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NY-LU-12    KEESPPPPKVVHPLIGLLGEYGGDSDYEEEEEEEQTPPPQPRTAQPQKREEQTKKENEEDKLTDWNKLACLLCRRQFPNKEVL 970
LUCA15      PELVRNGDEEHPLKRGLVAAYSGDSDNEE....................ELVERLESEEEKLADWKKMACLLCRRQFPNKDAL 662
DXS8237E    DLPKIASDDRPSPPRGLVAAYSGESDSEE....................EQERGGPEREEKLTDWQKLACLLCRRQFPSKEAL 233

NY-LU-12    IKHQQLSDLPKQHLEIHRKTKQSEQELAYLERRERE.GKFKGRGNDRREKLQSFDSPERKRIKYSRETDS..DRKLVDKEDID 1050
LUCA15      VRHQQLSDLHKQHMDIYRRSRLSEQELEALELREREMKYRDRAAERREKYGIPEPPEPKRKKQFDAGTV..NYEQPTKDGID 742
DXS8237E....IPHQQLSGLHKQHLKIHRRAHLSENELEALEKNIMEQNKYRDRAAERREKYGIPEPPEPKRRKYGGISTASVDFEQPTKDGLC 316

NY-LU-12    TSSKGCCVQQATGHRKGTGLGYQNPGLASSEEAEGRMHGPSVGASGRTSKRQSNETYRDAVRRVMFARYKELD 1123
LUCA15      HSHIGHKHLQAHGWREGSGLGRHQQGITAPIEAQVRLKGAGLGAKGSAYGLSGADSYKDAVRKAMFARFTEME 815
DXS8237E    SIRIGSRHIQAMGWKEGSGLGRKKQGIVTPIEAQTRVRGSGLGARGSSYGVTSTESYKETLHKTMVTRFNEAQ 389
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(57) Abstract

Various molecules associated with cancer are disclosed. The invention also discloses diagnostic and therapeutic methods based upon these molecules.

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CANCER ASSOCIATED NUCLEIC ACIDS AND POLYPEPTIDES

Field of the Invention

The invention relates to nucleic acids and encoded polypeptides which are cancer associated antigens expressed in patients afflicted with breast cancer. The invention also relates to agents which bind the nucleic acids or polypeptides. The nucleic acid molecules, polypeptides coded for by such molecules and peptides derived therefrom, as well as related antibodies and cytolytic T lymphocytes, are useful, *inter alia*, in diagnostic and therapeutic contexts.

Background of the Invention

The mechanism by which T cells recognize foreign materials has been implicated in cancer. A number of cytolytic T lymphocyte (CTL) clones directed against autologous melanoma antigens, testicular antigens, and melanocyte differentiation antigens have been described. In many instances, the antigens recognized by these clones have been characterized.

The use of autologous CTLs for identifying tumor antigens requires that the target cells which express the antigens can be cultured *in vitro* and that stable lines of autologous CTL clones which recognize the antigen-expressing cells can be isolated and propagated. While this approach has worked well for melanoma antigens, other tumor types, such as epithelial cancers including breast and colon cancer, have proved refractory to the approach.

More recently another approach to the problem has been described by Sahin et al. (*Proc. Natl. Acad. Sci. USA* 92:11810-11813, 1995). According to this approach, autologous antisera are used to identify immunogenic protein antigens expressed in cancer cells by screening expression libraries constructed from tumor cell cDNA. Antigen-encoding clones so identified have been found to have elicited an high-titer humoral immune response in the patients from which the antisera were obtained. Such a high-titer IgG response implies helper T cell recognition of the detected antigen. These tumor antigens can then be screened for the presence of MHC/HLA class I and class II motifs and reactivity with CTLs

The invention is elaborated upon in the disclosure which follows.

Summary of the Invention

Autologous antibody screening has now been applied to cancer using antisera from cancer patients. Numerous cancer associated antigens have been identified. The invention provides, *inter alia*, isolated nucleic acid molecules, expression vectors containing those molecules and host cells transfected with those molecules. The invention also provides isolated proteins and peptides, antibodies to those proteins and peptides and CTLs which recognize the proteins and peptides. Fragments including functional fragments and variants of the foregoing also are provided. Kits containing the foregoing molecules additionally are provided. The foregoing can be used in the diagnosis, monitoring, research, or treatment of conditions characterized by the expression of one or more cancer associated antigens.

Prior to the present invention, only a handful of cancer associated genes had been identified in the past 20 years. The invention involves the surprising discovery of many genes, some previously known and many previously unknown, which are expressed in individuals who have cancer. These individuals all have serum antibodies against the proteins (or fragments thereof) encoded by these genes. Thus, abnormally expressed genes are recognized by the host's immune system and therefore can form a basis for diagnosis, monitoring and therapy.

The invention involves the use of a single material, a plurality of different materials and even large panels and combinations of materials. For example, a single gene, a single protein encoded by a gene, a single functional fragment thereof, a single antibody thereto, etc. can be used in methods and products of the invention. Likewise, pairs, groups and even panels of these materials can be used for diagnosis, monitoring and therapy. The pairs, groups or panels can involve 2, 3, 4, 5... to as many as 25, 50, 100 or more genes, gene products, fragments thereof or agents that recognize such materials. A plurality of such materials are not only useful in monitoring, typing, characterizing and diagnosing cells abnormally expressing such genes, but a plurality of such materials can be used therapeutically. An example of the use of a plurality of such materials for the prevention, delay of onset, amelioration, etc. of cancer cells, which express or will express such genes prophylactically or acutely. Any and all combinations of the genes, gene products, and materials which recognize the genes and gene products can be tested and identified for use according to the invention. It would be far too lengthy to recite all such combinations; those skilled in the art, particularly in view of the teaching contained herein, will readily be able to determine which combinations are most appropriate for which circumstances.

As will be clear from the following discussion, the invention has *in vivo* and *in vitro* uses,

including for therapeutic, diagnostic, monitoring and research purposes. One aspect of the invention is the ability to fingerprint a cell expressing a number of the genes identified according to the invention. Such fingerprints will be characteristic, for example, of the stage of the cancer, the type of the cancer, or even the effect in animal models of a therapy on a cancer. Cells also can be screened to determine whether such cells abnormally express the genes identified according to the invention.

The invention, in one aspect, is a method of diagnosing a disorder characterized by expression of a cancer associated antigen precursor coded for by a nucleic acid molecule. The method involves the steps of contacting a biological sample isolated from a subject with an agent that specifically binds to the nucleic acid molecule, an expression product thereof, or a fragment of an expression product thereof complexed with an MHC, preferably an HLA, molecule, wherein the nucleic acid molecule is a NA Group 1 nucleic acid molecule, and determining the interaction between the agent and the nucleic acid molecule, the expression product or fragment of the expression product as a determination of the disorder.

In one embodiment the agent is selected from the group consisting of (a) a nucleic acid molecule comprising NA Group 1 nucleic acid molecules or a fragment thereof, (b) a nucleic acid molecule comprising NA Group 3 nucleic acid molecules or a fragment thereof, (c) a nucleic acid molecule comprising NA Group 17 nucleic acid molecules or a fragment thereof, (d) an antibody that binds to an expression product, or a fragment thereof, of NA group 1 nucleic acids, (e) an antibody that binds to an expression product, or a fragment thereof, of NA group 3 nucleic acids, (f) an antibody that binds to an expression product, or a fragment thereof, of NA group 17 nucleic acids, (g) and agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA Group 1 nucleic acid, (h) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA group 3 nucleic acid, and (I) an agent that binds to a complex of an MHC, preferably HLA, molecule and a fragment of an expression product of a NA Group 17 nucleic acid.

The disorder may be characterized by expression of a plurality of cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which is specific for a different human cancer associated antigen precursor, and wherein said plurality of agents is at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9 or at least 10 such agents.

In each of the above embodiments the agent may be specific for a human cancer associated antigen precursor that is a breast, a gastric, a lung, a prostate, a renal or a colon cancer associated antigen precursor.

In another aspect the invention is a method for determining regression, progression or onset of a condition characterized by expression of abnormal levels of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule. The method involves the steps of monitoring a sample, from a subject who has or is suspected of having the condition, for a parameter selected from the group consisting of (i) the protein, (ii) a peptide derived from the protein, (iii) an antibody which selectively binds the protein or peptide, and (iv) cytolytic T cells specific for a complex of the peptide derived from the protein and an MHC molecule, as a determination of regression, progression or onset of said condition. In one embodiment the sample is a body fluid, a body effusion or a tissue.

In another embodiment the step of monitoring comprises contacting the sample with a detectable agent selected from the group consisting of (a) an antibody which selectively binds the protein of (i), or the peptide of (ii), (b) a protein or peptide which binds the antibody of (iii), and (c) a cell which presents the complex of the peptide and MHC molecule of (iv). In a preferred embodiment the antibody, the protein, the peptide or the cell is labeled with a radioactive label or an enzyme. The sample in a preferred embodiment is assayed for the peptide.

According to another embodiment the nucleic acid molecule is one of the following: a NA Group 3 molecule, a NA Group 11 molecule, a NA Group 12 molecule, a NA Group 13 molecule, a NA Group 14 molecule, a NA Group 15 molecule, or a NA Group 16 molecule. In yet another embodiment the protein is a plurality of proteins, the parameter is a plurality of parameters, each of the plurality of parameters being specific for a different of the plurality of proteins.

The invention in another aspect is a pharmaceutical preparation for a human subject. The pharmaceutical preparation includes an agent which when administered to the subject enriches selectively the presence of complexes of an HLA molecule and a human cancer associated antigen, and a pharmaceutically acceptable carrier, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule which comprises a NA Group 1 molecule. In one embodiment the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

The agent in one embodiment comprises a plurality of agents, each of which enriches selectively in the subject complexes of an HLA molecule and a different human cancer associated antigen. Preferably the plurality is at least two, at least three, at least four or at least 5 different such agents.

In another embodiment the agent is selected from the group consisting of (1) an isolated polypeptide comprising the human cancer associated antigen, or a functional variant thereof, (2) an isolated nucleic acid operably linked to a promoter for expressing the isolated polypeptide, or functional variant thereof, (3) a host cell expressing the isolated polypeptide, or functional variant thereof, and (4) isolated complexes of the polypeptide, or functional variant thereof, and an HLA molecule.

The agent may be a cell expressing an isolated polypeptide. In one embodiment the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell is nonproliferative. In another embodiment the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell expresses an HLA molecule that binds the polypeptide. The cell can express one or both of the polypeptide and HLA molecule recombinantly. In another preferred embodiment the cell is nonproliferative. In yet another embodiment the agent is at least two, at least three, at least four or at least five different polypeptides, each representing a different human cancer associated antigen or functional variant thereof.

The agent in one embodiment is a PP Group 2 polypeptide. In other embodiments the agent is a PP Group 3 polypeptide or a PP Group 4 polypeptide.

In an embodiment each of the pharmaceutical preparations described herein also includes an adjuvant.

According to another aspect the invention, a composition is provided of an isolated agent that binds selectively a PP Group 1 polypeptide. In separate embodiments the agent binds selectively to a polypeptide selected from the following: a PP Group 3 polypeptide, a PP Group 11 polypeptide, a PP Group 12 polypeptide, a PP Group 13 polypeptide, a PP Group 14 polypeptide, a PP Group 15 polypeptide, and a PP Group 16 polypeptide. In other embodiments, the agent is a plurality of different agents that bind selectively at least two, at least three, at least four, or at least five different such polypeptides. In each of the above described embodiments the agent may be an antibody.

In another aspect the invention is a composition of matter .composed of a conjugate of the agent of the above-described compositions of the invention and a therapeutic or diagnostic agent. Preferably the conjugate is of the agent and a therapeutic or diagnostic that is an antineoplastic.

The invention in another aspect is a pharmaceutical composition of an isolated nucleic acid molecule selected from the group consisting of: (1) NA Group 1 molecules, and (2) NA Group 2 molecules, and a pharmaceutically acceptable carrier. In one embodiment the isolated nucleic acid molecule comprises a NA Group 3 or NA Group 4 molecule. In another embodiment the isolated nucleic acid molecule comprises at least two isolated nucleic acid molecules coding for two different polypeptides, each polypeptide comprising a different cancer associated antigen.

Preferably the pharmaceutical composition also includes an expression vector with a promoter operably linked to the isolated nucleic acid molecule. In another embodiment the pharmaceutical composition also includes a host cell recombinantly expressing the isolated nucleic acid molecule.

According to another aspect of the invention a pharmaceutical composition is provided. The pharmaceutical composition includes an isolated polypeptide comprising a PP Group 1 or a PP Group 2 polypeptide, and a pharmaceutically acceptable carrier. In one embodiment the isolated polypeptide comprises a PP Group 3 or a PP Group 4 polypeptide.

In another embodiment the isolated polypeptide comprises at least two different polypeptides, each comprising a different cancer associated antigen. In separate embodiments the isolated polypeptides are selected from the following: PP Group 11 polypeptides or HLA binding fragments thereof, PP Group 12 polypeptides or HLA binding fragments thereof, PP Group 13 polypeptides or HLA binding fragments thereof, PP Group 14 polypeptides or HLA binding fragments thereof, PP Group 15 polypeptides or HLA binding fragments thereof, or PP Group 16 polypeptides or HLA binding fragments thereof.

In an embodiment each of the pharmaceutical compositions described herein also includes an adjuvant.

Another aspect the invention is an isolated nucleic acid molecule comprising a NA Group 3 molecule. Another aspect the invention is an isolated nucleic acid molecule comprising a NA Group 4 molecule. In separate embodiments the isolated nucleic acid molecules are selected from the following: a Group 11 molecule or a functional fragment

thereof, a Group 12 molecule or a functional fragment thereof, a Group 13 molecule or a functional fragment thereof, a Group 14 molecule or a functional fragment thereof, a Group 15 molecule or a functional fragment thereof, or a Group 16 molecule or a functional fragment thereof.

The invention in another aspect is an isolated nucleic acid molecule selected from the group consisting of (a) a fragment of a nucleic acid selected from the group of nucleic acid molecules consisting of SEQ ID numbered below and comprising all nucleic acid sequences among SEQ ID NOs 1-816, of sufficient length to represent a sequence unique within the human genome, and identifying a nucleic acid encoding a human cancer associated antigen precursor, (b) complements of (a), provided that the fragment includes a sequence of contiguous nucleotides which is not identical to any sequence selected from the sequence group consisting of (1) sequences having the GenBank accession numbers of the sequence Group 1, (2) complements of (1), and (3) fragments of (1) and (2).

In one embodiment the sequence of contiguous nucleotides is selected from the group consisting of: (1) at least two contiguous nucleotides nonidentical to the sequence Group 1, (2) at least three contiguous nucleotides nonidentical to the sequence Group 1, (3) at least four contiguous nucleotides nonidentical to the sequence Group 1, (4) at least five contiguous nucleotides nonidentical to the sequence Group 1, (5) at least six contiguous nucleotides nonidentical to the sequence Group 1, or (6) at least seven contiguous nucleotides nonidentical to the sequence Group 1.

In another embodiment the fragment has a size selected from the group consisting of at least: 8 nucleotides, 10 nucleotides, 12 nucleotides, 14 nucleotides, 16 nucleotides, 18 nucleotides, 20, nucleotides, 22 nucleotides, 24 nucleotides, 26 nucleotides, 28 nucleotides, 30 nucleotides, 50 nucleotides, 75 nucleotides, 100 nucleotides, 200 nucleotides, 1000 nucleotides and every integer length therebetween.

In yet another embodiment the molecule encodes a polypeptide which, or a fragment of which, binds a human HLA receptor or a human antibody.

Another aspect of the invention is an expression vector comprising an isolated nucleic acid molecule of the invention described above operably linked to a promoter.

According to one aspect the invention is an expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 2 molecule. In another aspect the invention is an expression vector comprising a NA Group 1 or Group 2 molecule

and a nucleic acid encoding an MHC, preferably HLA, molecule.

In yet another aspect the invention is a host cell transformed or transfected with an expression vector of the invention described above.

In another aspect the invention is a host cell transformed or transfected with an expression vector comprising an isolated nucleic acid molecule of the invention described above operably linked to a promoter, or an expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 1 or 2 molecule and further comprising a nucleic acid encoding HLA.

According to another aspect of the invention an isolated polypeptide encoded by the isolated nucleic acid molecules the invention, described above, is provided. These include PP Group 1-17 polypeptides. The invention also includes a fragment of the polypeptide which is immunogenic. In one embodiment the fragment, or a portion of the fragment, binds HLA or a human antibody.

The invention includes in another aspect an isolated fragment of a human cancer associated antigen precursor which, or portion of which, binds HLA or a human antibody, wherein the precursor is encoded by a nucleic acid molecule that is a NA Group 1 molecule. In one embodiment the fragment is part of a complex with HLA. In another embodiment the fragment is between 8 and 12 amino acids in length. In another embodiment the invention includes an isolated polypeptide comprising a fragment of the polypeptide of sufficient length to represent a sequence unique within the human genome and identifying a polypeptide that is a human cancer associated antigen precursor.

According to another aspect of the invention a kit for detecting the presence of the expression of a cancer associated antigen precursor is provided. The kit includes a pair of isolated nucleic acid molecules each of which consists essentially of a molecule selected from the group consisting of (a) a 12-32 nucleotide contiguous segment of the nucleotide sequence of any of the NA Group 1 molecules and (b) complements of ("a"), wherein the contiguous segments are nonoverlapping. In one embodiment the pair of isolated nucleic acid molecules is constructed and arranged to selectively amplify an isolated nucleic acid molecule that is a NA Group 3 molecule. Preferably, the pair amplifies a human NA Group 3 molecule.

According to another aspect of the invention a method for treating a subject with a disorder characterized by expression of a human cancer associated antigen precursor is provided. The method includes the step of administering to the subject an amount of an agent,

which enriches selectively in the subject the presence of complexes of an HLA molecule and a human cancer associated antigen, effective to ameliorate the disorder, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule selected from the group consisting of (a) a nucleic acid molecule comprising NA group 1 nucleic acid molecules, (b) a nucleic acid molecule comprising NA group 3 nucleic acid molecules, (c) a nucleic acid molecule comprising NA group 17 nucleic acid molecules.

In one embodiment the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which enriches selectively in the subject the presence of complexes of an HLA molecule and a different human cancer associated antigen. Preferably the plurality is at least 2, at least 3, at least 4, or at least 5 such agents.

In another embodiment the agent is an isolated polypeptide selected from the group consisting of PP Group 1, PP Group 2, PP Group 3, PP Group 4, PP Group 5, PP Group 6, PP Group 7, PP Group 8, PP Group 9, PP Group 10, PP Group 11, PP Group 12, PP Group 13, PP Group 14, PP Group 15, PP Group 16 and PP Group 17 polypeptides.

In yet another embodiment the disorder is cancer.

According to another aspect the invention is a method for treating a subject having a condition characterized by expression of a cancer associated antigen precursor in cells of the subject. The method includes the steps of (I) removing an immunoreactive cell containing sample from the subject, (ii) contacting the immunoreactive cell containing sample to the host cell under conditions favoring production of cytolytic T cells against a human cancer associated antigen which is a fragment of the precursor, (iii) introducing the cytolytic T cells to the subject in an amount effective to lyse cells which express the human cancer associated antigen, wherein the host cell is transformed or transfected with an expression vector comprising an isolated nucleic acid molecule operably linked to a promoter, the isolated nucleic acid molecule being selected from the group of nucleic acid molecules consisting of NA Group 1, NA Group 2, NA Group 3, NA Group 4, NA Group 5, NA Group 6, NA Group 7, NA Group 8, NA Group 9, NA Group 10, NA Group 11, NA Group 12, NA Group 13, NA Group 14, NA Group 15, NA Group 16, and NA Group 17.

In one embodiment the host cell recombinantly expresses an HLA molecule which binds the human cancer associated antigen. In another embodiment the host cell endogenously

expresses an HLA molecule which binds the human cancer associated antigen.

The invention includes in another aspect a method for treating a subject having a condition characterized by expression of a cancer associated antigen precursor in cells of the subject. The method includes the steps of (I) identifying a nucleic acid molecule expressed by the cells associated with said condition, wherein said nucleic acid molecule is a NA Group 1 molecule (ii) transfecting a host cell with a nucleic acid selected from the group consisting of (a) the nucleic acid molecule identified, (b) a fragment of the nucleic acid identified which includes a segment coding for a cancer associated antigen, (c) deletions, substitutions or additions to (a) or (b), and (d) degenerates of (a), (b), or (c); (iii) culturing said transfected host cells to express the transfected nucleic acid molecule, and; (iv) introducing an amount of said host cells or an extract thereof to the subject effective to increase an immune response against the cells of the subject associated with the condition. Preferably, the antigen is a human antigen and the subject is a human.

In one embodiment the method also includes the step of (a) identifying an MHC molecule which presents a portion of an expression product of the nucleic acid molecule, wherein the host cell expresses the same MHC molecule as identified in (a) and wherein the host cell presents an MHC binding portion of the expression product of the nucleic acid molecule.

In another embodiment the method also includes the step of treating the host cells to render them non-proliferative.

In yet another embodiment the immune response comprises a B-cell response or a T cell response. Preferably the response is a T-cell response which comprises generation of cytolytic T-cells specific for the host cells presenting the portion of the expression product of the nucleic acid molecule or cells of the subject expressing the human cancer associated antigen.

In another embodiment the nucleic acid molecule is a NA Group 3 molecule.

Another aspect of the invention is a method for treating or diagnosing or monitoring a subject having a condition characterized by expression of an abnormal amount of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule. The method includes the step of administering to the subject an antibody which specifically binds to the protein or a peptide derived therefrom, the antibody being coupled to a therapeutically useful agent, in an amount effective to treat the condition.

In one embodiment the antibody is a monoclonal antibody. Preferably the monoclonal antibody is a chimeric antibody or a humanized antibody.

In another aspect the invention is a method for treating a condition characterized by expression in a subject of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule.. The method involves the step of administering to a subject at least one of the pharmaceutical compositions of the invention described above in an amount effective to prevent, delay the onset of, or inhibit the condition in the subject. In one embodiment the condition is cancer. In another embodiment the method includes the step of first identifying that the subject expresses in a tissue abnormal amounts of the protein. The invention in another aspect is a method for treating a subject having a condition characterized by expression of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method includes the steps of (I) identifying cells from the subject which express abnormal amounts of the protein; (ii) isolating a sample of the cells;. (iii) cultivating the cells, and (iv) introducing the cells to the subject in an amount effective to provoke an immune response against the cells.

In one embodiment the cells express a protein selected from the group consisting of a PP Group 11 protein, a PP Group 12 protein, a PP Group 13 protein, PP Group 14 protein, a PP Group 15 protein and a PP Group 16 protein.. In another embodiment the method includes the step of rendering the cells non-proliferative, prior to introducing them to the subject.

In another aspect the invention is a method for treating a pathological cell condition characterized by abnormal expression of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule. The method includes the step of administering to a subject in need thereof an effective amount of an agent which inhibits the expression or activity of the protein.

In one embodiment the agent is an inhibiting antibody which selectively binds to the protein and wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody. In another embodiment the agent is an antisense nucleic acid molecule which selectively binds to the nucleic acid molecule which encodes the protein. In yet another important embodiment the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

The invention includes in another aspect a composition of matter useful in stimulating an immune response to a plurality of a protein encoded by nucleic acid molecules that are NA Group 1 molecules. The composition is a plurality of peptides derived from the amino acid

sequences of the proteins, wherein the peptides bind to one or more MHC molecules presented on the surface of the cells which express an abnormal amount of the protein.

In one embodiment at least a portion of the plurality of peptides bind to MHC molecules and elicit a cytolytic response thereto. In another embodiment the composition of matter includes an adjuvant. In another embodiment the adjuvant is a saponin, GM-CSF, or an interleukin.

According to another aspect the invention is an isolated antibody which selectively binds to a complex of: (I) a peptide derived from a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule and (ii) and an MHC molecule to which binds the peptide to form the complex, wherein the isolated antibody does not bind to (I) or (ii) alone.

In one embodiment the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

The invention also involves the use of the genes, gene products, fragments thereof, agents which bind thereto, and so on in the preparation of medicaments. A particular medicament is for treating cancer and a more particular medicament is for treating breast cancer, lung cancer, renal cancer, colon cancer, prostate cancer or gastric cancer.

Detailed Description of the Invention

In the above summary and in the ensuing description, lists of sequences are provided. The lists are meant to embrace each single sequence separately, two or more sequences together where they form a part of the same gene, any combination of two or more sequences which relate to different genes, including and up to the total number on the list, as if each and every combination were separately and specifically enumerated. Likewise, when mentioning fragment size, it is intended that a range embrace the smallest fragment mentioned to the full-length of the sequence (-1 so that it is a fragment), each and every fragment length intended as if specifically enumerated. Thus, if a fragment could be between 10 and 15 in length, it is explicitly meant to mean 10, 11, 12, 13, 14, or 15 in length.

The summary and the claims mention antigen precursors and antigens. As used in the summary and in the claims, a precursor is substantially the full-length protein encoded by the coding region of the isolated DNA and the antigen is a peptide which complexes with MHC, preferably HLA, and which participates in the immune response as part of that complex. Such antigens are typically 9 amino acids long, although this may vary slightly.

As used herein, a subject is a human, non-human primate, cow, horse, pig, sheep, goat, dog, cat or rodent. In all embodiments human cancer antigens and human subjects are preferred.

The present invention in one aspect involves the cloning of cDNAs encoding human cancer associated antigen precursors using autologous antisera of subjects having cancer. The sequences of the clones representing genes identified according to the methods described herein are presented in the attached Sequence Listing, and the predicted amino acid sequences of some clones also are presented. Of the foregoing, it can be seen that some of the clones are considered completely novel as no nucleotide or amino acid homologies to coding regions were found in the databases searched. Other clones are novel but have some homology to sequences deposited in databases (mainly EST sequences). Nevertheless, the entire gene sequence was not previously known. In some cases no function was suspected and in other cases, even if a function was suspected, it was not know that the gene was associated with cancer. In all cases, it was not known or suspected that the gene encoded a cancer antigen which reacted with antibody from autologous sera. Analysis of the clone sequences by comparison to nucleic acid and protein databases determined that still other of the clones surprisingly are closely related to other previously-cloned genes. The sequences of these related genes is also presented in the Sequence Listing. The nature of the foregoing genes as encoding antigens recognized by the immune systems of cancer patients is, of course, unexpected.

The invention thus involves in one aspect cancer associated antigen polypeptides, genes encoding those polypeptides, functional modifications and variants of the foregoing, useful fragments of the foregoing, as well as diagnostics and therapeutics relating thereto.

Homologs and alleles of the cancer associated antigen nucleic acids of the invention can be identified by conventional techniques. Thus, an aspect of the invention is those nucleic acid sequences which code for cancer associated antigen precursors. Because this application contains so many sequences, the following chart is provided to identify the various groups of sequences discussed in the claims and in the summary:

"Nucleic Acid Sequences"

NA Group 1. (a) nucleic acid molecules which hybridize under stringent conditions to a molecule consisting of a nucleic acid sequence selected from the group consisting of nucleic acid sequences among SEQ ID NOs 1-816 and which code for a cancer associated antigen precursor,

(b) deletions, additions and substitutions which code for a respective cancer associated antigen precursor,

(c) nucleic acid molecules that differ from the nucleic acid molecules of (a) or (b) in codon sequence due to the degeneracy of the genetic code, and

(d) complements of (a), (b) or (c).

NA Group 2. Fragments of NA Group 1, which codes for a polypeptide which, or a portion of which, binds an MHC molecule to form a complex recognized by a an autologous antibody or lymphocyte.

NA Group 3. The subset of NA Group 1 where the nucleotide sequence is selected from the group consisting of:

(a) previously unknown human nucleic acids coding for a human cancer associated antigen precursor,

(b) deletions, additions and substitutions which code for a respective human cancer associated antigen precursor,

(c) nucleic acid molecules that differ from the nucleic acid molecules of (a) or (b) in codon sequence due to the degeneracy of the genetic code, and

(d) complements of (a), (b) or (c).

NA Group 4. Fragments of NA Group 3, which code for a polypeptide which, or a portion of which, binds to an MHC molecule to form a complex recognized by an autologous antibody or lymphocyte.

NA Group 5. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human breast cancer associated antigen precursor.

NA Group 6. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human colon cancer associated antigen precursor.

NA Group 7. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human gastric cancer associated antigen precursor.

NA Group 8. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human lung cancer associated antigen precursor.

NA Group 9. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human renal cancer associated antigen precursor.

NA Group 10. A subset of NA Group 1, wherein the nucleic acid molecule codes for a human prostate cancer associated antigen precursor.

NA Group 11. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human breast cancer associated antigen precursor.

NA Group 12. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human colon cancer associated antigen precursor.

NA Group 13. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human gastric cancer associated antigen precursor.

NA Group 14. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human lung cancer associated antigen precursor.

NA Group 15. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human renal cancer associated antigen precursor.

NA Group 16. A subset of NA Group 3, wherein the nucleic acid molecule codes for a human prostate cancer associated antigen precursor.

NA Group 17. A subset of NA Group 1, comprising human cancer associated antigens that react with allogenic cancer antisera.

Polypeptide Sequences

PP Group 1. Polypeptides encoded by NA Group 1.

PP Group 2. Polypeptides encoded by NA Group 2

PP Group 3. Polypeptides encoded by NA Group 3.

PP Group 4. Polypeptides encoded by NA Group 4.

PP Group 5. Polypeptides encoded by NA Group 5.

PP Group 6. Polypeptides encoded by NA Group 6.

PP Group 7. Polypeptides encoded by NA Group 7.

PP Group 8. Polypeptides encoded by NA Group 8.

PP Group 9. Polypeptides encoded by NA Group 9.

PP Group 10. Polypeptides encoded by NA Group 10.

PP Group 11. Polypeptides encoded by NA Group 11.

PP Group 12. Polypeptides encoded by NA Group 12.

PP Group 13. Polypeptides encoded by NA Group 13.

PP Group 14. Polypeptides encoded by NA Group 14.

PP Group 15. Polypeptides encoded by NA Group 15.

PP Group 16. Polypeptides encoded by NA Group 16.

PP Group 17. Polypeptides encoded by NA Group 17.

The term "stringent conditions" as used herein refers to parameters with which the art is familiar. Nucleic acid hybridization parameters may be found in references which compile such methods, e.g. *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989, or *Current Protocols in Molecular Biology*, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. More specifically, stringent conditions, as used herein, refers, for example, to hybridization at 65°C in hybridization buffer (3.5 x SSC, 0.02% Ficoll, 0.02% polyvinyl pyrrolidone, 0.02% Bovine Serum Albumin, 2.5mM NaH_2PO_4(pH7), 0.5% SDS, 2mM EDTA). SSC is 0.15M sodium chloride/0.15M sodium citrate, pH7; SDS is sodium dodecyl sulphate; and EDTA is ethylenediaminetetracetic acid. After hybridization, the membrane upon which the DNA is transferred is washed, for example, in 2 x SSC at room temperature and then at 0.1 - 0.5 x SSC/0.1 x SDS at temperatures up to 68°C.

There are other conditions, reagents, and so forth which can be used, which result in a similar degree of stringency. The skilled artisan will be familiar with such conditions, and thus they are not given here. It will be understood, however, that the skilled artisan will be able to

manipulate the conditions in a manner to permit the clear identification of homologs and alleles of cancer associated antigen nucleic acids of the invention (e.g., by using lower stringency conditions). The skilled artisan also is familiar with the methodology for screening cells and libraries for expression of such molecules which then are routinely isolated, followed by isolation of the pertinent nucleic acid molecule and sequencing.

In general homologs and alleles typically will share at least 40% nucleotide identity and/or at least 50% amino acid identity to the sequences of breast cancer associated antigen nucleic acid and polypeptides, respectively, in some instances will share at least 50% nucleotide identity and/or at least 65% amino acid identity and in still other instances will share at least 60% nucleotide identity and/or at least 75% amino acid identity. The homology can be calculated using various, publicly available software tools developed by NCBI (Bethesda, Maryland) that can be obtained through the internet (ftp:/ncbi.nlm.nih.gov/pub/). Exemplary tools include the BLAST system available at http://wwww.ncbi.nlm.nih.gov. Pairwise and ClustalW alignments (BLOSUM30 matrix setting) as well as Kyte-Doolittle hydropathic analysis can be obtained using the MacVetor sequence analysis software (Oxford Molecular Group). Watson-Crick complements of the foregoing nucleic acids also are embraced by the invention.

In screening for cancer associated antigen genes, a Southern blot may be performed using the foregoing conditions, together with a radioactive probe. After washing the membrane to which the DNA is finally transferred, the membrane can be placed against X-ray film to detect the radioactive signal. In screening for the expression of cancer associated antigen nucleic acids, Northern blot hybridizations using the foregoing conditions (see also the Examples) can be performed on samples taken from breast cancer patients or subjects suspected of having a condition characterized by expression of breast cancer associated antigen genes. Amplification protocols such as polymerase chain reaction using primers which hybridize to the sequences presented also can be used for detection of the cancer associated antigen genes or expression thereof.

The breast cancer associated genes correspond to SEQ ID NOs. 1-40 and 66. The preferred breast cancer associated antigens for the methods of diagnosis disclosed herein are those set forth in SEQ ID NOs:[31, 33 and 34], which were found to react with allogeneic breast cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The colon cancer associated genes correspond to SEQ ID Nos. 544-586, even numbers

only. The preferred colon cancer associated antigens for the methods of diagnosis disclosed herein are those, which were found to react with allogeneic colon cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The gastric cancer associated genes correspond to SEQ ID NOs 176-436 and 588-674. The preferred gastric cancer associated antigens for the methods of diagnosis disclosed herein are those, which were found to react with allogeneic gastric cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The renal cancer associated genes correspond to SEQ ID Nos. 89-169, odd numbers only, and 170, 172, and 174. The preferred renal cancer associated antigens for the methods of diagnosis disclosed herein are those, which were found to react with allogeneic renal cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The lung cancer associated genes correspond to SEQ ID Nos. 689, 691, 692, 694, 696-707, 709, 711, and 712. The preferred lung cancer associated antigens for the methods of diagnosis disclosed herein are those, which were found to react with allogeneic lung cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The prostate cancer associated genes correspond to SEQ ID NOs 437-543. The preferred prostate cancer associated antigens for the methods of diagnosis disclosed herein are those, which were found to react with allogeneic prostate cancer antisera. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis.

The invention also includes degenerate nucleic acids which include alternative codons to those present in the native materials. For example, serine residues are encoded by the codons TCA, AGT, TCC, TCG, TCT and AGC. Each of the six codons is equivalent for the purposes of encoding a serine residue. Thus, it will be apparent to one of ordinary skill in the art that any of the serine-encoding nucleotide triplets may be employed to direct the protein synthesis apparatus, *in vitro* or *in vivo*, to incorporate a serine residue into an elongating breast cancer associated antigen polypeptide. Similarly, nucleotide sequence triplets which encode other amino acid residues include, but are not limited to: CCA, CCC, CCG and CCT (proline codons); CGA, CGC, CGG, CGT, AGA and AGG (arginine codons); ACA, ACC, ACG and ACT (threonine codons); AAC and AAT (asparagine codons); and ATA, ATC and ATT (isoleucine codons). Other amino acid residues may be encoded similarly by multiple nucleotide sequences. Thus,

the invention embraces degenerate nucleic acids that differ from the biologically isolated nucleic acids in codon sequence due to the degeneracy of the genetic code.

The invention also provides isolated unique fragments of cancer associated antigen nucleic acid sequences or complements thereof. A unique fragment is one that is a 'signature' for the larger nucleic acid. It, for example, is long enough to assure that its precise sequence is not found in molecules within the human genome outside of the cancer associated antigen nucleic acids defined above (and human alleles). Those of ordinary skill in the art may apply no more than routine procedures to determine if a fragment is unique within the human genome. Unique fragments, however, exclude fragments completely composed of the nucleotide sequences of any of GenBank accession numbers listed in Table 1 or other previously published sequences as of the filing date of the priority documents for sequences listed in a respective priority document or the filing date of this application for sequences listed for the first time in this application which overlap the sequences of the invention.

A fragment which is completely composed of the sequence described in the foregoing GenBank deposits is one which does not include any of the nucleotides unique to the sequences of the invention. Thus, a unique fragment must contain a nucleotide sequence other than the exact sequence of those in GenBank or fragments thereof. The difference may be an addition, deletion or substitution with respect to the GenBank sequence or it may be a sequence wholly separate from the GenBank sequence.

Unique fragments can be used as probes in Southern and Northern blot assays to identify such nucleic acids, or can be used in amplification assays such as those employing PCR. As known to those skilled in the art, large probes such as 200, 250, 300 or more nucleotides are preferred for certain uses such as Southern and Northern blots, while smaller fragments will be preferred for uses such as PCR. Unique fragments also can be used to produce fusion proteins for generating antibodies or determining binding of the polypeptide fragments, or for generating immunoassay components. Likewise, unique fragments can be employed to produce nonfused fragments of the cancer associated antigen polypeptides, useful, for example, in the preparation of antibodies, and in immunoassays. Unique fragments further can be used as antisense molecules to inhibit the expression of cancer associated antigen nucleic acids and polypeptides, particularly for therapeutic purposes as described in greater detail below.

As will be recognized by those skilled in the art, the size of the unique fragment will depend upon its conservancy in the genetic code. Thus, some regions of cancer associated antigen sequences and complements thereof will require longer segments to be unique while others will require only short segments, typically between 12 and 32 nucleotides (e.g. 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31 and 32 or more bases long, up to the entire length of the disclosed sequence. As mentioned above, this disclosure intends to embrace each and every fragment of each sequence, beginning at the first nucleotide, the second nucleotide and so on, up to 8 nucleotides short of the end, and ending anywhere from nucleotide number 8, 9, 10 and so on for each sequence, up to the very last nucleotide, (provided the sequence is unique as described above).

Virtually any segment of the polypeptide coding region of novel cancer associated antigen nucleic acids, or complements thereof, that is 18 or more nucleotides in length will be unique. Those skilled in the art are well versed in methods for selecting such sequences, typically on the basis of the ability of the unique fragment to selectively distinguish the sequence of interest from other sequences in the human genome of the fragment to those on known databases typically is all that is necessary, although *in vitro* confirmatory hybridization and sequencing analysis may be performed. Especially preferred include nucleic acids encoding a series of epitopes, known as "polytopes". The epitopes can be arranged in sequential or overlapping fashion (*see, e.g.*, Thomson et al., *Proc. Natl. Acad. Sci. USA* 92:5845-5849, 1995; Gilbert et al., *Nature Biotechnol.* 15:1280-1284, 1997), with or without the natural flanking sequences, and can be separated by unrelated linker sequences if desired. The polytope is processed to generated individual epitopes which are recognized by the immune system for generation of immune responses.

Thus, for example, peptides derived from a polypeptide having an amino acid sequence encoded by one of the nucleic acid disclosed herein, and which are presented by MHC molecules and recognized by CTL or T helper lymphocytes, can be combined with peptides from one or more other cancer associated antigens (e.g. by preparation of hybrid nucleic acids or polypeptides) to form "polytopes". The two or more peptides (or nucleic acids encoding the peptides) can be selected from those described herein, or they can include one or more peptides of previously known cancer associated antigens. Exemplary cancer associated peptide antigens that can be administered to induce or enhance an immune response are derived from tumor associated genes and encoded proteins including MAGE-1, MAGE-2, MAGE-3, MAGE-4, MAGE-5, MAGE-6, MAGE-7,

MAGE-8, MAGE-9, MAGE-10, MAGE-11, GAGE-1, GAGE-2, GAGE-3, GAGE-4, GAGE-5, GAGE-6, BAGE-1, RAGE-1, LB33/MUM-1, PRAME, NAG, MAGE-Xp2, MAGE-Xp3, MAGE-Xp4, tyrosinase, brain glycogen phosphorylase, Melan-A, and MAGE-C1. See, for example, PCT application publication no. WO96/10577. Other examples will be known to one of ordinary skill in the art (for example, see Coulie, *Stem Cells* 13:393-403, 1995), and can be used in the invention in a like manner as those disclosed herein. One of ordinary skill in the art can prepare polypeptides comprising one or more peptides and one or more of the foregoing cancer associated peptides, or nucleic acids encoding such polypeptides, according to standard procedures of molecular biology.

Thus polytopes are groups of two or more potentially immunogenic or immune response stimulating peptides which can be joined together in various arrangements (e.g. concatenated, overlapping). The polytope (or nucleic acid encoding the polytope) can be administered in a standard immunization protocol, e.g. to animals, to test the effectiveness of the polytope in stimulating, enhancing and/or provoking an immune response.

The peptides can be joined together directly or via the use of flanking sequences to form polytopes, and the use of polytopes as vaccines is well known in the art (see, e.g., Thomson et al., *Proc. Acad. Natl. Acad. Sci USA* 92(13):5845-5849, 1995; Gilbert et al., *Nature Biotechnol.* 15(12):1280-1284, 1997; Thomson et al., *J. Immunol.* 157(2):822-826, 1996; Tam et al., *J. Exp. Med.* 171(1):299-306, 1990).for example, Tam showed that polytopes consisting of both MHC class I and class II binding epitopes successfully generated antibody and protective immunity in a mouse model. Tam also demonstrated that polytopes comprising "strings" of epitopes are processed to yield individual epitopes which are presented by MHC molecules and recognized by CTLs. Thus polytopes containing various numbers and combinations of epitopes can be prepared and tested for recognition by CTLs and for efficacy in increasing an immune response.

It is known that tumors express a set of tumor antigens, of which only certain subsets may be expressed in the tumor of any given patient (for examples of this, see the Examples below). Polytopes can be prepared which correspond to the different combination of epitopes representing the subset of tumor rejection antigens expressed in a particular patient. Polytopes also can be prepared to reflect a broader spectrum of tumor rejection antigens known to be expressed by a tumor type. Polytopes can be introduced to a patient in need of such treatment as polypeptide structures, or via the use of nucleic acid delivery systems known in the art (see, e.g., Allsopp et al., *Eur. J.*

Immunol. 26(8):1951-1959, 1996). Adenovirus, pox virus, Ty-virus like particles, adeno-associated virus, plasmids, bacteria, etc. can be used in such delivery. One can test the polytope delivery systems in mouse models to determine efficacy of the delivery system. The systems also can be tested in human clinical trials.

In instances in which a human HLA class I molecule presents tumor rejection antigens derived from cancer associated nucleic acids, the expression vector may also include a nucleic acid sequence coding for the HLA molecule that presents any particular tumor rejection antigen derived from these nucleic acids and polypeptides. Alternatively, the nucleic acid sequence coding for such a HLA molecule can be contained within a separate expression vector. In a situation where the vector contains both coding sequences, the single vector can be used to transfect a cell which does not normally express either one. Where the coding sequences for a cancer associated antigen precursor and the HLA molecule which presents it are contained on separate expression vectors, the expression vectors can be cotransfected. The cancer associated antigen precursor coding sequence may be used alone, when, e.g. the host cell already expresses a HLA molecule which presents a cancer associated antigen derived from precursor molecules. Of course, there is no limit on the particular host cell which can be used. As the vectors which contain the two coding sequences may be used in any antigen-presenting cells if desired, and the gene for cancer associated antigen precursor can be used in host cells which do not express a HLA molecule which presents a cancer associated antigen. Further, cell-free transcription systems may be used in lieu of cells.

As mentioned above, the invention embraces antisense oligonucleotides that selectively bind to a nucleic acid molecule encoding a cancer associated antigen polypeptide, to reduce the expression of cancer associated antigens. This is desirable in virtually any medical condition wherein a reduction of expression of cancer associated antigens is desirable, e.g., in the treatment of cancer. This is also useful for *in vitro* or *in vivo* testing of the effects of a reduction of expression of one or more cancer associated antigens.

As used herein, the term "antisense oligonucleotide" or "antisense" describes an oligonucleotide that is an oligoribonucleotide, oligodeoxyribonucleotide, modified oligoribonucleotide, or modified oligodeoxyribonucleotide which hybridizes under physiological conditions to DNA comprising a particular gene or to an mRNA transcript of that gene and, thereby, inhibits the transcription of that gene and/or the translation of that mRNA. The antisense molecules

are designed so as to interfere with transcription or translation of a target gene upon hybridization with the target gene or transcript. Those skilled in the art will recognize that the exact length of the antisense oligonucleotide and its degree of complementarity with its target will depend upon the specific target selected, including the sequence of the target and the particular bases which comprise that sequence. It is preferred that the antisense oligonucleotide be constructed and arranged so as to bind selectively with the target under physiological conditions, i.e., to hybridize substantially more to the target sequence than to any other sequence in the target cell under physiological conditions.

Based upon the sequences of nucleic acids encoding breast cancer associated antigen, or upon allelic or homologous genomic and/or cDNA sequences, one of skill in the art can easily choose and synthesize any of a number of appropriate antisense molecules for use in accordance with the present invention. In order to be sufficiently selective and potent for inhibition, such antisense oligonucleotides should comprise at least 10 and, more preferably, at least 15 consecutive bases which are complementary to the target, although in certain cases modified oligonucleotides as short as 7 bases in length have been used successfully as antisense oligonucleotides (Wagner et al., *Nature Biotechnol.* 14:840-844, 1996). Most preferably, the antisense oligonucleotides comprise a complementary sequence of 20-30 bases. Although oligonucleotides may be chosen which are antisense to any region of the gene or mRNA transcripts, in preferred embodiments the antisense oligonucleotides correspond to N-terminal or 5' upstream sites such as translation initiation, transcription initiation or promoter sites. In addition, 3'-untranslated regions may be targeted. Targeting to mRNA splicing sites has also been used in the art but may be less preferred if alternative mRNA splicing occurs. In addition, the antisense is targeted, preferably, to sites in which mRNA secondary structure is not expected (see, e.g., Sainio et al., *Cell Mol. Neurobiol.* 14(5):439-457, 1994) and at which proteins are not expected to bind. Finally, although the listed sequences are cDNA sequences, one of ordinary skill in the art may easily derive the genomic DNA corresponding to the cDNA of a cancer associated antigen. Thus, the present invention also provides for antisense oligonucleotides which are complementary to the genomic DNA corresponding to nucleic acids encoding breast cancer associated antigens. Similarly, antisense to allelic or homologous cDNAs and genomic DNAs are enabled without undue experimentation.

In one set of embodiments, the antisense oligonucleotides of the invention may be composed of "natural" deoxyribonucleotides, ribonucleotides, or any combination thereof. That is, the 5' end

of one native nucleotide and the 3' end of another native nucleotide may be covalently linked, as in natural systems, via a phosphodiester internucleoside linkage. These oligonucleotides may be prepared by art recognized methods which may be carried out manually or by an automated synthesizer. They also may be produced recombinantly by vectors.

In preferred embodiments, however, the antisense oligonucleotides of the invention also may include "modified" oligonucleotides. That is, the oligonucleotides may be modified in a number of ways which do not prevent them from hybridizing to their target but which enhance their stability or targeting or which otherwise enhance their therapeutic effectiveness.

The term "modified oligonucleotide" as used herein describes an oligonucleotide in which (1) at least two of its nucleotides are covalently linked via a synthetic internucleoside linkage (i.e., a linkage other than a phosphodiester linkage between the 5' end of one nucleotide and the 3' end of another nucleotide) and/or (2) a chemical group not normally associated with nucleic acids has been covalently attached to the oligonucleotide. Preferred synthetic internucleoside linkages are phosphorothioates, alkylphosphonates, phosphorodithioates, phosphate esters, alkylphosphonothioates, phosphoramidates, carbamates, carbonates, phosphate triesters, acetamidates, carboxymethyl esters and peptides.

The term "modified oligonucleotide" also encompasses oligonucleotides with a covalently modified base and/or sugar. For example, modified oligonucleotides include oligonucleotides having backbone sugars which are covalently attached to low molecular weight organic groups other than a hydroxyl group at the 3' position and other than a phosphate group at the 5' position. Thus modified oligonucleotides may include a 2'-O-alkylated ribose group. In addition, modified oligonucleotides may include sugars such as arabinose instead of ribose. The present invention, thus, contemplates pharmaceutical preparations containing modified antisense molecules that are complementary to and hybridizable with, under physiological conditions, nucleic acids encoding breast cancer associated antigen polypeptides, together with pharmaceutically acceptable carriers.

Antisense oligonucleotides may be administered as part of a pharmaceutical composition. Such a pharmaceutical composition may include the antisense oligonucleotides in combination with any standard physiologically and/or pharmaceutically acceptable carriers which are known in the art. The compositions should be sterile and contain a therapeutically effective amount of the antisense oligonucleotides in a unit of weight or volume suitable for administration to a patient. The term

"pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredients. The term "physiologically acceptable" refers to a non-toxic material that is compatible with a biological system such as a cell, cell culture, tissue, or organism. The characteristics of the carrier will depend on the route of administration. Physiologically and pharmaceutically acceptable carriers include diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials which are well known in the art, as further described below.

As used herein, a "vector" may be any of a number of nucleic acids into which a desired sequence may be inserted by restriction and ligation for transport between different genetic environments or for expression in a host cell. Vectors are typically composed of DNA although RNA vectors are also available. Vectors include, but are not limited to, plasmids, phagemids and virus genomes. A cloning vector is one which is able to replicate in a host cell, and which is further characterized by one or more endonuclease restriction sites at which the vector may be cut in a determinable fashion and into which a desired DNA sequence may be ligated such that the new recombinant vector retains its ability to replicate in the host cell. In the case of plasmids, replication of the desired sequence may occur many times as the plasmid increases in copy number within the host bacterium or just a single time per host before the host reproduces by mitosis. In the case of phage, replication may occur actively during a lytic phase or passively during a lysogenic phase. An expression vector is one into which a desired DNA sequence may be inserted by restriction and ligation such that it is operably joined to regulatory sequences and may be expressed as an RNA transcript. Vectors may further contain one or more marker sequences suitable for use in the identification of cells which have or have not been transformed or transfected with the vector. Markers include, for example, genes encoding proteins which increase or decrease either resistance or sensitivity to antibiotics or other compounds, genes which encode enzymes whose activities are detectable by standard assays known in the art (e.g., ß-galactosidase or alkaline phosphatase), and genes which visibly affect the phenotype of transformed or transfected cells, hosts, colonies or plaques (e.g., green fluorescent protein). Preferred vectors are those capable of autonomous replication and expression of the structural gene products present in the DNA segments to which they are operably joined.

As used herein, a coding sequence and regulatory sequences are said to be "operably" joined

when they are covalently linked in such a way as to place the expression or transcription of the coding sequence under the influence or control of the regulatory sequences. If it is desired that the coding sequences be translated into a functional protein, two DNA sequences are said to be operably joined if induction of a promoter in the 5' regulatory sequences results in the transcription of the coding sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the coding sequences, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a promoter region would be operably joined to a coding sequence if the promoter region were capable of effecting transcription of that DNA sequence such that the resulting transcript might be translated into the desired protein or polypeptide.

The precise nature of the regulatory sequences needed for gene expression may vary between species or cell types, but shall in general include, as necessary, 5' non-transcribed and 5' non-translated sequences involved with the initiation of transcription and translation respectively, such as a TATA box, capping sequence, CAAT sequence, and the like. Especially, such 5' non-transcribed regulatory sequences will include a promoter region which includes a promoter sequence for transcriptional control of the operably joined gene. Regulatory sequences may also include enhancer sequences or upstream activator sequences as desired. The vectors of the invention may optionally include 5' leader or signal sequences. The choice and design of an appropriate vector is within the ability and discretion of one of ordinary skill in the art.

Expression vectors containing all the necessary elements for expression are commercially available and known to those skilled in the art. See, e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989. Cells are genetically engineered by the introduction into the cells of heterologous DNA (RNA) encoding a breast cancer associated antigen polypeptide or fragment or variant thereof. That heterologous DNA (RNA) is placed under operable control of transcriptional elements to permit the expression of the heterologous DNA in the host cell.

Preferred systems for mRNA expression in mammalian cells are those such as pRc/CMV (available from Invitrogen, Carlsbad, CA) that contain a selectable marker such as a gene that confers G418 resistance (which facilitates the selection of stably transfected cell lines) and the

human cytomegalovirus (CMV) enhancer-promoter sequences. Additionally, suitable for expression in primate or canine cell lines is the pCEP4 vector (Invitrogen), which contains an Epstein Barr Virus (EBV) origin of replication, facilitating the maintenance of plasmid as a multicopy extrachromosomal element. Another expression vector is the pEF-BOS plasmid containing the promoter of polypeptide Elongation Factor 1α, which stimulates efficiently transcription *in vitro*. The plasmid is described by Mishizuma and Nagata (*Nuc. Acids Res.* 18:5322, 1990), and its use in transfection experiments is disclosed by, for example, Demoulin (*Mol. Cell. Biol.* 16:4710-4716, 1996). Still another preferred expression vector is an adenovirus, described by Stratford-Perricaudet, which is defective for E1 and E3 proteins (*J. Clin. Invest.* 90:626-630, 1992). The use of the adenovirus as an Adeno.P1A recombinant for the expression of an antigen is disclosed by Warnier et al., in intradermal injection in mice for immunization against P1A (*Int. J. Cancer*, 67:303-310, 1996). Additional vectors for delivery of nucleic acid are provided below.

The invention also embraces so-called expression kits, which allow the artisan to prepare a desired expression vector or vectors. Such expression kits include at least separate portions of a vector and one or more of the previously discussed breast cancer associated antigen nucleic acid molecules. Other components may be added, as desired, as long as the previously mentioned nucleic acid molecules, which are required, are included. The invention also includes kits for amplification of a breast cancer associated antigen nucleic acid, including at least one pair of amplification primers which hybridize to a breast cancer associated antigen nucleic acid. The primers preferably are 12-32 nucleotides in length and are non-overlapping to prevent formation of "primer-dimers". One of the primers will hybridize to one strand of the breast cancer associated antigen nucleic acid and the second primer will hybridize to the complementary strand of the breast cancer associated antigen nucleic acid, in an arrangement which permits amplification of the breast cancer associated antigen nucleic acid. Selection of appropriate primer pairs is standard in the art. For example, the selection can be made with assistance of a computer program designed for such a purpose, optionally followed by testing the primers for amplification specificity and efficiency.

The invention also permits the construction of cancer associated antigen gene "knock-outs" in cells and in animals, providing materials for studying certain aspects of cancer and immune system responses to cancer.

The invention also provides isolated polypeptides (including whole proteins and partial

proteins) encoded by the foregoing cancer associated antigen nucleic acids. Such polypeptides are useful, for example, alone or as fusion proteins to generate antibodies, as components of an immunoassay or diagnostic assay or as therapeutics. Cancer associated antigen polypeptides can be isolated from biological samples including tissue or cell homogenates, and can also be expressed recombinantly in a variety of prokaryotic and eukaryotic expression systems by constructing an expression vector appropriate to the expression system, introducing the expression vector into the expression system, and isolating the recombinantly expressed protein. Short polypeptides, including antigenic peptides (such as are presented by MHC molecules on the surface of a cell for immune recognition) also can be synthesized chemically using well-established methods of peptide synthesis.

A unique fragment of a cancer associated antigen polypeptide, in general, has the features and characteristics of unique fragments as discussed above in connection with nucleic acids. As will be recognized by those skilled in the art, the size of the unique fragment will depend upon factors such as whether the fragment constitutes a portion of a conserved protein domain. Thus, some regions of breast cancer associated antigens will require longer segments to be unique while others will require only short segments, typically between 5 and 12 amino acids (e.g. 5, 6, 7, 8, 9, 10, 11 or 12 or more, including each integer up to the full length, amino acids long).

Unique fragments of a polypeptide preferably are those fragments which retain a distinct functional capability of the polypeptide. Functional capabilities which can be retained in a unique fragment of a polypeptide include interaction with antibodies, interaction with other polypeptides or fragments thereof, selective binding of nucleic acids or proteins, and enzymatic activity. One important activity is the ability to act as a signature for identifying the polypeptide. Another is the ability to complex with HLA and to provoke in a human an immune response. Those skilled in the art are well versed in methods for selecting unique amino acid sequences, typically on the basis of the ability of the unique fragment to selectively distinguish the sequence of interest from non-family members. A comparison of the sequence of the fragment to those on known databases typically is all that is necessary.

The invention embraces variants of the cancer associated antigen polypeptides described above. As used herein, a "variant" of a cancer associated antigen polypeptide is a polypeptide which contains one or more modifications to the primary amino acid sequence of a cancer associated antigen polypeptide. Modifications which create a cancer associated antigen variant can be made to

a cancer associated antigen polypeptide 1) to reduce or eliminate an activity of a cancer associated antigen polypeptide; 2) to enhance a property of a cancer associated antigen polypeptide, such as protein stability in an expression system or the stability of protein-protein binding; 3) to provide a novel activity or property to a cancer associated antigen polypeptide, such as addition of an antigenic epitope or addition of a detectable moiety; or 4) to provide equivalent or better binding to an HLA molecule. Modifications to a cancer associated antigen polypeptide are typically made to the nucleic acid which encodes the cancer associated antigen polypeptide, and can include deletions, point mutations, truncations, amino acid substitutions and additions of amino acids or non-amino acid moieties. Alternatively, modifications can be made directly to the polypeptide, such as by cleavage, addition of a linker molecule, addition of a detectable moiety, such as biotin, addition of a fatty acid, and the like. Modifications also embrace fusion proteins comprising all or part of the cancer associated antigen amino acid sequence. One of skill in the art will be familiar with methods for predicting the effect on protein conformation of a change in protein sequence, and can thus "design" a variant cancer associated antigen polypeptide according to known methods. One example of such a method is described by Dahiyat and Mayo in *Science* 278:82-87, 1997, whereby proteins can be designed *de novo*. The method can be applied to a known protein to vary a only a portion of the polypeptide sequence. By applying the computational methods of Dahiyat and Mayo, specific variants of a cancer associated antigen polypeptide can be proposed and tested to determine whether the variant retains a desired conformation.

In general, variants include cancer associated antigen polypeptides which are modified specifically to alter a feature of the polypeptide unrelated to its desired physiological activity. For example, cysteine residues can be substituted or deleted to prevent unwanted disulfide linkages. Similarly, certain amino acids can be changed to enhance expression of a breast cancer associated antigen polypeptide by eliminating proteolysis by proteases in an expression system (e.g., dibasic amino acid residues in yeast expression systems in which KEX2 protease activity is present).

Mutations of a nucleic acid which encode a cancer associated antigen polypeptide preferably preserve the amino acid reading frame of the coding sequence, and preferably do not create regions in the nucleic acid which are likely to hybridize to form secondary structures, such a hairpins or loops, which can be deleterious to expression of the variant polypeptide.

Mutations can be made by selecting an amino acid substitution, or by random mutagenesis of

a selected site in a nucleic acid which encodes the polypeptide. Variant polypeptides are then expressed and tested for one or more activities to determine which mutation provides a variant polypeptide with the desired properties. Further mutations can be made to variants (or to non-variant cancer associated antigen polypeptides) which are silent as to the amino acid sequence of the polypeptide, but which provide preferred codons for translation in a particular host. The preferred codons for translation of a nucleic acid in, e.g., *E. coli*, are well known to those of ordinary skill in the art. Still other mutations can be made to the noncoding sequences of a cancer associated antigen gene or cDNA clone to enhance expression of the polypeptide. The activity of variants of cancer associated antigen polypeptides can be tested by cloning the gene encoding the variant cancer associated antigen polypeptide into a bacterial or mammalian expression vector, introducing the vector into an appropriate host cell, expressing the variant cancer associated antigen polypeptide, and testing for a functional capability of the cancer associated antigen polypeptides as disclosed herein. For example, the variant cancer associated antigen polypeptide can be tested for reaction with autologous or allogeneic sera as disclosed in the Examples. Preparation of other variant polypeptides may favor testing of other activities, as will be known to one of ordinary skill in the art.

The skilled artisan will also realize that conservative amino acid substitutions may be made in cancer associated antigen polypeptides to provide functionally equivalent variants of the foregoing polypeptides, i.e, the variants retain the functional capabilities of the cancer associated antigen polypeptides. As used herein, a "conservative amino acid substitution" refers to an amino acid substitution which does not alter the relative charge or size characteristics of the protein in which the amino acid substitution is made. Variants can be prepared according to methods for altering polypeptide sequence known to one of ordinary skill in the art such as are found in references which compile such methods, e.g. *Molecular Cloning: A Laboratory Manual*, J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989, or *Current Protocols in Molecular Biology*, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. Exemplary functionally equivalent variants of the cancer associated antigen polypeptides include conservative amino acid substitutions of in the amino acid sequences of SEQ ID proteins disclosed herein. Conservative substitutions of amino acids include substitutions made amongst amino acids within the following groups: (a) M, I, L, V; (b) F, Y, W; (c) K, R, H; (d) A, G; (e) S, T; (f) Q, N; and (g) E, D.

For example, upon determining that a peptide derived from a cancer associated antigen polypeptide is presented by an MHC molecule and recognized by CTLs (e.g., as described in the Examples), one can make conservative amino acid substitutions to the amino acid sequence of the peptide, particularly at residues which are thought not to be direct contact points with the MHC molecule. For example, methods for identifying functional variants of HLA class II binding peptides are provided in a published PCT application of Strominger and Wucherpfennig (PCT/US96/03182). Peptides bearing one or more amino acid substitutions also can be tested for concordance with known HLA/MHC motifs prior to synthesis using, e.g. the computer program described by D'Amaro and Drijfhout (D'Amaro et al., *Human Immunol.* 43:13-18, 1995; Drijfhout et al., *Human Immunol.* 43:1-12, 1995). The substituted peptides can then be tested for binding to the MHC molecule and recognition by CTLs when bound to MHC. These variants can be tested for improved stability and are useful, *inter alia*, in vaccine compositions.

Conservative amino-acid substitutions in the amino acid sequence of cancer associated antigen polypeptides to produce functionally equivalent variants of cancer associated antigen polypeptides typically are made by alteration of a nucleic acid encoding a cancer associated antigen polypeptide. Such substitutions can be made by a variety of methods known to one of ordinary skill in the art. For example, amino acid substitutions may be made by PCR-directed mutation, site-directed mutagenesis according to the method of Kunkel (Kunkel, *Proc. Nat. Acad. Sci. U.S.A.* 82: 488-492, 1985), or by chemical synthesis of a gene encoding a cancer associated antigen polypeptide. Where amino acid substitutions are made to a small unique fragment of a cancer associated antigen polypeptide, such as an antigenic epitope recognized by autologous or allogeneic sera or cytolytic T lymphocytes, the substitutions can be made by directly synthesizing the peptide. The activity of functionally equivalent fragments of cancer associated antigen polypeptides can be tested by cloning the gene encoding the altered cancer associated antigen polypeptide into a bacterial or mammalian expression vector, introducing the vector into an appropriate host cell, expressing the altered cancer associated antigen polypeptide, and testing for a functional capability of the cancer associated antigen polypeptides as disclosed herein. Peptides which are chemically synthesized can be tested directly for function, e.g., for binding to antisera recognizing associated antigens.

The invention as described herein has a number of uses, some of which are described elsewhere herein. First, the invention permits isolation of the cancer associated antigen protein

molecules. A variety of methodologies well-known to the skilled practitioner can be utilized to obtain isolated cancer associated antigen molecules. The polypeptide may be purified from cells which naturally produce the polypeptide by chromatographic means or immunological recognition. Alternatively, an expression vector may be introduced into cells to cause production of the polypeptide. In another method, mRNA transcripts may be microinjected or otherwise introduced into cells to cause production of the encoded polypeptide. Translation of mRNA in cell-free extracts such as the reticulocyte lysate system also may be used to produce polypeptide. Those skilled in the art also can readily follow known methods for isolating cancer associated antigen polypeptides. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography and immune-affinity chromatography.

The isolation and identification of cancer associated antigen genes also makes it possible for the artisan to diagnose a disorder characterized by expression of cancer associated antigens. These methods involve determining expression of one or more cancer associated antigen nucleic acids, and/or encoded cancer associated antigen polypeptides and/or peptides derived therefrom. In the former situation, such determinations can be carried out via any standard nucleic acid determination assay, including the polymerase chain reaction, or assaying with labeled hybridization probes. In the latter situation, such determinations can be carried out by screening patient antisera for recognition of the polypeptide.

The invention also makes it possible isolate proteins which bind to cancer associated antigens as disclosed herein, including antibodies and cellular binding partners of the cancer associated antigens. Additional uses are described further herein.

The invention also provides, in certain embodiments, "dominant negative" polypeptides derived from cancer associated antigen polypeptides. A dominant negative polypeptide is an inactive variant of a protein, which, by interacting with the cellular machinery, displaces an active protein from its interaction with the cellular machinery or competes with the active protein, thereby reducing the effect of the active protein. For example, a dominant negative receptor which binds a ligand but does not transmit a signal in response to binding of the ligand can reduce the biological effect of expression of the ligand. Likewise, a dominant negative catalytically-inactive kinase which interacts normally with target proteins but does not phosphorylate the target proteins can reduce phosphorylation of the target proteins in response to a cellular signal. Similarly, a dominant

negative transcription factor which binds to a promoter site in the control region of a gene but does not increase gene transcription can reduce the effect of a normal transcription factor by occupying promoter binding sites without increasing transcription.

The end result of the expression of a dominant negative polypeptide in a cell is a reduction in function of active proteins. One of ordinary skill in the art can assess the potential for a dominant negative variant of a protein, and using standard mutagenesis techniques to create one or more dominant negative variant polypeptides. For example, given the teachings contained herein of cancer-associated antigens, especially those which are similar to known proteins which have known activities, one of ordinary skill in the art can modify the sequence of the cancer associated antigens by site-specific mutagenesis, scanning mutagenesis, partial gene deletion or truncation, and the like. See, e.g., U.S. Patent No. 5,580,723 and Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989. The skilled artisan then can test the population of mutagenized polypeptides for diminution in a selected and/or for retention of such an activity. Other similar methods for creating and testing dominant negative variants of a protein will be apparent to one of ordinary skill in the art.

The invention also involves agents such as polypeptides which bind to cancer associated antigen polypeptides. Such binding agents can be used, for example, in screening assays to detect the presence or absence of cancer associated antigen polypeptides and complexes of cancer associated antigen polypeptides and their binding partners and in purification protocols to isolated cancer associated antigen polypeptides and complexes of cancer associated antigen polypeptides and their binding partners. Such agents also can be used to inhibit the native activity of the cancer associated antigen polypeptides, for example, by binding to such polypeptides.

The invention, therefore, embraces peptide binding agents which, for example, can be antibodies or fragments of antibodies having the ability to selectively bind to cancer associated antigen polypeptides. Antibodies include polyclonal and monoclonal antibodies, prepared according to conventional methodology.

Significantly, as is well-known in the art, only a small portion of an antibody molecule, the paratope, is involved in the binding of the antibody to its epitope (see, in general, Clark, W.R. (1986) The Experimental Foundations of Modern Immunology Wiley & Sons, Inc., New York; Roitt, I. (1991) Essential Immunology, 7th Ed., Blackwell Scientific Publications, Oxford). The

pFc' and Fc regions, for example, are effectors of the complement cascade but are not involved in antigen binding. An antibody from which the pFc' region has been enzymatically cleaved, or which has been produced without the pFc' region, designated an $F(ab')_2$ fragment, retains both of the antigen binding sites of an intact antibody. Similarly, an antibody from which the Fc region has been enzymatically cleaved, or which has been produced without the Fc region, designated an Fab fragment, retains one of the antigen binding sites of an intact antibody molecule. Proceeding further, Fab fragments consist of a covalently bound antibody light chain and a portion of the antibody heavy chain denoted Fd. The Fd fragments are the major determinant of antibody specificity (a single Fd fragment may be associated with up to ten different light chains without altering antibody specificity) and Fd fragments retain epitope-binding ability in isolation.

Within the antigen-binding portion of an antibody, as is well-known in the art, there are complementarity determining regions (CDRs), which directly interact with the epitope of the antigen, and framework regions (FRs), which maintain the tertiary structure of the paratope (see, in general, Clark, 1986; Roitt, 1991). In both the heavy chain Fd fragment and the light chain of IgG immunoglobulins, there are four framework regions (FR1 through FR4) separated respectively by three complementarity determining regions (CDR1 through CDR3). The CDRs, and in particular the CDR3 regions, and more particularly the heavy chain CDR3, are largely responsible for antibody specificity.

It is now well-established in the art that the non-CDR regions of a mammalian antibody may be replaced with similar regions of conspecific or heterospecific antibodies while retaining the epitopic specificity of the original antibody. This is most clearly manifested in the development and use of "humanized" antibodies in which non-human CDRs are covalently joined to human FR and/or Fc/pFc' regions to produce a functional antibody. Thus, for example, PCT International Publication Number WO 92/04381 teaches the production and use of humanized murine RSV antibodies in which at least a portion of the murine FR regions have been replaced by FR regions of human origin. Such antibodies, including fragments of intact antibodies with antigen-binding ability, are often referred to as "chimeric" antibodies.

Thus, as will be apparent to one of ordinary skill in the art, the present invention also provides for $F(ab')_2$, Fab, Fv and Fd fragments; chimeric antibodies in which the Fc and/or FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous

human or non-human sequences; chimeric $F(ab')_2$ fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; chimeric Fab fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; and chimeric Fd fragment antibodies in which the FR and/or CDR1 and/or CDR2 regions have been replaced by homologous human or non-human sequences. The present invention also includes so-called single chain antibodies.

Thus, the invention involves polypeptides of numerous size and type that bind specifically to cancer associated antigen polypeptides, and complexes of both cancer associated antigen polypeptides and their binding partners. These polypeptides may be derived also from sources other than antibody technology. For example, such polypeptide binding agents can be provided by degenerate peptide libraries which can be readily prepared in solution, in immobilized form or as phage display libraries. Combinatorial libraries also can be synthesized of peptides containing one or more amino acids. Libraries further can be synthesized of peptoids and non-peptide synthetic moieties.

Phage display can be particularly effective in identifying binding peptides useful according to the invention. Briefly, one prepares a phage library (using e.g. m13, fd, or lambda phage), displaying inserts from 4 to about 80 amino acid residues using conventional procedures. The inserts may represent, for example, a completely degenerate or biased array. One then can select phage-bearing inserts which bind to the cancer associated antigen polypeptide. This process can be repeated through several cycles of reselection of phage that bind to the cancer associated antigen polypeptide. Repeated rounds lead to enrichment of phage bearing particular sequences. DNA sequence analysis can be conducted to identify the sequences of the expressed polypeptides. The minimal linear portion of the sequence that binds to the cancer associated antigen polypeptide can be determined. One can repeat the procedure using a biased library containing inserts containing part or all of the minimal linear portion plus one or more additional degenerate residues upstream or downstream thereof. Yeast two-hybrid screening methods also may be used to identify polypeptides that bind to the cancer associated antigen polypeptides. Thus, the cancer associated antigen polypeptides of the invention, or a fragment thereof, can be used to screen peptide libraries, including phage display libraries, to identify and select peptide binding partners of the cancer

associated antigen polypeptides of the invention. Such molecules can be used, as described, for screening assays, for purification protocols, for interfering directly with the functioning of cancer associated antigen and for other purposes that will be apparent to those of ordinary skill in the art.

As detailed herein, the foregoing antibodies and other binding molecules may be used for example to identify tissues expressing protein or to purify protein. Antibodies also may be coupled to specific diagnostic labeling agents for imaging of cells and tissues that express cancer associated antigens or to therapeutically useful agents according to standard coupling procedures. Diagnostic agents include, but are not limited to, barium sulfate, iocetamic acid, iopanoic acid, ipodate calcium, diatrizoate sodium, diatrizoate meglumine, metrizamide, tyropanoate sodium and radiodiagnostics including positron emitters such as fluorine-18 and carbon-11, gamma emitters such as iodine-123, technitium-99m, iodine-131 and indium-111, nuclides for nuclear magnetic resonance such as fluorine and gadolinium. Other diagnostic agents useful in the invention will be apparent to one of ordinary skill in the art. As used herein, "therapeutically useful agents" include any therapeutic molecule which desirably is targeted selectively to a cell expressing one of the cancer antigens disclosed herein, including antineoplastic agents, radioiodinated compounds, toxins, other cytostatic or cytolytic drugs, and so forth. Antineoplastic therapeutics are well known and include: aminoglutethimide, azathioprine, bleomycin sulfate, busulfan, carmustine, chlorambucil, cisplatin, cyclophosphamide, cyclosporine, cytarabidine, dacarbazine, dactinomycin, daunorubicin, doxorubicin, taxol, etoposide, fluorouracil, interferon-α, lomustine, mercaptopurine, methotrexate, mitotane, procarbazine HCl, thioguanine, vinblastine sulfate and vincristine sulfate. Additional antineoplastic agents include those disclosed in Chapter 52, Antineoplastic Agents (Paul Calabresi and Bruce A. Chabner), and the introduction thereto, 1202-1263, of Goodman and Gilman's "The Pharmacological Basis of Therapeutics", Eighth Edition, 1990, McGraw-Hill, Inc. (Health Professions Division). Toxins can be proteins such as, for example, pokeweed anti-viral protein, cholera toxin, pertussis toxin, ricin, gelonin, abrin, diphtheria exotoxin, or *Pseudomonas* exotoxin. Toxin moieties can also be high energy-emitting radionuclides such as cobalt-60.

In the foregoing methods, antibodies prepared according to the invention also preferably are specific for the cancer associated antigen/MHC complexes described herein.

When "disorder" is used herein, it refers to any pathological condition where the cancer associated antigens are expressed. An example of such a disorder is cancer, breast, colon, gastric,

renal, prostate and lung cancers as particular examples.

Samples of tissue and/or cells for use in the various methods described herein can be obtained through standard methods such as tissue biopsy, including punch biopsy and cell scraping, and collection of blood or other bodily fluids by aspiration or other methods.

In certain embodiments of the invention, an immunoreactive cell sample is removed from a subject. By "immunoreactive cell" is meant a cell which can mature into an immune cell (such as a B cell, a helper T cell, or a cytolytic T cell) upon appropriate stimulation. Thus immunoreactive cells include $CD34^+$ hematopoietic stem cells, immature T cells and immature B cells. When it is desired to produce cytolytic T cells which recognize a cancer associated antigen, the immunoreactive cell is contacted with a cell which expresses a cancer associated antigen under conditions favoring production, differentiation and/or selection of cytolytic T cells; the differentiation of the T cell precursor into a cytolytic T cell upon exposure to antigen is similar to clonal selection of the immune system.

Some therapeutic approaches based upon the disclosure are premised on a response by a subject's immune system, leading to lysis of antigen presenting cells, such as breast cancer cells which present one or more cancer associated antigens. One such approach is the administration of autologous CTLs specific to a cancer associated antigen/MHC complex to a subject with abnormal cells of the phenotype at issue. It is within the ability of one of ordinary skill in the art to develop such CTLs *in vitro*. An example of a method for T cell differentiation is presented in International Application number PCT/US96/05607. Generally, a sample of cells taken from a subject, such as blood cells, are contacted with a cell presenting the complex and capable of provoking CTLs to proliferate. The target cell can be a transfectant, such as a COS cell of the type described herein. These transfectants present the desired complex of their surface and, when combined with a CTL of interest, stimulate its proliferation. COS cells, such as those used herein are widely available, as are other suitable host cells. Specific production of a CTL clone is described herein, and is well known in the art. The clonally expanded autologous CTLs then are administered to the subject.

Another method for selecting antigen-specific CTL clones has recently been described (Altman et al., *Science* 274:94-96, 1996; Dunbar et al., *Curr. Biol.* 8:413-416, 1998), in which fluorogenic tetramers of MHC class I molecule/peptide complexes are used to detect specific CTL clones. Briefly, soluble MHC class I molecules are folded *in vitro* in the presence of β_2-

microglobulin and a peptide antigen which binds the class I molecule. After purification, the MHC/peptide complex is purified and labeled with biotin. Tetramers are formed by mixing the biotinylated peptide-MHC complex with labeled avidin (e.g. phycoerythrin) at a molar ratio or 4:1. Tetramers are then contacted with a source of CTLs such as peripheral blood or lymph node. The tetramers bind CTLs which recognize the peptide antigen/MHC class I complex. Cells bound by the tetramers can be sorted by fluorescence activated cell sorting to isolate the reactive CTLs. The isolated CTLs then can be expanded *in vitro* for use as described herein.

To detail a therapeutic methodology, referred to as adoptive transfer (Greenberg, *J. Immunol.* 136(5): 1917, 1986; Riddel et al., *Science* 257: 238, 1992; Lynch et al, *Eur. J. Immunol.* 21: 1403-1410,1991; Kast et al., *Cell* 59: 603-614, 1989), cells presenting the desired complex are combined with CTLs leading to proliferation of the CTLs specific thereto. The proliferated CTLs are then administered to a subject with a cellular abnormality which is characterized by certain of the abnormal cells presenting the particular complex. The CTLs then lyse the abnormal cells, thereby achieving the desired therapeutic goal.

The foregoing therapy assumes that at least some of the subject's abnormal cells present the relevant HLA cancer associated antigen complex. This can be determined very easily, as the art is very familiar with methods for identifying cells which present a particular HLA molecule, as well as how to identify cells expressing DNA of the pertinent sequences, in this case a cancer associated antigen sequence. Once cells presenting the relevant complex are identified via the foregoing screening methodology, they can be combined with a sample from a patient, where the sample contains CTLs. If the complex presenting cells are lysed by the mixed CTL sample, then it can be assumed that a cancer associated antigen is being presented, and the subject is an appropriate candidate for the therapeutic approaches set forth *supra*.

Adoptive transfer is not the only form of therapy that is available in accordance with the invention. CTLs can also be provoked *in vivo*, using a number of approaches. One approach is the use of non-proliferative cells expressing the complex. The cells used in this approach may be those that normally express the complex, such as irradiated tumor cells or cells transfected with one or both of the genes necessary for presentation of the complex (i.e. the antigenic peptide and the presenting HLA molecule). Chen et al. (*Proc. Natl. Acad. Sci. USA* 88: 110-114,1991) exemplifies this approach, showing the use of transfected cells expressing HPVE7 peptides in a therapeutic

regime. Various cell types may be used. Similarly, vectors carrying one or both of the genes of interest may be used. Viral or bacterial vectors are especially preferred. For example, nucleic acids which encode a breast cancer associated antigen polypeptide or peptide may be operably linked to promoter and enhancer sequences which direct expression of the cancer associated antigen polypeptide or peptide in certain tissues or cell types. The nucleic acid may be incorporated into an expression vector. Expression vectors may be unmodified extrachromosomal nucleic acids, plasmids or viral genomes constructed or modified to enable insertion of exogenous nucleic acids, such as those encoding cancer associated antigen, as described elsewhere herein. Nucleic acids encoding a cancer associated antigen also may be inserted into a retroviral genome, thereby facilitating integration of the nucleic acid into the genome of the target tissue or cell type. In these systems, the gene of interest is carried by a microorganism, e.g., a Vaccinia virus, retrovirus or adenovirus, and the materials de facto "infect" host cells. The cells which result present the complex of interest, and are recognized by autologous CTLs, which then proliferate.

A similar effect can be achieved by combining the cancer associated antigen or a stimulatory fragment thereof with an adjuvant to facilitate incorporation into antigen presenting cells *in vivo*. The breast cancer associated antigen polypeptide is processed to yield the peptide partner of the HLA molecule while a cancer associated antigen peptide may be presented without the need for further processing. Generally, subjects can receive an intradermal injection of an effective amount of the cancer associated antigen. Initial doses can be followed by booster doses, following immunization protocols standard in the art.. Preferred cancer associated antigens include those found to react with allogeneic cancer antisera, such as the nucleic acids (and encoded polypeptides and peptides) of SEQ ID NO:31,33 and 34 and others, for example, shown in the examples below.

The invention involves the use of various materials disclosed herein to “immunize” subjects or as “vaccines”. As used herein, “immunization” or “vaccination” means increasing or activating an immune response against an antigen. It does not require elimination or eradication of a condition but rather contemplates the clinically favorable enhancement of an immune response toward an antigen. Generally accepted animal models can be used for testing of immunization against breast cancer using a cancer associated antigen nucleic acid. For example, cancer cells can be introduced into a mouse to create a tumor, and one or more cancer associated antigen nucleic acids can be delivered by the methods described herein. The effect on the cancer cells (e.g., reduction of tumor

size) can be assessed as a measure of the effectiveness of the cancer associated antigen nucleic acid immunization. Of course, testing of the foregoing animal model using more conventional methods for immunization include the administration of one or more cancer associated antigen polypeptides or peptides derived therefrom, optionally combined with one or more adjuvants and/or cytokines to boost the immune response. Methods for immunization, including formulation of a vaccine composition and selection of doses, route of administration and the schedule of administration (e.g. primary and one or more booster doses), are well known in the art. The tests also can be performed in humans, where the end point is to test for the presence of enhanced levels of circulating CTLs against cells bearing the antigen, to test for levels of circulating antibodies against the antigen, to test for the presence of cells expressing the antigen and so forth.

As part of the immunization compositions, one or more cancer associated antigens or stimulatory fragments thereof are administered with one or more adjuvants to induce an immune response or to increase an immune response. An adjuvant is a substance incorporated into or administered with antigen which potentiates the immune response. Adjuvants may enhance the immunological response by providing a reservoir of antigen (extracellularly or within macrophages), activating macrophages and stimulating specific sets of lymphocytes. Adjuvants of many kinds are well known in the art. Specific examples of adjuvants include monophosphoryl lipid A (MPL, SmithKline Beecham), a congener obtained after purification and acid hydrolysis of *Salmonella minnesota* Re 595 lipopolysaccharide; saponins including QS21 (SmithKline Beecham), a pure QA-21 saponin purified from *Quillja saponaria* extract; DQS21, described in PCT application WO96/33739 (SmithKline Beecham); QS-7, QS-17, QS-18, and QS-L1 (So et al., *Mol. Cells* 7:178-186, 1997); incomplete Freund's adjuvant; complete Freund's adjuvant; montanide; and various water-in-oil emulsions prepared from biodegradable oils such as squalene and/or tocopherol. Preferably, the peptides are administered mixed with a combination of DQS21/MPL. The ratio of DQS21 to MPL typically will be about 1:10 to 10:1, preferably about 1:5 to 5:1 and more preferably about 1:1. Typically for human administration, DQS21 and MPL will be present in a vaccine formulation in the range of about 1 μg to about 100 μg. Other adjuvants are known in the art and can be used in the invention (*see, e.g.* Goding, *Monoclonal Antibodies: Principles and Practice*, 2nd Ed., 1986). Methods for the preparation of mixtures or emulsions of peptide and adjuvant are well known to those of skill in the art of vaccination.

Other agents which stimulate the immune response of the subject can also be administered to the subject. For example, other cytokines are also useful in vaccination protocols as a result of their lymphocyte regulatory properties. Many other cytokines useful for such purposes will be known to one of ordinary skill in the art, including interleukin-12 (IL-12) which has been shown to enhance the protective effects of vaccines (*see, e.g., Science* 268: 1432-1434, 1995), GM-CSF and IL-18. Thus cytokines can be administered in conjunction with antigens and adjuvants to increase the immune response to the antigens.

There are a number of immune response potentiating compounds that can be used in vaccination protocols. These include costimulatory molecules provided in either protein or nucleic acid form. Such costimulatory molecules include the B7-1 and B7-2 (CD80 and CD86 respectively) molecules which are expressed on dendritic cells (DC) and interact with the CD28 molecule expressed on the T cell. This interaction provides costimulation (signal 2) to an antigen/MHC/TCR stimulated (signal 1) T cell, increasing T cell proliferation and effector function. B7 also interacts with CTLA4 (CD152) on T cells and studies involving CTLA4 and B7 ligands indicate that the B7-CTLA4 interaction can enhance antitumor immunity and CTL proliferation, Zheng P., et al. *PNAS* 95 (11) 6284-6289 (1998).

B7 typically is not expressed on tumor cells so they are not efficient antigen presenting cells (APCs) for T cells. Induction of B7 expression would enable the tumor cells to stimulate more efficiently CTL proliferation and effector function. A combination of B7/IL-6/IL-12 costimulation has been shown to induce IFN-gamma and a Th1 cytokine profile in the T cell population leading to further enhanced T cell activity, Gajewski et al., *J. I mmunol*, 154:5637-5648 (1995). Tumor cell transfection with B7 has ben discussed in relation to *in vitro* CTL expansion for adoptive transfer immunotherapy by Wang et al., J Immunol, 19:1-8 (1986). Other delivery mechanisms for the B7 molecule would include nucleic acid (naked DNA) immunization Kim J., et al. *Nat Biotechnol.*, 15:7:641-646 (1997) and recombinant viruses such as adeno and pox (Wendtner et al., *Gene Ther*, 4:7:726-735 (1997)). These systems are all amenable to the construction and use of expression cassettes for the coexpression of B7 with other molecules of choice such as the antigens or fragment(s) of antigens discussed herein (including polytopes) or cytokines. These delivery systems can be used for induction of the appropriate molecules *in vitro* and for *in vivo* vaccination situations. The use of anti-CD28 antibodies to directly stimulate T cells *in vitro* and *in vivo* could also be

considered.

Lymphocyte function associated antigen-3 (LFA-3) is expressed on APCs and some tumor cells and interacts with CD2 expressed on T cells. This interaction induces T cell IL-2 and IFN-gamma production and can thus complement but not substitute, the B7/CD28 costimulatory interaction, Parra et al., *J. Immunol.*, 158:637-642 (1997), Fenton et al., *J. Immunother*, 21:2:95-108 (1989).

Lymphocyte function associated antigen-1 (LFA-1) is expressed on leukocytes and interacts with ICAM-1 expressed on APCs and some tumor cells. This interaction induces T cell IL-2 and IFN-gamma production and can thus complement but not substitute, the B7/CD28 costimulatory interaction, Fenton et al., *J. Immunothera*, 21:2:95-108 (1998). LFA-1 is thus a further example of a costimulatory molecule that could be provided in a vaccination protocol in the various ways discussed above for B7.

Complete CTL activation and effector function requires Th cell help through the interaction between the Th cell CD40L (CD40 ligand) molecule and the CD40 molecule expressed by DCS, Ridge et al., *Nature*, 393:474 (1998), Bennett et al., *Nature*, 393:478 (1998), Schoenberger et al., *Nature*, 393:480 (1998). This mechanism of this costimulatory signal is likely to involve upregulation of B7 and associated IL-6/IL-12 production by the DC (APC). The CD40-CD40L interaction thus complements the signal 1 (antigen/MHC-TCR) and signal 2 (B7-CD28) interactions.

The use of anti-CD40 antibodies to stimulate DC cells directly, would be expected to enhance a response to tumor antigens which are normally encountered outside of a inflammatory context or are presented by non-professional APCs (tumor cells). In these situations Th help and B7 costimulation signals are not provided. This mechanism might be used in the context of antigen pulsed DC based therapies or in situations where Th epitopes have not been defined within known TRA precursors.

A cancer associated antigen polypeptide, or a fragment thereof, also can be used to isolate their native binding partners. Isolation of such binding partners may be performed according to well-known methods. For example, isolated cancer associated antigen polypeptides can be attached to a substrate (e.g., chromatographic media, such as polystyrene beads, or a filter), and then a solution suspected of containing the binding partner may be applied to the substrate. If a binding partner which can interact with cancer associated antigen polypeptides is present in the solution,

then it will bind to the substrate-bound cancer associated antigen polypeptide. The binding partner then may be isolated.

It will also be recognized that the invention embraces the use of the cancer associated antigen cDNA sequences in expression vectors, as well as to transfect host cells and cell lines, be these prokaryotic (e.g., *E. coli*), or eukaryotic (e.g., dendritic cells, B cells, CHO cells, COS cells, yeast expression systems and recombinant baculovirus expression in insect cells). Especially useful are mammalian cells such as human, mouse, hamster, pig, goat, primate, etc. They may be of a wide variety of tissue types, and include primary cells and cell lines. Specific examples include keratinocytes, peripheral blood leukocytes, bone marrow stem cells and embryonic stem cells. The expression vectors require that the pertinent sequence, i.e., those nucleic acids described *supra*, be operably linked to a promoter.

The invention also contemplates delivery of nucleic acids, polypeptides or peptides for vaccination. Delivery of polypeptides and peptides can be accomplished according to standard vaccination protocols which are well known in the art. In another embodiment, the delivery of nucleic acid is accomplished by *ex vivo* methods, i.e. by removing a cell from a subject, genetically engineering the cell to include a breast cancer associated antigen, and reintroducing the engineered cell into the subject. One example of such a procedure is outlined in U.S. Patent 5,399,346 and in exhibits submitted in the file history of that patent, all of which are publicly available documents. In general, it involves introduction *in vitro* of a functional copy of a gene into a cell(s) of a subject, and returning the genetically engineered cell(s) to the subject. The functional copy of the gene is under operable control of regulatory elements which permit expression of the gene in the genetically engineered cell(s). Numerous transfection and transduction techniques as well as appropriate expression vectors are well known to those of ordinary skill in the art, some of which are described in PCT application WO95/00654. *In vivo* nucleic acid delivery using vectors such as viruses and targeted liposomes also is contemplated according to the invention.

In preferred embodiments, a virus vector for delivering a nucleic acid encoding a cancer associated antigen is selected from the group consisting of adenoviruses, adeno-associated viruses, poxviruses including vaccinia viruses and attenuated poxviruses, Semliki Forest virus, Venezuelan equine encephalitis virus, retroviruses, Sindbis virus, and Ty virus-like particle. Examples of viruses and virus-like particles which have been used to deliver exogenous nucleic acids include:

replication-defective adenoviruses (e.g., Xiang et al., *Virology* 219:220-227, 1996; Eloit et al., *J. Virol* 7:5375-5381, 1997; Chengalvala et al., *Vaccine* 15:335-339, 1997), a modified retrovirus (Townsend et al., *J. Virol.* 71:3365-3374, 1997), a nonreplicating retrovirus (Irwin et al., *J. Virol.* 68:5036-5044, 1994), a replication defective Semliki Forest virus (Zhao et al., *Proc. Natl. Acad. Sci. USA* 92:3009-3013, 1995), canarypox virus and highly attenuated vaccinia virus derivative (Paoletti, *Proc. Natl. Acad. Sci. USA* 93:11349-11353, 1996), non-replicative vaccinia virus (Moss, *Proc. Natl. Acad. Sci. USA* 93:11341-11348, 1996), replicative vaccinia virus (Moss, *Dev. Biol. Stand.* 82:55-63, 1994), Venzuelan equine encephalitis virus (Davis et al., *J. Virol.* 70:3781-3787, 1996), Sindbis virus (Pugachev et al., *Virology* 212:587-594, 1995), and Ty virus-like particle (Allsopp et al., *Eur J. Immunol* 26:1951-1959, 1996). In preferred embodiments, the virus vector is an adenovirus.

Another preferred virus for certain applications is the adeno-associated virus, a double-stranded DNA virus. The adeno-associated virus is capable of infecting a wide range of cell types and species and can be engineered to be replication-deficient. It further has advantages, such as heat and lipid solvent stability, high transduction frequencies in cells of diverse lineages, including hematopoietic cells, and lack of superinfection inhibition thus allowing multiple series of transductions. The adeno-associated virus can integrate into human cellular DNA in a site-specific manner, thereby minimizing the possibility of insertional mutagenesis and variability of inserted gene expression. In addition, wild-type adeno-associated virus infections have been followed in tissue culture for greater than 100 passages in the absence of selective pressure, implying that the adeno-associated virus genomic integration is a relatively stable event. The adeno-associated virus can also function in an extrachromosomal fashion.

In general, other preferred viral vectors are based on non-cytopathic eukaryotic viruses in which non-essential genes have been replaced with the gene of interest. Non-cytopathic viruses include retroviruses, the life cycle of which involves reverse transcription of genomic viral RNA into DNA with subsequent proviral integration into host cellular DNA. Adenoviruses and retroviruses have been approved for human gene therapy trials. In general, the retroviruses are replication-deficient (i.e., capable of directing synthesis of the desired proteins, but incapable of manufacturing an infectious particle). Such genetically altered retroviral expression vectors have general utility for the high-efficiency transduction of genes *in vivo*. Standard protocols for

producing replication-deficient retroviruses (including the steps of incorporation of exogenous genetic material into a plasmid, transfection of a packaging cell lined with plasmid, production of recombinant retroviruses by the packaging cell line, collection of viral particles from tissue culture media, and infection of the target cells with viral particles) are provided in Kriegler, M., "Gene Transfer and Expression, A Laboratory Manual," W.H. Freeman C.O., New York (1990) and Murry, E.J. Ed. "Methods in Molecular Biology," vol. 7, Humana Press, Inc., Cliffton, New Jersey (1991).

Preferably the foregoing nucleic acid delivery vectors: (1) contain exogenous genetic material that can be transcribed and translated in a mammalian cell and that can induce an immune response in a host, and (2) contain on a surface a ligand that selectively binds to a receptor on the surface of a target cell, such as a mammalian cell, and thereby gains entry to the target cell.

Various techniques may be employed for introducing nucleic acids of the invention into cells, depending on whether the nucleic acids are introduced *in vitro* or *in vivo* in a host. Such techniques include transfection of nucleic acid-$CaPO_4$ precipitates, transfection of nucleic acids associated with DEAE, transfection or infection with the foregoing viruses including the nucleic acid of interest, liposome mediated transfection, and the like. For certain uses, it is preferred to target the nucleic acid to particular cells. In such instances, a vehicle used for delivering a nucleic acid of the invention into a cell (e.g., a retrovirus, or other virus; a liposome) can have a targeting molecule attached thereto. For example, a molecule such as an antibody specific for a surface membrane protein on the target cell or a ligand for a receptor on the target cell can be bound to or incorporated within the nucleic acid delivery vehicle. Preferred antibodies include antibodies which selectively bind a cancer associated antigen, alone or as a complex with a MHC molecule. Especially preferred are monoclonal antibodies. Where liposomes are employed to deliver the nucleic acids of the invention, proteins which bind to a surface membrane protein associated with endocytosis may be incorporated into the liposome formulation for targeting and/or to facilitate uptake. Such proteins include capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half life, and the like. Polymeric delivery systems also have been used successfully to deliver nucleic acids into cells, as is known by those skilled in the art. Such systems even permit oral delivery of nucleic acids.

When administered, the therapeutic compositions of the present invention can be

administered in pharmaceutically acceptable preparations. Such preparations may routinely contain pharmaceutically acceptable concentrations of salt, buffering agents, preservatives, compatible carriers, supplementary immune potentiating agents such as adjuvants and cytokines and optionally other therapeutic agents.

The therapeutics of the invention can be administered by any conventional route, including injection or by gradual infusion over time. The administration may, for example, be oral, intravenous, intraperitoneal, intramuscular, intracavity, subcutaneous, or transdermal. When antibodies are used therapeutically, a preferred route of administration is by pulmonary aerosol. Techniques for preparing aerosol delivery systems containing antibodies are well known to those of skill in the art. Generally, such systems should utilize components which will not significantly impair the biological properties of the antibodies, such as the paratope binding capacity (see, for example, Sciarra and Cutie, "Aerosols," in Remington's Pharmaceutical Sciences, 18th edition, 1990, pp 1694-1712; incorporated by reference). Those of skill in the art can readily determine the various parameters and conditions for producing antibody aerosols without resort to undue experimentation. When using antisense preparations of the invention, slow intravenous administration is preferred.

The compositions of the invention are administered in effective amounts. An "effective amount" is that amount of a cancer associated antigen composition that alone, or together with further doses, produces the desired response, e.g. increases an immune response to the cancer associated antigen. In the case of treating a particular disease or condition characterized by expression of one or more cancer associated antigens, such as cancer, the desired response is inhibiting the progression of the disease. This may involve only slowing the progression of the disease temporarily, although more preferably, it involves halting the progression of the disease permanently. This can be monitored by routine methods or can be monitored according to diagnostic methods of the invention discussed herein. The desired response to treatment of the disease or condition also can be delaying the onset or even preventing the onset of the disease or condition.

Such amounts will depend, of course, on the particular condition being treated, the severity of the condition, the individual patient parameters including age, physical condition, size and weight, the duration of the treatment, the nature of concurrent therapy (if any), the specific route of

administration and like factors within the knowledge and expertise of the health practioner. These factors are well known to those of ordinary skill in the art and can be addressed with no more than routine experimentation. It is generally preferred that a maximum dose of the individual components or combinations thereof be used, that is, the highest safe dose according to sound medical judgment. It will be understood by those of ordinary skill in the art, however, that a patient may insist upon a lower dose or tolerable dose for medical reasons, psychological reasons or for virtually any other reasons.

The pharmaceutical compositions used in the foregoing methods preferably are sterile and contain an effective amount of breast cancer associated antigen or nucleic acid encoding cancer associated antigen for producing the desired response in a unit of weight or volume suitable for administration to a patient. The response can, for example, be measured by determining the immune response following administration of the cancer associated antigen composition via a reporter system as described herein, by measuring downstream effects such as gene expression, or by measuring the physiological effects of the breast cancer associated antigen composition, such as regression of a tumor or decrease of disease symptoms. Other assays will be known to one of ordinary skill in the art and can be employed for measuring the level of the response.

The doses of cancer associated antigen compositions (e.g., polypeptide, peptide, antibody, cell or nucleic acid) administered to a subject can be chosen in accordance with different parameters, in particular in accordance with the mode of administration used and the state of the subject. Other factors include the desired period of treatment. In the event that a response in a subject is insufficient at the initial doses applied, higher doses (or effectively higher doses by a different, more localized delivery route) may be employed to the extent that patient tolerance permits.

In general, for treatments for eliciting or increasing an immune response, doses of cancer associated antigen are formulated and administered in doses between 1 ng and 1 mg, and preferably between 10 ng and 100 μg, according to any standard procedure in the art. Where nucleic acids encoding cancer associated antigen of variants thereof are employed, doses of between 1 ng and 0.1 mg generally will be formulated and administered according to standard procedures. Other protocols for the administration of cancer associated antigen compositions will be known to one of ordinary skill in the art, in which the dose amount, schedule of injections, sites of injections, mode of administration (e.g., intra-tumoral) and the like vary from the foregoing. Administration of cancer

associated antigen compositions to mammals other than humans, e.g. for testing purposes or veterinary therapeutic purposes, is carried out under substantially the same conditions as described above.

As part of the immunization compositions, the peptide antigens are administered with one or more adjuvants to induce an immune response or to increase an immune response. An adjuvant is a substance incorporated into or administered with antigen which potentiates the immune response. Adjuvants may enhance the immunological response by providing a reservoir of antigen (extracellularly or within macrophages), activating macrophages and stimulating specific sets of lymphocytes. Adjuvants of many kinds are well known in the art. Specific examples of adjuvants include monophosphoryl lipid A (MPL, SmithKline Beecham), a congener obtained after purification and acid hydrolysis of *Salmonella minnesota* Re 595 lipopolysaccharide; saponins including QS21 (SmithKline Beecham), a pure QA-21 saponin purified from *Quillja saponaria* extract; DQS21, described in PCT application WO96/33739 (SmithKline Beecham); QS-7, QS-17, QS-18, and QS-L1 (So et al., *Mol. Cells* 7:178-186, 1997); incomplete Freund's adjuvant; complete Freund's adjuvant; montanide; and various water-in-oil emulsions prepared from biodegradable oils such as squalene and/or tocopherol. Other adjuvants are known in the art and can be used in the invention (*see, e.g.* Goding, *Monoclonal Antibodies: Principles and Practice*, 2nd Ed., 1986). Methods for the preparation of mixtures or emulsions of peptide and adjuvant are well known to those of skill in the art of vaccination.

Where cancer associated antigen peptides are used for vaccination, modes of administration which effectively deliver the cancer associated antigen and adjuvant, such that an immune response to the antigen is increased, can be used. For administration of a cancer associated antigen peptide in adjuvant, preferred methods include intradermal, intravenous, intramuscular and subcutaneous administration. Although these are preferred embodiments, the invention is not limited by the particular modes of administration disclosed herein. Standard references in the art (e.g., *Remington's Pharmaceutical Sciences*, 18th edition, 1990) provide modes of administration and formulations for delivery of immunogens with adjuvant or in a non-adjuvant carrier.

When administered, the pharmaceutical preparations of the invention are applied in pharmaceutically-acceptable amounts and in pharmaceutically-acceptable compositions. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the

effectiveness of the biological activity of the active ingredients. Such preparations may routinely contain salts, buffering agents, preservatives, compatible carriers, and optionally other therapeutic agents. When used in medicine, the salts should be pharmaceutically acceptable, but non-pharmaceutically acceptable salts may conveniently be used to prepare pharmaceutically-acceptable salts thereof and are not excluded from the scope of the invention. Such pharmacologically and pharmaceutically-acceptable salts include, but are not limited to, those prepared from the following acids: hydrochloric, hydrobromic, sulfuric, nitric, phosphoric, maleic, acetic, salicylic, citric, formic, malonic, succinic, and the like. Also, pharmaceutically-acceptable salts can be prepared as alkaline metal or alkaline earth salts, such as sodium, potassium or calcium salts.

A breast cancer associated antigen composition may be combined, if desired, with a pharmaceutically-acceptable carrier. The term "pharmaceutically-acceptable carrier" as used herein means one or more compatible solid or liquid fillers, diluents or encapsulating substances which are suitable for administration into a human. The term "carrier" denotes an organic or inorganic ingredient, natural or synthetic, with which the active ingredient is combined to facilitate the application. The components of the pharmaceutical compositions also are capable of being co-mingled with the molecules of the present invention, and with each other, in a manner such that there is no interaction which would substantially impair the desired pharmaceutical efficacy.

The pharmaceutical compositions may contain suitable buffering agents, including: acetic acid in a salt; citric acid in a salt; boric acid in a salt; and phosphoric acid in a salt.

The pharmaceutical compositions also may contain, optionally, suitable preservatives, such as: benzalkonium chloride; chlorobutanol; parabens and thimerosal.

The pharmaceutical compositions may conveniently be presented in unit dosage form and may be prepared by any of the methods well-known in the art of pharmacy. All methods include the step of bringing the active agent into association with a carrier which constitutes one or more accessory ingredients. In general, the compositions are prepared by uniformly and intimately bringing the active compound into association with a liquid carrier, a finely divided solid carrier, or both, and then, if necessary, shaping the product.

Compositions suitable for oral administration may be presented as discrete units, such as

capsules, tablets, lozenges, each containing a predetermined amount of the active compound. Other compositions include suspensions in aqueous liquids or non-aqueous liquids such as a syrup, elixir or an emulsion.

Compositions suitable for parenteral administration conveniently comprise a sterile aqueous or non-aqueous preparation of breast cancer associated antigen polypeptides or nucleic acids, which is preferably isotonic with the blood of the recipient. This preparation may be formulated according to known methods using suitable dispersing or wetting agents and suspending agents. The sterile injectable preparation also may be a sterile injectable solution or suspension in a non-toxic parenterally-acceptable diluent or solvent, for example, as a solution in 1,3-butane diol. Among the acceptable vehicles and solvents that may be employed are water, Ringer's solution, and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose any bland fixed oil may be employed including synthetic mono-or di-glycerides. In addition, fatty acids such as oleic acid may be used in the preparation of injectables. Carrier formulation suitable for oral, subcutaneous, intravenous, intramuscular, etc. administrations can be found in *Remington's Pharmaceutical Sciences*, Mack Publishing Co., Easton, PA.

Examples

Example 1: Preparation of breast cancer cDNA expression libraries

Step 1: Purification of total RNA from tumors.

Total RNA was isolated from tumor samples using the guanidium thiocyanate-phenol-chloroform extraction protocol described by Chomczynski and Sacci (*Anal. Biochem.* 162:156-159, 1987).

Step 2: Purification of mRNA.

A Dynabeads mRNA isolation kit (Dynal, Cat.No. 610.01) was used to isolate mRNA from the pool of total RNA isolated in step 1 above according to the manufacturer's instructions.

Step 3: cDNA synthesis.

cDNA synthesis was performed using a ZAP-cDNA synthesis Kit (Stratagene, La Jolla CA; Cat. No. 200400) according to the manufacturer's protocol. A specific linker-primer which contains a XbaI cloning site was designed and used in this protocol, to facilitate subcloning into TriplEx

vector. The sequence of the primer was:

GAGAGAGAGAGAGAGAGAGAAGTCGACTCTAGATTTTTTTTTTTTTTTTT-Xba 1 site

Step 4: Ligation into the TriplEx vector arms.

The cDNAs generated in step 3 above were ligated into TriplEx vector arms (Clontech, Palo Alto, CA; Cat. No. 6162-1); the arms were predigested with EcoR I/Xba I.

Step 5: Packaging into phages with Gigapack III kit.

The ligation mix (TriplEx/cDNA) from step 4 was packed into phages using the Gigapack III Gold Cloning Kit (Stratagene, Cat. N.200450) according to the protocol supplied with the kit.

Step 6: Titering and amplification of generated libraries was performed accoding to the Stratagene protocols.

The foregoing protocol was used to prepare several libraries from tumor sample of different patients. Some libraries were prepared using the UNI-ZAP XR vector system (Stratagene) according to the manufacturer's protocol, and some using the TriplEx system as described above.

Table 2

UNI-ZAP Libraries		
Code for tumors	Titer of the library	Histopathological diagnosis
HBR173	1.8×10^6 pfu	Ductal Carcinoma, Grade III
HBR184	3.5×10^6 pfu	Invasive Ductal Carcinoma,Grade II
TriplEx libraries		
Code for tumors	Titer of the library	Histopoathological diagnosis
HBR173	2.3×10^6 pfu	Ductal Carcinoma, Grade III
HBR184	1.1×10^6 pfu	Ivasive Ductal Carcinoma, Grade II
HBR257	2.5×10^6 pfu	Invasive Ductal Carcinoma, Grade II
HBR297	4.0×10^6 pfu	Ductal Carcinoma, Grade II
HBR248	1.0×10^6 pfu	Invasive Ductal Carcinoma with Vascular Permeation,Grade III

HBR271	2.5 x 10^6 pfu	Medullary Carcimoma
HBR263	10.0 x 10^6 pfu	Inv. Pleiomorphic Lobular Carcinoma, Grade II

All libraries were screened with the exception of HBR173 (no autologous serum). No serum-positive clones were found by screening HBR271 library.

Example 2: Immunoscreening

Sera was obtained from donors undergoing routine diagnostic and therapeutic procedures. It was stored at - 70°C prior to absorption. Sera, at a dilution of 1:10 in Tris buffered saline (TBS, pH 7.5), was sequentially passed through Sepharose 4B columns which had been coupled to lysates from *E. coli* Y1090 and bacteriophage infected *E. coli* BNN97 (5 Prime 3 Prime, Inc. Boulder, Co.). Final serum dilutions were prepared in 0.2% non-fat dried milk/TBS (NFDM) and stored at 4°C. Library screening was performed as described by Sahin et al.(*Proc. Natl. Acad. Sci. USA* 92:11810-11813, 1995) with following modifications. Recombinant phage at a concentration of 4 x 10^3 per 15 cm plate were amplified for 6 hours and transferred to nitrocellulose membranes for an additional 15 hours at 37°C. Membranes were then blocked with 5% NFDM. As an alternative to generation of IgG subtracted libraries, membranes were pre-screened in a 1:2000 dilution of peroxidase conjugated, Fc fragment specific, goat anti-human IgG (Jackson Immunoresearch Laboratories Inc., West Grove, PA) for 1 hour at room temperature. Color was developed with 3,3' diaminobenzidine tetrahydrochloride and IgG encoding clones were scored. Membranes were then incubated in a 1:100 dilution of absorbed autologous sera for 15 hours at room temperature. Following serum exposure, filters were incubated in a 1:3000 dilution of alkaline phosphatase conjugated, Fc fragment specific, goat anti-human IgG (Jackson Immunoresearch Laboratories Inc.) for 1 hour at room temperature and processed for 4-nitro blue tetrazolium chloride/5-bromo-4-chloro- 3-indolyl-phosphate color development. Serum positive clones were subcloned and retested for serum reactivity as above except nitrocellulose transfer was decreased to 3 hours. For the determination of allogeneic serum reactivity, plates containing an equal number of serum positive clones and negative control plaques were similarly processed less the IgG prescreening steps. A minimum of 5 x 10^5 recombinants were screened per cDNA library, a number

which approximates a point at which the likelihood of repeat isolations of previously identified clones outweigh the prospect of identifying new clones.

Example 3: DNA Sequencing

Phage cDNA clones were converted to pBKCMV phagemid forms by in vivo excision. Plasmid DNA was purified on Qiaprep spin columns (Qiagen Inc. Chatsworth, CA) and subjected to EcoRI/XbaI restriction enzyme digestion. Clones representing different cDNA inserts were ~~sequenced at Cornell University DNA services (Ithaca, NY) using an ABI Prism (Perkin Elmer)~~ automated DNA sequencer. The sequences of the clones were compared with sequences in GenBank and HGI databases to detect homologous nucleic acid and/or protein sequences. The following table lists exemplary related sequences.

Table 3: Sequences Related to Breast Cancer Associated Antigen Clones

Clone	Nucleotide Homology	Clone	Nucleotide Homology	Clone	Nucleotide Homology
LONY-Br-1	L34543	LONY-Br-23	AA262134; U74628	LONY-Br-44	D15057
LONY-Br-2	S75417	LONY-Br-24	AA282633	LONY-Br-45	AB000815
LONY-Br-3	J05211	LONY-Br-25	M62324	LONY-Br-46	L04733
LONY-Br-4	X15187	LONY-Br-26	M99389	LONY-Br-47	X88791
LONY-Br-5	X62083	LONY-Br-27	X79389	LONY-Br-48	AF000430
LONY-Br-6	J04965	LONY-Br-28	D44466	LONY-Br-49	none
LONY-Br-7	D63784	LONY-Br-29	M33197	LONY-Br-50	AA226732
LONY-Br-8	U11292	LONY-Br-30	M17886	LONY-Br-51	AA046574
LONY-Br-9	HSB06D102	LONY-Br-31	L38941	LONY-Br-52	none
LONY-Br-10	none	LONY-Br-32	X17644	LONY-Br-53	AB002307
LONY-Br-11	none	LONY-Br-33	X75342	92	AA127328
LONY-Br-12	AA430998	LONY-Br-33	X75342	101	AA167314
LONY-Br-13	D83032	LONY-Br-34	U43368	102	AA508139
LONY-Br-14	AA034417	LONY-Br-35	X15882	107	none
LONY-Br-15	AA167070	LONY-Br-37	AA121558	109	AA220229

LONY-Br-16	none	LONY-Br-38	AA211771	110	W67775
LONY-Br-17	AA161103	LONY-Br-39	AA367417	111	AA280070
LONY-Br-19	R13835	LONY-Br-40	AA188052	112	AF004292
LONY-Br-20	HUMORF003	LONY-Br-41	THC83518	131	none
LONY-Br-21	S74572	LONY-Br-42	none	143	AA481578
LONY-Br-22	AA070233	LONY-Br-43	HU35246	162	AA481578

Example 4: Reverse transcriptase (RT) PCR and Rapid Amplification of cDNA Ends (RACE)

The mRNA expression pattern of selected cDNA clones was determined by RT- PCR using a panel of normal tissue RNA. This test panel consisted of lung, testis, small intestine, colon, breast, liver, and placenta, and was purchased from Clontech Laboratories Inc. (Palo Alto, CA). Colon tumor RNA was also included in this panel and was prepared as described above. As a control for genomic DNA contamination, all cDNA synthesis reactions were set up in duplicate with the additional sample lacking reverse transcriptase. Gene specific PCR primers were designed to amplify 5' fragments of 300-400 bp and were purchased commercially (Gibco BRL, Grand Island, NY). PCR reactions were undertaken at an annealing temperature of 68°C using a Perkin Elmer thermal cycler. In certain cases, RT-PCR products were subcloned into the pCR2.1 plasmid vector (Invitrogen) and multiple clones were subjected to DNA sequencing as described. 5' and 3' RACE reactions were undertaken using gene specific and adapter primers in conjunction with Marathon Ready normal colon cDNA and KlenTaq polymerase (Clontech) as per manufacturers protocol. Products were then subcloned into the pCR2.1 plasmid vector (Invitrogen) and screened by PCR with internal primers for presence of the desired insert. Multiple RACE clones were subjected to DNA sequencing as described.

Example 5: Northern blot analysis

Northern blots containing the transfer yields of 2 μg poly A^+ RNA from a panel of normal tissues were obtained commercially (Clontech). Random primed ^{32}P labeled probes consisting of 300-600 bp PCR products from 5 prime coding sequences of serum positive cDNA clones were hybridized for 1.5 hours in Expresshyb (Clontech) at 68°C and washed at high stringency (2 times,

30 min. each, 0.1X SSC/0.1% SDS at 68°C). Resultant blots were used to expose Biomax MS autoradiography film (Eastman Kodak Co., Rochester, NY).

Table 4: Breast Cancer Associated Antigen Clone mRNA sizes

Clone	Size (kb)	Clone	Size (kb)	Clone	Size (kb)
LONY-Br-1	1.8	LONY-Br-17	1.0	LONY-Br-33	2.6
LONY-Br-2	2.9	LONY-Br-19	1.5	LONY-Br-34	2.1
LONY-Br-3	4.8	LONY-Br-20	2.4	LONY-Br-35	1.9
LONY-Br-4	1.2	LONY-Br-21	2.4	LONY-Br-36	0.8
LONY-Br-5	0.9	LONY-Br-22	1.6	LONY-Br-37	1.0
LONY-Br-6	1.4	LONY-Br-23	1.3	LONY-Br-38	2.2
LONY-Br-7	1.3	LONY-Br-24	3.9	LONY-Br-39	1.9
LONY-Br-8	0.9	LONY-Br-25	1.9	LONY-Br-40	3.4
LONY-Br-9	6.0	LONY-Br-26	1.5	LONY-Br-41	3.9
LONY-Br-10	3.6	LONY-Br-27	1.2	LONY-Br-42	0.6
LONY-Br-11	4.6	LONY-Br-28	0.5	LONY-Br-43	1.4
LONY-Br-12	2.2	LONY-Br-29	0.6	LONY-Br-44	0.7
LONY-Br-13	1.2	LONY-Br-30	0.8	LONY-Br-45	3.0
LONY-Br-14	0.8	LONY-Br-31	0.4	LONY-Br-46	3.7
LONY-Br-15	0.9	LONY-Br-32	2.2	LONY-Br-47	0.5
LONY-Br-16	2.5	LONY-Br-33	2.6	LONY-Br-48	1.6

Example 6: Isolation of gastric and prostate clones

A stomach cancer cDNA library was established, using standard techniques, then the library was screened, using the SEREX methodology described supra, and set forth by Sahin et al., *Proc. Natl. Acad. Sci. USA* 92: 11810 (1995), and by Chen et al., *Proc. Natl. Acad. Sci. USA* 94: 1914 (1997), incorporated by reference in their entirety.

To be specific, total RNA was isolated by homogenizing tumor samples in 4M guanidium thiocyanate/0.5% sodium N-lauryl sarcosine/ and 25 mM EDTA followed by centrifugation in 5.7 M CsCl/25 mM sodium acetate/10 uM EDTA at 320,000 rpm. Total mRNA was removed by passing the sample over an oligo-dT cellulose column. The cDNA libraries were then constructed

by taking 5 ug of mRNA, using standard methodologies to reverse transcribe the material.

Libraries were prepared from four different stomach cancer patients, referred to as "SM", "CK" and "SS" and "KM" respectively. A total of $2.5x10^6$, $1.1x10^6$, and $1.7x10^6$ cDNA clones were obtained from the "SM", "CK" and "SS" individuals. Additional libraries were prepared from prostate cancer patient "OT".

The cDNA was used to construct a lambda phage library, and 500 phages were plated onto XL1-Blue MRF E. coli, and incubated for eight hours at 37°C. A nitrocellulose membrane was then placed on the plate, followed by overnight incubation. The membrane was then washed, four times, without TBS which contained 0.05% Tween, and was then immersed in TBS containing 5% non-fat dried milk. After one hour, the membrane was incubated with conjugates of peroxidase-goat anti human IgG specific for Fc portions of huma antibody (1:2000, diluted in TBS with 1% BSA. The incubation was carried out for one hour, at room temperature, and the membrane was then washed three times with TBS. Those clones which produced antibodies were visualized with 0.06%, 3,3'diamino benzidine tetrachloride, and 0.015% H_2O_2, in 50 mM Tris (pH 7.5). Any clones which produced immunoglobulin were marked, and then the membrane was washed, two further times, with TBS that contained 0.05% Tween, and then twice with "neat" TBS.

The membranes were then incubated in 1:100 diluted patient serum, overnight, at 4°C. The patient serum had been pretreated. Specifically, 5 ml samples were diluted to 10 ml with TBS containing 1% bovine serum albumin, and 0.02% Na_3N. The serum had been treated to remove antibodies to bacteriophage, by passing it through a 5 ml Sepharose column, to which a lysate of E. coli Y1090 had been attached, followed by passage over a second column which had E. coli lysate and lysate of E. coli infected with lambda bacteriophage. The screening was carried out five time. The samples were then diluted to 50 ml, and kept at -80°C, until used as described herein.

Following the overnight incubation with the membrane, the membrane was washed twice with TBS/0.05% Tween 20, and then once with TBS. A further incubation was carried out, using the protocols discussed supra, for the POD labelled antibodies.

The positive clones were then sequenced, using standard techniques. Following comparison of the sequences to information available in data banks, a total of 36 clones were resolved into known and unknown genes. In the table that follows, the "+" and "-" signs are essentially used to compare signals to each other. All were positive. Table 5, which follows, summarizes some of this

work isolation and sequencing of "SM" clones. Specifically, with reference to the first page of the table, previously identified human proteins and the nucleotide sequences, set forth in SEQ ID NOS:588-626 are known. The four molecules which follow in SEQ ID NOs:627-634 (gelsolin, zinc finger protein family, variant zinc finger motif protein goliath and homeodomain proteins), have not been identified in humans previously, although there are related molecules found in other species. Finally, with reference to Table 5, the last four moieties, i.e., prepro-α collagen, heterogeneous ribonucleoprotein D, nucleosome assembly protein 2, and NY-ESO-2/Ulsn NRP/V1 small nuclear ribonucleoprotein, are also known. Nucleotide sequences are set forth at SEQ ID NOS:635-642. The nucleic acid molecules having the nucleotide sequences set forth at SEQ ID NOS:643-670 represent molecules for which no related sequences were found. SEQ ID NO:671 combines the sequences of SEQ ID NOS:627-630, inclusive. SEQ ID NO:672 combines SEQ ID NOS:643-656, SEQ ID NO:673 combines SEQ ID NOS:657, 659 and 662, while SEQ ID NO:674 combines SEQ ID NOS: 658, 660, 661 and 663.

SEREX analysis of clones from libraries derived from patients "CK", "SS", "KM" (all gastric cancer) and patient "OT" (prostate cancer) was carried out as described above. The nucleotide sequences of clones derived from gastric cancer patients are presented as SEQ ID NOs:176-436. The nucleotide sequences of clones derived from prostate cancer patient "OT" are presented as SEQ ID Nos:437-543.

Example 7:Isolation and analysis of colon clones

Colon tumor samples were obtained as surgical samples, and were frozen at -80°C until ready for use.

Total RNA was then isolated from the samples, using the guanidium thiocyanate method of Chirgwin, et al., *Biochemistry* 18: 5294-5299 (1979), incorporated by reference. The total RNA thus obtained was then purified to isolate all poly A^+ RNA, using commercially available products designed for this purpose.

The poly A^+ RNA was then converted into cDNA, and ligated into λZAP, a commercially available expression vector, according to the manufacturer's suggested protocol.

Three cDNA libraries were constructed in this way, using colorectal carcinoma samples. A fourth library, also from colorectal carcinoma, was prepared, albeit in a different way. The

fourth library was an IgG subtraction library, prepared by using a subtraction partner, generated by PCR amplification of a cDNA clone which encoded an IgG molecule. *See, e.g.*, Ace et al, *Endocrinology* 134: 1305-1309 (1994), and incorporated by reference in its entirety. IgG subtraction is done to eliminate any false, positive signals resulting from interaction of cDNA clones which encode IgG, with the IgG then interacting with the anti-human IgG used in the SEREX assay, as described herein. PCR products were biotinylated, and hybridized with denatured second strand cDNA, at 68°C for 18 hours. Biotinylated hybrid molecules were coupled to streptavidin, and then removed by phenol chloroform extraction. Any remaining cDNA was also ligated into λZAP. All libraries were amplified, prior to immunoscreening.

Immunoscreening was carried out using sera obtained from patients undergoing routine diagnostic and therapeutic procedures. The sera were stored at -70°C prior to use. Upon thawing, the sera were diluted at 1:10 in Tris buffered saline (pH 7.5), and were then passed through Sepharose 4B columns. First, the sera were passed through columns which had E. coli Y1090 lysates coupled thereto, and then lysates from bacteriophage infected E. coli BNN97 lysates. Final serum dilutions were then prepared in 0.2% non-fat dried milk/Tris buffered saline.

The method of Sahin et al., *Proc. Natl. Acad. Sci. USA* 92:11810-11813 (1995), and U.S. Patent No. 5,698,396, both of which are incorporated by reference, was used, with some modifications. Specifically, recombinant phages at a concentration of $4x10^3$ phages per 15 cm plate (pfus), were amplified for six hours, after which they were transferred to nitrocellulose membranes for 15 hours. The membranes then were blocked with 5% nonfat dried milk.

As an alternative to the IgG subtraction procedure discussed above, membranes were prescreened in a 1:2000 dilution of peroxidase conjugated, Fc fragment specific goat anti-human IgG, for one hour, at room temperature. Color was developed using 3,3'-diaminobenzidine tetrahydrochloride, which permitted scoring of IgG encoding clones.

Membranes were then incubated in 1:100 dilutions of autologous sera, which had been pretreated with the Sepharose 4B columns, as described supra. The filters were then incubated, in a 1:3000 dilution of alkaline phosphatase conjugated Fc fragment specific, goat anti-human IgG, for one hour, at room temperature. The indicator system 4-nitroblue tetrazolium chloride/5-bromo-4-chloro-3-indolyl-phosphate was then added, and color development assessed. Any positive clones were subcloned, and retested, except the time on the nitrocellulose membrane was reduced to three

hours.

Positive clones were isolated and sequenced according to standard procedures. The nucleotide sequences of the clones are set forth in the even numbered sequences from SEQ ID Nos:544-586. The odd numbered sequences from SEQ ID Nos:545-587 represent the translated amino acid sequences of the colon nucleic acid clones. Analysis of probes for SEQ ID NOS:544 and 546 confirmed their universal expression.

The foregoing results reflect SEREX isolation of colon cancer clones using autologous serum. ~~The positive clones were then rescreened, using allogeneic serum, following the same~~ method discussed supra, in example 2, except IgG prescreening was omitted. The allogeneic sera was obtained from sixteen normal blood donors, and twenty nine patients who had been diagnosed with colorectal cancer.

The analysis with the two types of serum revealed that fourteen reacted with a subset of sera from normal and cancer patients, twenty-eight only with autologous sera, and six with both allogeneic and autologous sera. Over 60% of the allogeneic serum samples tested reacted with at least one of these positive clones. About 20% reacted with two or more.

In view of the results described above, further experiments were carried out using serum samples from patients with other forms of cancer, i.e., renal cancer (13 samples), lung cancer (23 samples), and breast cancer (10 samples). The results are set forth in Table 6 which follows:

Table 6: Allogeneic serotyping using colon cancer clones

Clone Number	Normal Sera	Colon Cancer	Renal Cancer	Lung Cancer	Breast Cancer
NY-Co-8	0/16	8/29	1/13	0/23	0/10
NY-Co-9	0/16	5/29	1/13	1/23	0/10
NY-Co-13	0/16	5/29	0/13	0/23	0/10
NY-Co-16	0/16	3/29	0/13	0/23	0/10
NY-Co-20	0/16	4/29	0/13	0/23	0/10
NY-Co-38	0/16	4/29	3/13	0/23	1/10

Of the six clones which were identified as being reactive with autologous and allogeneic

cancer serum, and not with normal serum, two were found to be identical to previously identified molecules (NY-Co-. Four others were found to have little or no homology to known sequences and thus are preferred allogeneic-reactive colon cancer clones. These nucleic acids and their polypeptide translations are presented as SEQ ID NOS: 544-551: SEQ ID NO: 544/545 (NY-CO-8), SEQ ID NO: 546/547 (NY-CO-9), SEQ ID NO: 548/549 (NY-CO-16) and SEQ ID NO: 550/551 (NY-CO-38). . Of twenty seven allogeneic colon cancer serum samples tested, 67% reacted with at least one of these antigens.

~~The expression pattern of mRNA corresponding to SEQ ID NOS:544, 546 and 550, as~~ well as other sequences identified via the preceding examples was determined. To do this, RT-PCR was carried out on a panel of RNA samples, taken from normal tissue. The panel contained RNA of lung, testis, small intestine, colon, breast, liver and placenta tissues. The RNA was purchased from a commercial source. RNA from a colon tumor sample was also included. All samples were set up for duplicate runs, so that genomic DNA contamination could be accounted for. In the controls, no reverse transcriptase was used.

Primers were designed which were specific for the cDNA, which would amplify 5'-fragments, from 300-400 base pairs in length. The PCR reactions were undertaken at an annealing temperature of 68°C. Where appropriate, 5' and 3'-RACE reactions were undertaken, using gene specific primers, and adapter primers, together with commercially available reagents. Specifically, SEQ ID NOS: 546 and 550 were tested using RACE. The resulting products were subcloned into vector pCR 2.1, screened via PCR using internal primers, and then sequenced.

SEQ ID NOS:544 and 546 were found to be amplified in all tissues tested. SEQ ID NO:550 was found in colon tumor, colon metastasis, gastric cancer, renal cancer and colon cancer cell lines Colo 204 and HT29, as well as in normal colon, small intestine, brain, stomach, testis, pancreas, liver, lung, heart, fetal brain, mammary gland, bladder, adrenal gland tissues. It is was not found in normal uterine, skeletal muscle, peripheral blood lymphocytes, placental, spleen thymus, or esophagus tissue, nor in lung cancer.

The analysis also identified differential expression of a splice variant of SEQ ID NO:550, i.e., SEQ ID NO:552. When the two sequences were compared, it was found that SEQ ID NO:550 encodes a putative protein of 652 amino acids (SEQ ID NO:551), and molecular weight of 73,337 daltons. SEQ ID NO:552, in contrast, lacks an internal 74 base pairs, corresponding to

nucleotides 1307-1380 of SEQ ID NO:550. The deletion results in formation of a stop codon at the splice function, and a putative protein of 403 amino acids (SEQ ID NO:553), and molecular weight 45,839. The missing segment results in the putative protein lacking a PEST protein degradation sequence, thereby suggesting a longer half life for this protein.

In additional experiments, primers designed not to differentiate between SEQ ID NOS: 550 and 552 resulted in almost universal amplification (placenta being the only exception). In contrast, when primers specific for SEQ ID NO:552 were used differences were seen in normal pancreatic, liver, lung, heart, fetal brain, mammary gland, bladder, and adrenal gland tissue, where there was no expression of SEQ ID NO:552 found.

Northern blotting was also carried out for SEQ ID NOS: 544, 546, 550 and 552. These experiments employed the same commercially available RNA libraries discussed above were used.

Samples (2 ug) of polyA$^+$ RNA were analyzed from these samples, using random, ^{32}P labelled probes 300-360 nucleotides in length, obtained from PCR products. These probes were hybridized to the RNA, for 1.5 hours, at 68°C, followed by two washes at 0.1xSSC, 0.1% SDS, 68°C, for 30 minutes each time.

SEQ ID NOs:544 and 546 were again found to be universally expressed.

Further screening identified additional isoforms of SEQ ID NOS:544 and 550. These are set forth as SEQ ID NOS: 554, 556, 558 and 560. The isoform represented by SEQ ID NO:554 (translated as SEQ ID NO:555) is a naturally occurring splice variant of SEQ ID NO:544, found in normal colon. SEQ ID NO:556 (translated as SEQ ID NO:557), which is an isoform of SEQ ID NO:550 (translated as SEQ ID NO:551), was found in brain tissue, primarily spinal chord and medulla. SEQ ID NO:558 (translated as SEQ ID NO:559), was found in normal kidney and in colon tumors, metastasized colon cancer, renal cancer, gastric cancer, and in colon cancer cell line Colo 205. It was not found in any normal tissue other than kidney.

The nucleic acid molecule whose nucleotide sequence set forth as SEQ ID NO:560 (translated as SEQ ID NO:561), is a further isoform of SEQ ID NO:552. It is similar to SEQ ID NO:558, except it contains a long nucleotide insert encoding a longer COOH terminus. It was expressed in normal bladder and kidney cells, and renal cancer cells. It was not expressed in colon cancer cells.

It is reported above that fourteen clones reacted with subsets of serum from both normal

and cancer patients, while twenty eight reacted with autologous sera only. These clones were sequenced, in accordance with standard, art recognized methods. Of the clones which reacted only with autologous sera, nine appear to be previously unidentified sequences. These are set forth as SEQ ID NOS: 562, 564, 566, 568, 570, 572, 574, 576 and 578. SEQ ID NO:562 (translated as SEQ ID NO:563) is 1445 nucleotides long, and shows some similarity to known sequences for myosin and tropomyosin. SEQ ID NO:564 (translated as SEQ ID NO:565), which is 1226 nucleotides long, contains a TPR motif. The sequence set forth in SEQ ID NO:566 (translated as SEQ ID NO:567) is 1857 nucleotides long, and shows similarity to cyclophillins. The nucleotide sequence set forth in SEQ ID NO:568 (translated as SEQ ID NO:569) is 1537 nucleotides long, and shows similarity to murine gene 22A3, which has unknown function, but resembles an unconventional form of myosin, as well as an EST for heat shock inducible mRNA. As for the molecule set forth in SEQ ID NO:570 (translated as SEQ ID NO:571), it appears to resemble a nucleic targeting signal protein. SEQ ID NO: 572 (translated as SEQ ID NO:573) is 604 nucleotides long, and may encode a lysosymal protein. The molecule set forth in SEQ ID NO:574 (translated as SEQ ID NO:575) is 742 nucleotides long, and encodes a protein with an SH3 domain and which shows some similarity to GRB2 and human neutrophil oxidase factor. The molecule set forth in SEQ ID NO:576 (translated as SEQ ID NO:577) is 1087 nucleotides long, and encodes a protein which contains coiled core domains. The molecule set forth in SEQ ID NO:578 (translated as SEQ ID NO:579) is 2569 nucleotides long, shows some similarity with Drosophila homeotic material tudor protein, and has a DY(F)GN repeat.

Additional sequences were identified which were expressed in both normal sera and cancer cells. The sequence set forth in SEQ ID NO:580 (translated as SEQ ID NO:581), e.g., is 2077 nucleotides long, and was expressed by both colorectal cancer and normal cells. Analysis of the sequence showed that it possesses a nuclear targeting sequence. The molecule set forth in SEQ ID NO:582 (translated as SEQ ID NO:583) is 3309 nucleotides long, was expressed by colorectal cancer and normal cells, and is similar to heat shock protein 110 family members. The molecule presented in SEQ ID NO:584 (translated as SEQ ID NO:585) was expressed in a colon to lung metastasis, as well as by normal tissue. It is 2918 nucleotides in length. Analysis shows that it contains 2 zinc finger domains. The nucleotide sequence of SEQ ID NO:586 (translated as SEQ ID NO:587) was also expressed in a colon to lung metastasis, is 1898 nucleotides long, and is

also expressed by normal tissue. Specifically, the reactivity of the molecules was as follows:

Table 7

SEQ ID NO:	Normal Sera Reactivity	Tumor Sera Reactivity
580	2/16	2/16
582	2/16	3/16
584	2/16	2/16
586	2/8	1/16

A more extensive set of RT-PCR experiments were carried out to study the expression pattern of SEQ ID NOS: 550, 552, 558 and 560. The results follow.

Table 8: RT-PCR analysis of colon SEREX clones

normal tissue	SEQ ID NO.:550	SEQ ID NO.:552	SEQ ID NO.:558	SEQ ID NO.:560
kidney	+	Negative	Negative	Negative
colon	+	Negative	Negative	Negative
small		Negative	Negative	Negative
intest.	+	Negative	Negative	Negative
brain	+	Negative	Negative	Negative
stomach	+	Negative	Negative	Negative
testis	+	Negative	Negative	Negative
pancreas	+	Negative	Negative	Negative
lung	+	Negative	Negative	Negative
liver	+	Negative	Negative	Negative
heart	+	Negative	Negative	Negative
fetal		Negative	Negative	Negative
brain	+	Negative	Negative	Negative
mammary		Negative	Negative	Negative
gland	+	Negative	Negative	Negative
bladder	+	Negative	Negative	Negative
adrenal		Negative	Negative	Negative
gland	+	Negative	Negative	Negative
uterus	Negative	Negative	Negative	Negative
skeletal		Negative	Negative	Negative
muscle	Negative	Negative	Negative	Negative
PBL	Negative	Negative	Negative	Negative
placenta	Negative	Negative	Negative	Negative

spleen	Negative	Negative	Negative	Negative
thymus	Negative	Negative	Negative	Negative
esophagus	Negative	Negative	Negative	Negative
<u>Tumor Tissue</u>				
renal cancer (4)	+ (2/4)	+ (2/4)	+ (2/4)	+ (2/4)
colon primary tumors (10)	+ (10/10)	+ (10/10)	+(10/10)	Negative
colon mets (4)	+ (4/4)	+ (4/4)	+ (4/4)	Negative
breast cancer (6)	+ (3/6)	Negative	Negative	Negative
lung cancer (6)	+ (6/6)	Negative	Negative	Negative
gastric cancer (1)	+	+	+	Not tested
<u>colon cancer cell lines</u>				
colo 205	+	+	+	Negative
HT29	+	+	Negative	Negative
HCT15	Negative	Negative	Negative	Negative

Example 8: Isolation and analysis of additional clones

For the establishment of a cDNA library from human tissue total RNA was obtained from 0.5 g of a renal clear cell carcinoma and established according to the method of Chomzynski as described above. The mRNA was extracted from total RNA with oligo-dT-cellulose. The synthesis of the first strand cDNA was accomplished by the method described by Gubler and Hoffmann, *Gene* 25: 263 (1983) using RNase H and DNA polymerase I. For adaptation of the cDNA Klenow enzyme, adaptors with EcoRI restriction enzyme sites were ligated to the cDNA ends using T4 DNA ligase (Ferretti L and Sgamerella V, *Nucl. Acids Res.* 9: 3695 (1981)). Following restriction enzymatic digestion with the enzyme XhoI, cDNA molecules of different length were separated using Sephacryl 400 and transfected into λZAPII phage vectors (Short JM et al., *Nucleic Acids Res.* 16: 7583 (1988)). The recombinant phage DNA was packaged into phages after ligation with packaging extracts and used for the transfection of *E. coli* bacteria. The titration of the library resulted in 1.8 x 10^6 recombinant primary clones. The total cDNA library was transfected in *E. coli* and amplified. The titer of the cDNA library after amplification was 10^{11} plaque forming units per ml (pfu/ml). These transfected cells were used in experiments which follow.

In accordance with the invention as described above, identification of immunogenic material was achieved by using human sera which has been completely depleted of antibodies directed against antigens derived from native and lytic λ phage-transfected *E. coli* bacteria. To this end, the serum was absorbed, as follows.

E. coli bacteria of the strain XL1-blue were cultured in 50 ml LB medium overnight. After achieving an optical density of $OD_{600} = 1.0$, the bacteria were pelleted by centrifugation, resuspended in 5 ml phosphate buffered saline (PBS), and lysed by sonication. The bacterial lysate was bound onto a matrix of activated Sepharose, which was then put into a column and used for the absorption of the human serum. The serum was run over this column 10 times.

A culture of *E. coli* XL1 blue bacteria in the exponential growth phase was pelleted by centrifugation, transfected in 0.01 M magnesium sulfate with 10^6 λZAPII phages without a recombinant insert and incubated in 5 ml LB medium for four hours. The lysate of the transfected bacteria was used in the same manner as the untransfected bacteria, with the human serum described supra being passed through the column an addition ten times.

To complete the depletion of the serum, interfering antibodies from lytically transfected *E. coli* bacteria were cultured on agar plates and their proteins were blotted onto nitrocellulose membranes after 10 hours of culture at 37°C. Following this, the serum which had been preabsorbed according to the above steps was transferred to the blotted nitrocellulose membrane, and the absorption procedure was repeated five times. The serum, which was processed in accordance with the invention, was totally depleted of antibodies directed against antigens derived from *E. coli* and phages.

In this, a renal cancer-specific antigen was identified via the following steps. Bacteria of the strain XL1 blue were transfected with recombinant phages derived from the described cDNA library and plated at a density of 4-5x10^3 plaque forming units (pfu) per plate in LB-medium with isopropylthiogalactopyranoside ("IPTG"). After 12 hours of incubation at 37°C, nitrocellulose membranes were put on top of the cultures and culture plates were incubated for another four hours. This was followed by incubation of the nitrocellulose membrane for one hour in Tris-buffered saline (PBS) with 5% milk powder. After washing the nitrocellulose membranes three times in TBS, the stripped human serum secured following Example 2 was diluted 1:1000 in TBS/0.5% (w/v) milk power and incubated overnight with gentle shaking. After the incubation with the nitrocellulose

membrane the serum was removed and kept for additional testing. Following incubation with serum, the nitrocellulose membranes were washed three times in TBS, and incubated with a polyclonal alkaline phosphatase-conjugated goat anti-human IgG serum for one hour. Following this, the nitrocellulose membranes were washed repeatedly with TBS/0.01% (v/v Tween 20). The reaction was developed using nitroblue tetrazolium chloride and bromochloro-indoyl-phosphate in TBS. The binding of human antibodies to the expressed protein became visible by a blue ring-formed color deposit on the nitro-cellulose membrane. The efficient preabsorption of the serum made in possible to develop the membrane at 37°C over several hours without compromising the quality of the test because of background reactivity caused by antibodies against *E. coli* and phage antigens.

Positive clones were localized on the agar plates, transferred into transfection buffer, and used for a second round of transfection and subcloning. A total of 1.8×10^6 recombinant clones were subjected to screening and five different positive-reacting clones were identified.

Positive clones, i.e., those which had bound antibodies derived from the processed human serum, were subcloned to monoclonality by repeated rounds of transfection and testing of reactivity with the processed human serum. P-bluescript phagemids with the respective cDNA inserts were cloned by in vivo excision (Hay B and Short JM, *Strategies* 5: 16-19, 1992) from the λZAPII phage vectors and used for the transfection of E. coli SOLR bacteria. Plasmids were isolated from the bacteria after alkaline lysis with NaOH in a modification of the method of Birnboim HC and Doly J. *J. Nucl. Acids Res.* 7: 1513 (1979). The recombinant plasmid DNA was sequenced according to standard methods using M13-forward and M13-reverse oligonucleotides. The DNA sequence obtained and the resulting amino acid sequence were compared with nucleic acid and protein data banks (Gene Bank, EMBL, Swiss Prot). The sequencing of the cDNA inserts was continued using internal oligonucleotides. Analysis showed no homology with any sequences deposited in the data banks. The full length cDNA clone, referred to as SK313, was cloned with the RACE method (Frohman MA, Dush MK, Martin GR, *Proc. Natl. Acad Sci. USA* 85: 8998 (1988)), and had a carbonic anhydrase domain at the 5' end.

As a continuation of these experiments, RNA was isolated from a spectrum of malignant and normal human tissues and Northern blots were performed with labeled SK313 (also referred to as clone HOM-RCC-313). The Norther blot analysis demonstrated that the mRNA of clone HOM-

RCC-313 was overexpressed in 4 out of 19 renal cell carcinomas compared to normal kidneys. Very weak expression was found only in colonic mucosal tissue and in normal kidney. Expression in other tissues was not observed.

To determine the incidence of antibodies against antigens which are identified above, allogeneic sera from healthy individuals and tumor patients were analyzed. To this end, the sera were processed as described above and depleted from antibodies against antigens derived from *E. coli* and phages. For the detection of antigen-specific antibodies, phages derived from reactive clones were mixed with non-reactive phages derived from the same cDNA library at a ratio of 1:10 and tested as described above for reactivity with antibodies in the human test serum. The serum which had been used for the identification of the antigen was used as a positive control. The non-reactive phages served as a negative control. A serum sample was positive for antigen reactive antibodies, if the expected percentage of the phage plaques showed a positive reaction. In the case of the renal cell carcinoma antigen represented by clone HOM-RCC-313, the analysis of a spectrum of human sera showed that only sera from renal cell carcinoma patients contained reactive antibodies. Sera from healthy controls and patients with other tumors did not contain such antibodies.

The cDNA for clone HOM-RCC-313 was excised from the plasmid DNA by digestion with the restriction enzyme EcoR1, was separated by agarose gel electrophoresis, followed by extraction from the gel. This was then used to create a vector which expresses a fusion protein with the bacterial protein anthranilate synthetase. A relevant fragment in the exact open reading frame was cloned into pATH plasmid vectors (Koerner et al., *Meth. Enzymol.* 194: 477 (1991)). Induction of protein expression was obtained after transformation of the plasmids into E. coli of strain BL21 as described (Spindleret al., *J. Virol.* 49: 132 (1984)). Expressed fusion proteins were separated by SDS gel electrophoresis, excised from the gel, eluted and freeze dried. Rabbits were immunized by subcutaneous injection with 100 µg of the lyophilisate combined with Freund's adjuvant according to standard procedures. Immunization was repeated three times at two-week intervals using incomplete Freund's adjuvant. The rabbit was bled and antiserum was obtained. The obtained antiserum was depleted from antibodies reactive with E. coli and phages as described above and tested for reactivity against the renal carcinoma antigen as described for the human serum. Reactivity was detected at dilutions of 1: >100,000.

Additional clones were identified from pancreatic cancer tumor specimen using the SEREX method of Sahin et al., (1995). A cDNA library was prepared and reacted with high titer IgG in sera of pancreatic carcinoma patients. A total of $8x10^5$ clones were screened with autologous serum, and $4.5x10^3$ clones were screened with three different allogeneic sera. Twenty three clones, representing seven different transcripts were found. Four were previously unknown, unisolated genes. Of the remaining three, glycolytic enzyme aldolase A was found (SEQ ID Nos:799 and 800). Another molecule was "known" in that it was homologous to the rat eIF-5 gene (SEQ ID Nos:801 and 802), which is a eukaryotic translation initiation factor. The human eIF-5 gene was not previously known.

When hepatocelullar carcinoma libraries were studied in the same way, a total of $1.5x10^6$ clones were screened, and 98 positives were found. A total of 59 of these were sequenced, and corresponded to at least 20 different transcripts. Nine of these were assayed with allogeneic sera from hepatocellular cancer (HCC) patients and normal patients. High titered antibody was restricted to HCC patients. The majority of isolated sequences did not correspond to known molecules. Three which did were human albumin (SEQ ID Nos:803 and 804), senescence marker protein SMP30 (SEQ ID NOs:805 and 806), and C3VS (SEQ ID NOs:807 and 808). The latter was overexpressed in 2 of 4 hepatocarcinoma tissues, as compared to normal. Expression of SMP30 was found to vary highly.

The methodology was combined with subtractive cDNA techniques when assaying leukemia cells (T-ALL). An antigen was found which was identical to a broadly expressed, DNA repair enzyme.

Further assays identified the known molecule galectin-9 (SEQ ID NOs:809 and 810), as being highly expressed on human macrophages and dendritic cells. Expression is upregulated during differentiation of monocytes to macrophages. Highest levels were found on monocyte derived, dendritic cells.

Fusion proteins "LD1-mFc" and "LD2-mFc" were constructed to help analyze galectin-9. These consist of murine IgG heavy chain fragments, and a lectin domain (LD1, or LD2), as the N-terminus. Analysis indicated that the C-terminal lectin domain binds to the surface ligands, while the cell surface ligands recognized by the C-terminal lectin domain of galactin-9 was expressed only in a small, subpopulation of dendritic cells.

Further analysis of ovarian cancer cells (500,000 clones, using the SEREX method described

above), identified previously known antigens MAGE-4 (SEQ ID Nos:811 and 812) and restin (SEQ ID Nos:813 and 814), and six other newly identified molecules.

Further experiments were carried out which involved restin. A variation of restin is known, i.e., "CLIP170", which was reported to mediate binding of endosomes to microlubules. It was found that both resin and CLIP 170 are highly expressed in dendritic cells, and are involved in the formation and transport of macropinosomes, a feature of professional antigen presenting cells. Expression of restin was induced after 48 hours of culture of monocytes in GM-CSF/IL-4 supplemented medium. Highest levels were found in immature dendritic cells. When microlubile systems, which are essential for the activity of restin/CLIP-170 were disrupted, macropinocytosis was lost completely.

Further work with the methodology disclosed herein on glioma identified a clone encoding nm23-H2 protein (SEQ ID Nos:815 and 816). This clone corresponds to subunit B of nucleoside diphosphate kinase, which is implicated in tumor metastasis control. It is also known as PuF, a transcriptional factor, for c-myc proto-oncogenes. Antibodies against the protein were found in 1 of 18 sera of brain malignancy patients, 3 of 20 melanoma patients, and 2 of 20 sera from healthy patients. When expression studies were carried out using RT-PCR, 25 of 28 brain tumor, and 4 or 5 mengioma tumor samples were found to express the gene.

Example 9:Isolation and analysis of lung cancer clones

A cDNA library was constructed from a case of moderately differentiated adenocarcinoma of the lung, obtained from the Department of Pathology at The New York Hospital. The library was constructed in a λZAP Express vector using a cDNA library kit (Stratagene, La Jolla, CA).

The cDNA library was screened with autologous patient's serum as described previously [Sahin, U. et al., *Proc Natl Acad Sci USA* 92:11810-3 (1995); Chen, Y.T. et al. *Proc Natl Acad Sci USA*. 94:1914-8 (1997)]. Briefly, the serum was diluted 1:10, pre-absorbed with transfected *E. coli* lysate, and a 1:10 dilution of the absorbed serum (final dilution of serum 1:100) was incubated overnight at room temperature with the nitrocellulose membranes containing the phage plaques. After washing, the filters were incubated with alkaline phosphatase-conjugated goat anti-human Fc γ secondary antibodies and the reactive phage plaques were visualized by incubating with 5-bromo-4-chloro-3-indolyl-phosphate and nitroblue tetrazolium. Phagemid clones encoding human

immunoglobulin sequences were subsequently eliminated during the secondary screening.

The reactive clones were subcloned, purified, and *in vitro* excised to pBK-CMV plasmid forms (Stratagene). Plasmid DNA was prepared using Wizard Miniprep DNA Purification System (Promega, Madison, WI). The inserted DNA was evaluated by EcoRI-XbaI restriction mapping, and clones representing different cDNA inserts were sequenced. The sequencing reactions were performed by DNA Services at Cornell University (Ithaca, NY) using ABI PRISM (Perkin Elmer) automated sequencers.

To evaluate the mRNA expression pattern of the cloned cDNA in normal and malignant tissues, gene-specific oligonucleotide primers for PCR were designed to amplify cDNA segments of 300-400bp in length, with the estimated primer melting temperature in the range of 65-70°C. All primers were commercially synthesized (Operon Technologies, Alameda, CA). RT-PCR were performed using 35 amplification cycles in a thermal cycler (Perkin Elmer) at an annealing temperature of 60°C.

Genomic DNA were extracted from cell lines and frozen tumor tissue. Following restriction enzyme digestion, the DNA was separated on a 0.7% agarose gel, blotted onto nitrocellulose filters, and hybridized to an $\alpha^{32}P$-labeled DNA probe at high stringency (65°C, aqueous buffer). Washing of the blot was also under high stringency conditions, with a final wash in 0.2XSSC with 0.2% SDS at 65°C.

To identify the 5'end of the mRNA transcripts, RACE (rapid amplification of cDNA ends) methodology was utilized using the Marathon cDNA amplification kit (Clontech) and adaptor-ligated testicular cDNA as the substrate. The PCR products, after separation by agarose gel electrophoresis, were cloned into the direct PCR cloning vector pGEM-T (Promega).

Single-strand conformation polymorphism (SSCP) analysis was performed to analyze cDNA from various tissues, using previously described protocols [Dracopoli, C.D. et al., New York: John Wiley and Sons, Inc. (1997)]. Briefly, PCR was performed with 5 μl RT product in a final volume of 25 μl, with 2μCi of $\alpha^{32}P$-dCTP (~3000 Ci/mmole, New England Nuclear) per reaction. The PCR conditions was as described for RT-PCR above. After the PCR, 1 μl of the mixture was diluted with 5 μl of denaturing buffer (95% formamide, 20 mM EDTA, 0.05% bromophenol blue, 0.05% xylene cyanol), heat-denatured at 98°C for 2 min, and electrophoresed through an 8% polyacrylamide gel with 10% glycerol. As controls, aliquots of the same samples were diluted with a standard non-

denaturing DNA loading dye and electrophoresed in parallel. The electrophoresis was performed at room temperature at a constant power of 10-12 watts. The gel was then dried and autoradiography performed for 15-24 hours with an intensifying screen.

Identification of Immunoreactive cDNA clones

A cDNA expression library of 1.42×10^7 primary clones was prepared from Lu15, a specimen of moderately differentiated adenocarcinoma of the lung and 8×10^5 phage plaques were immunoscreened with absorbed autologous patient serum at 1:100 dilution. Excluding false-positive clones encoding immunoglobulin gene fragments, 20 positive clones were identified. These clones were purified and sequence analyzed. Comparisons of the sequences showed that these clones represented cDNAs from 12 distinct genes, designated NY-LU-1 through NY-LU-12 (Table 9). A homology search through the GenBank/EMBO databases revealed that 4 of the 12 genes corresponded to previously known molecules, and 8 others were unknown genes, with sequence identity limited only to short segments of known genes or to expressed sequence tags (ESTs).

Table 9: NY-LU clones

Gene Designation	Gene/Sequence Identity [Accession Number]	cDNA	Comments
NY-LU-1	Aldolase A (N and H type) [X06352]	Lu-15/24, 72, 83, 158, 219, 241	Human fructose, 1,6 diphosphate aldolase A: Expressed in muscle (M type), but also in most other tissues (N and H types). Levels increased in most lung cancers; released into blood upon trauma and in several cancers.
NY-LU-2	hASNA-1 [U60276]	Lu-15/26, 66	Human homolog of the ATP-biding ars A component of the bacterial arsenite transporter. Previously cloned by SEREX from a testicular library (Chen et al., unpolished). Ubiquitously expressed.
NY-LU-3	Annexin 1X [L19605]	LU-15/64	Homosapiens 56K autoantigen. Antibodies to Annexin 1X are found in multiple autoimmune diseases. ubiquitously expressed.

NY-LU-4	Rip-1 [U55766]	Lu-15/65	Human HIV Rev-interacting protein. Expressed in B cells, monocytes and rhabdomyoma cells.
NY-LU-5	Unknown [W61291, W92962, etc.]	Lu-15/80	Expressed ubiquitously (by RT-PCR).
NY-LU-6	Unknown [none]	Lu-15/85	Sequence contains no ORF, expressed ubiquitously (by RT-PCR).
NY-LU-7	Unknown [W23466, AA167732, etc.]	Lu-15/135,217	Expressed in neuron, pregnant uterus, lung ca., parathyroid tumors, etc.
NY-LU-8	Unknown [Z78323, N39225, etc.]	Lu-15/139	Expressed in fetal heart, retin, multiple sclerosis, etc.
NY-LU-9	Unknown [W26569, AA036884, etc.]	Lu-15/145	Expressed in retina, pregnant uterus, fetal liver-spleen, etc.
NY-LU-10	Unknown [M29204, etc.]	Lu-15/154	Expressed in colon, pancreas, pregnant uterus, fibroblasts, etc.
NY-LU-11	Unknown [W23466, AA057400, etc.]	Lu-15/270	Expressed in retina, pregnant uterus, fetal heart, fetal liver-spleen, parathyroid tumors, etc.
NY-LU-12	g16	Lu-15/251	Located at the 3p21 TSG locus (see text)

Of the 4 known genes, aldolase A (NY-LU-1; SEQ ID NOs:689 and 690) was most frequently isolated, representing 6 of 20 primary positive clones in the entire screening. NY-LU-2 (SEQ ID NO:691), represented by two isolates, was the human homolog of the ATP-binding arsA component of the bacterial arsenite transporter, a gene which has been shown to be ubiquitously expressed in various tissues [Kurdi-Haidar, B. et al., *Genomics* 36:486-91 (1996)]. NY-LU-3 (SEQ ID Nos:692 and 693) encodes annexin XI, which is a 56KD ubiquitously expressed antigen to which autoantibodies have been described in sera from patients with various autoimmune diseases [Misaki, Y. et al., *J Biol Chem* 269:4240-6 (1994); Misaki, Y. et al., *J Rheumatol.* 22:97-102 (1995)]. The last gene in this group, NY-LU-4 (SEQ ID NOs:694 and 695), codes for the human HIV Rev interacting protein Rip-1, which has been shown to be expressed in the monocyte cell line U937, the rhabdomyoma cell line RD, as well as in adherent monocytes and primary lymphocytes [Refaeli, Y.

et al., *Proc Natl Acad Sci USA* 92:3621-5 (1995)].

Of the eight unknown genes, 6 (NY-LU-5, 7, 8, 9, 10, 11; SEQ ID Nos:696, 698, 699, 700, 701 and 702/703, respectively) shared sequence identify with reported expressed sequence tags (EST), likely representing cDNA products derived from the same genes. These ESTs were derived from various somatic tissues unrelated to lung, e.g., neuron, pregnant uterus, colon, endothelial cells, etc., suggesting that these genes are widely expressed in human tissues (Table 9), making them unlikely candidates for vaccine-based tumor immunotherapy. These clones were not further investigated. The only novel gene in this group, NY-LU-6 (SEQ ID NO:697), showed no sequence identity to deposited sequences in the public databases. The tissue expression pattern of this gene was evaluated by RT-PCR analysis using gene-specific primers and a normal tissue RNA panel consisting of lung, colon, kidney, liver, brain and testis. Results showed universal expression in these tissues, and this clone was not further analyzed.

<u>NY-LU-12 is on *TSG* locus of chromosome 3p21.</u>

The last gene in the unknown gene group, NY-LU-12, was represented by the immunoreactive clone Lu15-251. This clone, 1081bp in length, contained an uninterrupted open reading frame (ORF) of 952 bp, followed by a 129bp 3'untranslated region. No translation initiation codon was identified, indicating that this was a partial cDNA clone.

A sequence homology search revealed that this gene shared up to 30% homology with two different human proteins at its C-terminus (Fig. 1), LUCA15 and DXS8237E (GenBank accession numbers U23946, and P98175) and also shared homology to S1-1, the rat counterpart of DXS8237E [Inoue, A. et al., *Nucleic Acids Res*. 24:2990-7 (1996)]. LUCA15 was subsequently proven to be a gene immediately centromeric to NY-LU-12 on the *TSG* locus on chromosome 3p21 (see below and [Wei, M.H. et al., *Cancer Res*. 56: 2487-92 (1996))]. Our analysis of LUCA15 revealed the presence of a nuclear localization signal in the putative LUCA15 protein. DXS8237E, was located on chromosome Xp11.23 [Coleman, M.P. et al., *Genomics* 31:135-8 (1996)] and its rat homolog, S1-1, has been shown to be an RNA-binding protein [Inoue, A. et al., *Nucleic Acids Res*. 24:2990-7 (1996)].

Of particular interest, however, was that a short segment (92bp) at the 5' end of NY-LU-12 was identical to a previously identified gene, g16 (GenBank accession number U50839), which was

mapped to chromosome 3p21.3 and was interrupted in the small cell lung cancer line NCI-H740.

To compare NY-LU-12 with g16, the full-length NY-LU-12 cDNA sequence was obtained from normal testicular mRNA through a combination of 5'RACE and direct PCR cloning strategies. The predominant cDNA form ~~(SEQ ID No:707), excluding the poly A tail, is of~~ 3591bp in length. An open-reading-frame of 1123 amino acid residues (SEQ ID No:708) was identified (nt. 102-3470), with 101bp of 5' untranslated and 129bp of the 3' untranslated region. The nucleotide and amino acid sequences are shown in Fig. 2.

~~Comparison with the g16 sequence verified that these two are identical genes and mapped~~ NY-LU-12 to *TSG* locus on 3p21. However, the reported g16 sequence, 2433 bp in length, lacks the 5' end 110 bases which include the translational initiation codon at nucleotide 102, and also the 3' end 980 nucleotides of NY-LU-12. In addition, 74bp DNA segment (nt. 1587-1659 of NY-LU-12) was absent in the reported g16 sequence. Oligonucleotide primers flanking this 74 bp region were designed and used to amplify RNA from 1 normal lung, 5 lung cancer cell lines, and 6 lung cancer specimens. Two RT-PCR products were seen in every specimen, corresponding to the sizes of the two cDNA variants. It was thus concluded that this variation represents an alternate splicing event which occurs in both normal and cancerous lung tissues. Of interest, however, was the difference in the putative translational products resulting from this additional 74bp exon. In the absence of this exon, the open-reading-frame of NY-LU-12 would end in the termination codon at nt.1736, as reported for g16, with a total length of 520 amino acid residues (in contrast to 1123 residues in the longer transcript). Moreover, this shorter form would not encode the C-terminal portion of the NY-LU-12 protein, the segment responsible for the immunoreactivity of Lu15-251 to the autologous patient serum.

Additional cDNA variants of NY-LU-12

In the process of 5'RACE cloning of the full-length NY-LU-12, three minor forms of cDNA products were identified which varied in their transcriptional initiation site and in their exon usage in the 5' segment of this gene. These variants will be described as transcripts B, C, and D (SEQ ID Nos:709, 711 and 712). Fig. 3 shows the comparison of these transcripts to the predominant cDNA form (transcript A, see Fig. 2).

Transcript B (Fig. 3A, bottom) contains an additional exon of 208 base pairs, inserted at

nucleotide 145 of the NY-LU-12 sequence. The original ORF of NY-LU-12 is disrupted due to this inserted sequence, and the AUG initiation codon used by transcript A is thus unlikely to be used by this transcript. A new potential translational initiation site, however, is found within this new exon and would continue the translation into the ORF of transcript A. The final product would be a protein of 1177 amino acids (SEQ ID NO:710), with the 69 residues at the N-terminus different from transcript A. Interestingly, this new exon encodes for a signal peptide not present in the transcript A (Fig. 3A, bottom), and it is possible that these two products are localized to different subcellular compartments.

Similar to transcript B, transcripts C and D both contained additional exon(s) not present in transcript A. Transcript C contained two extra exons in tandem and a length of 364bp, only one of which (137bp) was present in transcript D, Figure 3B. These extra exon(s), inserted at the same alternate splicing site as transcript B, disrupted the original ORF, and the only long ORF would initiate at nucleotide position 498 of NY-LU-12 (959 of transcript C, 635 of transcript D). Considering the long untranslated region at the 5' end, it is doubtful whether transcripts C and D are indeed translated *in vivo*.

Correlating with this variation of NY-LU-12 mRNA, Northern blot analysis showed several RNA species in normal tissues, ranging approximately from 3 to 4.4 Kb. The intensity of individual bands also appear to vary among different tissues, suggesting post-transcriptional tissue specific regulation of NY-LU-12 mRNA.

Features of NY-LU-12 and its putative gene product

Analysis of the NY-LU-12 amino acid sequence showed 20 inexact 6 amino acid repeats with a consensus sequence of D(F/Y)RGR(D/E) close to the N-terminus (Fig. 2). These repeats were separated by 4 to 6 amino acid intervals, which showed no apparent sequence homology among each other. This feature in primary sequence is distinctive among known proteins. Hydrophilicity plot revealed that this region, although hydrophilic in general, has regular hydrophobic turns, and these cycles of hydrophilicity changes correspond to the hexapeptide repeats. Although the significance of this characteristic is unclear at present, this segment of sequence is highly rich in arginine and aspartic acid, a feature shared by RNA binding proteins. Similar motifs, rich in arginine and aspartic acid residues, were found in other RNA-binding proteins [Witte, M.M.

et al., *Proc Natl Acad Sci USA* 94: 1212-7 (1997); Wilson, R. et al., *Nature* 368:32-8 (1994); Seraphin, B. et al., *Nature* 337:84-7 (1989); Takagaki, Y. et al., *Proc Natl Acad Sci USA* 89:1403-7 (1992)], e.g., RNA [Seraphin, B. et al., *Nature* 337:84-7 (1989)] hnRNA 3'end cleavage stimulation factor [Takagaki, Y. et al., *Proc Natl Acad Sci USA* 89:1403-7 (1992)], etc., indicating that NY-LU-12 is likely to be an RNA-binding protein. Consistent with this, PROSITE analysis of the putative NY-LU-12 protein identified a bipartite nuclear localization signal between amino acids 1016-1032 and a 4-residue nuclear localization pattern (PRKR) at amino acid 604-607 (Fig. 2), suggesting that NY-LU-12 is a nuclear protein. Analysis for post-translational modification sites showed potential sites for tyrosine sulfation, amidation, as well as phosphorylation sites for protein kinase A, C, casein kinase II, and tyrosine kinase. A PEST region, peptide sequences consistently found among unstable proteins with short half lives, was identified at amino acids 897-928 (Fig. 2), implying NY-LU-12 as an unstable protein.

Southern blot analysis of NY-LU-12 in normal and tumor tissues

To investigate the status of NY-LU-12 in normal and tumor cells, Southern blot analysis was performed on 9 lung cancer cell lines (3 adenocarcinoma, 2 squamous, and 3 large cell anaplastic), Lu15 tumor DNA, and a colon cancer cell line HT29 (Fig. 4). (HT29 was included due to the finding of an EST identified in the GenBank, accession number AA079461, which appeared to be a fusion sequence between semaphorin IV gene and NY-LU-12.) Using a 1.1Kb cDNA probe (nucleotide 1095-2140) and HindIII digested DNA, the results showed that one of the two hybridizing bands was absent in NCI-H740, confirming that NY-LU-12 was partially deleted in this cell line. The breakpoint of this deletion, by using primers from different regions, was further defined to be between nucleotides 1433 and 1777 of NY-LU-12, with the 3' sequences homozygously deleted. Besides NCI-H740, however, no evidence of homozygous deletion was seen in any other tumor cell line sample or in LU15. The similar band intensities and identical sizes of the DNA signals in all specimens also argued against the possibility of a heterozygous deletion or translocation of this gene, at least in the region analyzed. No change was found in HT29, suggesting that the semaphorin IV/NY-LU-12 fusion sequence in the GenBank probably represents a cloning artifact.

<u>SSCP and sequence analysis of NY-LU-12 in Lu15 tumor DNA.</u>

The mapping of NY-LU-12 to the lung cancer *TSG* locus raised the possibility that an altered protein product due to mutational event may be the basis for the autologous immune recognition. This possibility was explored using DNA sequencing and single-strand confirmational polymorphism (SSCP) analysis.

The DNA sequence contained in the immunoreactive clone Lu15-251 (nucleotide 2518-3599 of NY-LU-12) was obtained from the normal counterpart by RT-PCR cloning using autologous ~~normal lung tissue, and no mutations were found when compared to Lu15-251.~~

RT-PCR SSCP was then used to analyze the entire NY-LU-12 gene, comparing Lu15 tumor tissue and autologous normal lung tissue. To encompass the whole sequence, 10 sets of primer pairs were designed, each amplifying a range of 205 to 603 bps. For products >400bps, a restriction enzyme digestion step was added prior to the electrophoresis step to further reduce the fragment sizes and increase the assay sensitivity. Results showed no reproducible changes between normal and tumor tissues, and thus no evidence of mutation in Lu15 tumor cDNA. A representative set of SSCP analysis is shown in Fig. 5.

<u>Serological response to NY-LU-12 in lung cancer patient</u>

The frequency of anti-NY-LU-12 response was examined among normal adult and patient sera using the phage plaque assay identical to the original immunoscreening procedure. Of 21 absorbed sera from allogeneic lung cancer patients, one (Lu22) reacted strongly with the Lu15-251 plaque at 1:1000 dilution, and another (Lu7) also reacted at 1:1000, but only weakly. Nineteen other lung cancer patient sera were non-reactive, nor were the sera from 16 healthy donors, 15 colon cancer, 5 breast cancer, 1 renal cancer, 1 prostate cancer, 1 esophageal cancer, and 1 melanoma patients.

<u>Example 10: Expression analysis of additional cancer associated nucleic acids</u>

The clone RING 3 was isolated from breast SEREX analysis as LONY-Br-5 (see above). The gene was identified as homologous to the "bromodomain testis" gene (BRDT; GenBank accession number AF019085). Analysis of related genes identified BRDT as a gene expressed only in testis, which was then investigated by RT-PCR analysis as described above.

The primers used to perform RT-PCR had the following sequences:

BRDT F1: CAAGAAAGGCACTCAACAG (bp 543-563 of BRDT)

BRDT R1: TTCACTACTTGCTTTAACTGC (bp 776-797 of BRDT)

The meiotic protein H1T (Histone 1 Testis; GenBank accession number M60094) was identified through a literature search for meiotic proteins (testis specific expression).

The primers used to perform RT-PCR had the following sequences:

H1F1: TGCCGAACCTCTCTGTGTC (bp 116-135 of H1T)

~~H1R1: GCTTCGTGTAGATTTAGGAATC (bp 344-366 of H1T)~~

Table 10: RT-PCR analysis

Normal Tissue	BRDT	H1T
mammary gland	-	-
liver	-	-
small intestine	-	-
brain	-	+/- (very weak)
lung	-	-
fetal brain	-	-
placenta	+	+
kidney	-	-
skeletal muscle	-	-
pancreas	-	-
adrenal gland	-	-
heart	-	-
thymus	-	-
uterus	-	-
prostate	-	+/- (very weak)
spleen	-	-
Testis	+	+

Tumor Tissue	BRDT	H1T
Colon	0/6	0/6
Breast	0/6	6/6+
Melanoma	0/12	3/12+
Lung	8/26+	4/26+
Renal	0/2	0/2
Ovary	0/2	0/2
Esophageal	0/1	0/1

Gastric	0/1	0/1
Bladder	0/2	0/2

Lung cancer specific expression of BRDT was observed (see table above). BRDT was expressed only in normal testis and possibly in placenta. The expression analysis of H1T revealed that all breast tumor samples (6 of 6) and ~30% lung cancers and melanoma tissue samples expressed H1T. H1T was expressed in normal testis and possibly in placenta and brain.

Example 11: allogeneic serotyping

To confirm the cancer associated expression of SEREX clones, allogenic sera screening of gastric cancer patients' sera was conducted. Sera from normal patients (gastritis) was used as a control for expression of the clones in non-gastric cancer. The screening procedure used was as described above for the SEREX screening, except for the absorption of anti-bacterial and anti-bacteriophage antibodies. The modifications were as follows.

Serum from a stomach cancer patient or a normal individual was diluted to 1:10 in TBS (Tris buffered saline; final volume 5 ml) and passed through a column (BIO-RAD Poly-Prep Chromatography Column, Hercules. CA, USA) containing 0.5 ml Sepharose-4B cross linked to E. coli Y1090 lysate and 0.5 ml Sepharose-4B cross linked to E. coli BNN97 (5 Prime 3 Prime, Inc, Boulder, CO, USA). After repeating the column chromatography 10 times, serum was then diluted to 1:100 in TBS containing 1% BSA and 0.02% sodium azide. To remove antibodies to bacteria and baceteriophages further, 10 ml absorbed serum was incubated overnight with a 82 mm nitrocellulose membrane on which XL-1 Blue MRF' bacteria and lambda ZAP Express phages (Stratagene, La Jolla, CA USA) were immobilized. The serum was stored at - 80°C until use. For allogeneic typing, an equal numbers of positive phage and negative phage were mixed and plated and processed by the standard SEREX screening procedure.

The results of the allogenic screening experiments follow:

Table 11: Allogenic Sera Screening of SEREX Sequences from Gastric Patients

Sequence Gene/Clone	Number	Isolated in Serex Patients	Allogenic Serotyping Gastric Cancer Sera	Allogenic Serotyping Normal Sera
RPB-J H-2K binding factor		SM1	6/12	6/16
Telomeric repeat binding protein		SM1	1/12	0/16
Ser/Thr protein kinase		SM1	1/12	0/16
SRY interacting protein-1		SM1	2/12	1/16
Sterol carrier protein X		SM1	2/12	0/16
Archain		SM1	1/12	1/16
HEM-1		SM1	2/12	1/16
Id-1 helix-loop-helix protein		SM1	1/12	0/16
helix-loop-helix transcription factor		SM1	1/12	0/16
Follistatin related precursor protein		SM1,CK, KM	6/12	0/16
Translation initiation factor eIF-4gamma		SM1,SS1, KM	5/12	2/16
M phase phophoprotein I		SM1,SS1	8/12	5/16
Lysal tRNA synthase		SM1	1/12	0/16
Gelsolin		SM1	4/12	0/16
Zinc finger protein		SM1	1/12	1/16
Goliath		SM1	2/12	1/16
zhx-1		SM1	1/12	1/16
SG24		SM1,SS1, KM	5/12	0/16
SG132		SM1	3/12	0/16
S553		SM1	7/12	7/16
S134		SM1	3/12	0/16
S328		SM1	2/12	1/16
S365		SM1, KM	2/12	0/16

FKBP25		KM, SS1	5/12	0/16
Pros-27		KM, CK	3/12	1/16
BS4		KM	1/12	1/16
GnRH-II		KM	1/12	0/16
CTBP		KM	1/12	0/16
ETF		KM	3/12	1/16
KIAA0438		KM	1/12	5/16
KIAA0367		KM	4/12	3/16
APK1		KM	2/12	0/16
IPP		KM	1/12	0/16
Tropomyosin		KM	1/12	0/16
p63		KM	1/12	0/16
KIAA0181		KM	1/12	0/16
KIAA0349		KM	1/12	0/16
RPB1		KM	5/12	9/15
PPIM		KM	1/12	-
EB virus		KM	3/12	-
G.KM073		KM	6/12	-
G.KM403		KM	1/12	-
KM192		KM	1/12	-
KM294		KM	1/12	-
KM362		KM	1/12	-
KM031		KM	1/12	-
KM081		KM	3/12	-
KM201		KM	1/12	-
KM1496		KM	1/12	-
KM334		KM	1/12	-
KM313		KM	1/12	
E-cad/Y		CK	1/12	0/16
IPBP		SS1	1/4	-
OS-9		SS1	1/4	-

Kinesin light chain		SS1	1/4	-

The screening results shown above confirm the association of the SEREX clones with cancer. There is a higher correlation of cancer and the expression of certain clones, in particular, follistatin related precursor protein, the translation initiation factor eIF-4gamma, the unknown sequence SG24, the FK506-binding protein 25, and the unknown sequence G.KM073. These clones are well suited to serve as diagnostic indicators of disease and as targets for therapeutics (e.g., vaccine compositions) development.

Example 12: Preparation of recombinant cancer associated antigens

To facilitate screening of patients' sera for antibodies reactive with cancer associated antigens, for example by ELISA, recombinant proteins are prepared according to standard procedures. In one method, the clones encoding cancer associated antigens are subcloned into a baculovirus expression vector, and the recombinant expression vectors are introduced into appropriate insect cells. Baculovirus/insect cloning systems are preferred because post-translational modifications are carried out in the insect cells. Another preferred eukaryotic system is the *Drosophila* Expression System from Invitrogen. Clones which express high amounts of the recombinant protein are selected and used to produce the recombinant proteins. The recombinant proteins are tested for antibody recognition using serum from the patient which was used to isolated the particular clone, or in the case of cancer associated antigens recognized by allogeneic sera, e.g. certain breast cancer and gastric cancer associated antigens, by the sera from any of the patients used to isolate the clones or sera which recognize the clones' gene products.

Alternatively, the cancer associated antigen clones are inserted into a prokaryotic expression vector for production of recombinant proteins in bacteria. Other systems, including yeast expression systems and mammalian cell culture systems also can be used.

Example 13: Preparation of antibodies to cancer associated antigens

The recombinant cancer associated antigens produced as in Example 12 above are used to generate polyclonal antisera and monoclonal antibodies according to standard procedures. The antisera and antibodies so produced are tested for correct recognition of the cancer associated

antigens by using the antisera/antibodies in assays of cell extracts of patients known to express the particular cancer associated antigen (e.g. an ELISA assay). These antibodies can be used for experimental purposes (e.g. localization of the cancer associated antigens, immunoprecipitations, Western blots, etc.) as well as diagnostic purposes (e.g., testing extracts of tissue biopsies, testing for the presence of cancer associated antigens).

Example 14: Expression of cancer associated antigens in cancers of similar and different origin.

The expression of one or more of the cancer associated antigens is tested in a range of tumor samples to determine which, if any, other malignancies should be diagnosed and/or treated by the methods described herein. Tumor cell lines and tumor samples are tested for cancer associated antigen expression, preferably by RT-PCR according to standard procedures. Northern blots also are used to test the expression of the cancer associated antigens. Antibody based assays, such as ELISA and western blot, also can be used to determine protein expression. A preferred method of testing expression of cancer associated antigens (in other cancers and in additional same type cancer patients) is allogeneic serotyping using a modified SEREX protocol (as described above for gastric clones).

In all of the foregoing, extracts from the tumors of patients who provided sera for the initial isolation of the cancer associated antigens are used as positive controls. The cells containing recombinant expression vectors described in the Examples above also can be used as positive controls.

The results generated from the foregoing experiments provide panels of multiple cancer associated nucleic acids and/or polypeptides for use in diagnostic (e.g. determining the existence of cancer, determining the prognosis of a patient undergoing therapy, etc.) and therapeutic methods (e.g., vaccine composition, etc.).

Example 15: HLA typing of patients positive for cancer associated antigen

To determine which HLA molecules present peptides derived from the cancer associated antigens, cells of the patients which express the cancer associated antigens are HLA typed. Peripheral blood lymphocytes are taken from the patient and typed for HLA class I or class II, as

well as for the particular subtype of class I or class II. Tumor biopsy samples also can be used for typing. HLA typing can be carried out by any of the standard methods in the art of clinical immunology, such as by recognition by specific monoclonal antibodies, or by HLA allele-specific PCR (e.g. as described in WO97/31126).

Example 16: Characterization of breast cancer associated antigen peptides presented by MHC class I and class II molecules.

Antigens which provoke an antibody response in a subject may also provoke a cell-mediated immune response. Cells process proteins into peptides for presentation on MHC class I or class II molecules on the cell surface for immune surveillance. Peptides presented by certain MHC/HLA molecules generally conform to motifs. These motifs are known in some cases, and can be used to screen the breast cancer associated antigens for the presence of potential class I and/or class II peptides. Summaries of class I and class II motifs have been published (e.g., Rammensee et al., *Immunogenetics* 41:178-228, 1995). Based on the results of experiments such as those described in Example 15, the HLA types which present the individual breast cancer associated antigens are known. Motifs of peptides presented by these HLA molecules thus are preferentially searched.

One also can search for class I and class II motifs using computer algorithms. For example, computer programs for predicting potential CTL epitopes based on known class I motifs has been described (*see, e.g.*, Parker et al, *J. Immunol.* 152:163, 1994; D'Amaro et al., *Human Immunol.* 43:13-18, 1995; Drijfhout et al., *Human Immunol.* 43:1-12, 1995). HLA binding predictions can conveniently be made using an algorithm available via the Internet on the National Institutes of Health World Wide Web site at URL http://bimas.dcrt.nih.gov. Methods for determining HLA class II peptides and making substitutions thereto are also known (e.g. Strominger and Wucherpfennig (PCT/US96/03182)).

The lung cancer SEREX clone polypeptides NY-LU-12 and NY-LU-12B (variant B), SEQ ID NOs: 708 and 710, were subjected to the HLA binding peptide analysis described above, using the NIH website, to identify HLA binding peptides for several common HLA molecules (HLA-A1, A2, A3, A24, B7, B44, and B52). The results are listed below in Table 12.

Table 12: Identification of HLA binding peptides in lung SEREX clones

HLA	peptide	amino acids of NY-LU-12 protein	SEQ ID NO
A1	NVEE-HSFSY	67 - 75	713
	PVDP-NILDY	287 - 295	714
	DTDY-RSMEY	398 - 406	715
A2	SLLE-DAIGC	506 - 514	716
	TLMI-QDKEV	521 - 529	717
	YVSSLDFWYC	533 - 542	718
	VIVEVLEPYV	671 - 680	719
	KLTD-WNKLA	948 - 956	720
	QLSDLHKQNL	975 - 984	721
	KQSEQELAYL	991 - 1000	722
	KLVDKEDIDT	1042 - 1051	723
	VMFA-RYKEL	1114 - 1122	724
A3	QMFG-YGQSK	417 - 425	725
	GMPVKNLQLK	481 - 490	726
	GLPE-EEEIK	823 - 831	727
	LLCRRQFPNK	958 - 967	728
A24	EYRD-VDHRL	405 - 413	729
	GYVC-VEFSL	499 - 507	730
	DYGY-VCVEF	497 - 505	731
	WYCKRCKANI	540 - 549	732
	TYPQPQKTSI	574 - 583	733
	IYRSTPPEVI	663 - 672	734
	HYYQ-GKKYF	754 - 762	735
	VYVP-QDPGL	816 - 824	736
B7	WNRDYPPPPL	26 - 35	737
	MPPV-DPNIL	285 - 293	738
	TARD-AQRDL	432 - 440	739
	GPSEEKPSRL	448 - 457	740
	TPPEVIVEVL	667 - 676	741
	RVMFARYKEL	1113 - 1122	742
B44	REMG-SCMEF	272 - 280	743
	EEQSSDAGLF	376 - 385	744
	KEYN-TGYDY	490 - 498	745
	TEAKQELITY	566 - 575	746
	VEALRVVKIL	710 - 719	747
	GEYG-GDSDY	906 - 914	748
	LERREREGKF	1000 - 1009	749

B52	RQDGESKTIM	650 - 659	750
	TPPEVIVEVL	667 - 676	751
	YGFIDLDSHV	701 - 710	752
	RQFP-NKEVL	962 - 970	753

NY-LU-12B (variant B)

A1	NVEE-HSFSY	121 - 129	754
	PVDP-NILDY	341 - 349	755
	DTDY-RSMEY	452 - 460	756
A2	WQSA-RFYYL	41 - 49	757
	SLLE-DAIGC	560 - 568	758
	TLMI-QDKEV	575 - 583	759
	YVSSLDFWYC	587 - 596	760
	VIVEVLEPYV	725 - 734	761
	KLTD-WNKLA	1002 - 1010	762
	QLSDLHKQNL	1029 - 1038	763
	KQSEQELAYL	1045 - 1054	764
	KLVDKEDIDT	1096 - 1105	765
	VMFA-RYKEL	1168 - 1176	766
A3	QMFG-YGQSK	471 - 479	767
	GMPVKNLQLK	535 - 544	768
	GLPE-EEEIK	877 - 885	769
	LLCRRQFPNK	1012 - 1021	770
A24	YYLN-ATDVL	47 - 55	771
	FYYLNATDVL	46 - 55	772
	EYRD-VDHRL	459 - 467	773
	GYVC-VEFSL	553 - 561	774
	DYGY-VCVEF	551 - 559	775
	WYCKRCKANI	594 - 603	776
	TYPQPQKTSI	628 - 637	777
	IYRSTPPEVI	717 - 726	778
	HYYQ-GKKYF	808 - 816	779
	VYVP-QDPGL	870 - 878	780
B7	WNRDYPPPPL	80 - 89	781
	MPPV-DPNIL	339 - 347	782
	TARD-AQRDL	486 - 494	783
	GPSEEKPSRL	502 - 511	784
	TPPEVIVEVL	721 - 730	785
	RVMFARYKEL	1167 - 1176	786

B44	SEAWSSNEKF	59 - 68	787
	REMG-SCMEF	326 - 334	788
	EEQSSDAGLF	430 - 439	789
	KEYN-TGYDY	544 - 552	790
	TEAKQELITY	620 - 629	791
	VEALRVVKIL	764 - 773	792
	GEYG-GDSDY	960 - 968	793
	LERREREGKF	1054 - 1063	794
B52	RQDGESKTIM	704 - 713	795
	TPPEVIVEVL	721 - 730	796
	YGFIDLDSHV	755 - 764	797
	RQFP-NKEVL	1016 - 1024	798

Likewise, other clones identified herein can be analyzed for the presence of candidate HLA binding peptides using no more than routine experimentation.

Example 17: Identification of the portion of a cancer associated polypeptide encoding an antigen

To determine if the cancer associated antigens isolated as described above can provoke a cytolytic T lymphocyte response, the following method is performed. CTL clones are generated by stimulating the peripheral blood lymphocytes (PBLs) of a patient with autologous normal cells transfected with one of the clones encoding a cancer associated antigen polypeptide or with irradiated PBLs loaded with synthetic peptides corresponding to the putative protein and matching the consensus for the appropriate HLA class I molecule (as described above) to localize an antigenic peptide within the cancer associated antigen clone (*see*, e.g., Knuth et al., *Proc. Natl. Acad. Sci. USA* 81:3511-3515, 1984; van der Bruggen et al., *Eur. J. Immunol.*24:3038-3043, 1994). These CTL clones are screened for specificity against COS cells transfected with the cancer associated antigen clone and autologous HLA alleles as described by Brichard et al. (*Eur. J. Immunol.* 26:224-230, 1996). CTL recognition of a cancer associated antigen is determined by measuring release of TNF from the cytolytic T lymphocyte or by ^{51}Cr release assay (Herin et al., *Int. J. Cancer* 39:390-396, 1987). If a CTL clone specifically recognizes a transfected COS cell, then shorter fragments of the cancer associated antigen clone transfected in that COS cell are tested to identify the region of the gene that encodes the peptide. Fragments of the cancer associated antigen clone are prepared by

exonuclease III digestion or other standard molecular biology methods. Synthetic peptides are prepared to confirm the exact sequence of the antigen.

Optionally, shorter fragments of cancer associated antigen cDNAs are generated by PCR. Shorter fragments are used to provoke TNF release or ^{51}Cr release as above.

Synthetic peptides corresponding to portions of the shortest fragment of the cancer associated antigen clone which provokes TNF release are prepared. Progressively shorter peptides are synthesized to determine the optimal cancer associated antigen tumor rejection antigen peptides for a given HLA molecule.

A similar method is performed to determine if the cancer associated antigen contains one or more HLA class II peptides recognized by CTLs. One can search the sequence of the cancer associated antigen polypeptides for HLA class II motifs as described above. In contrast to class I peptides, class II peptides are presented by a limited number of cell types. Thus for these experiments, dendritic cells or B cell clones which express HLA class II molecules preferably are used.

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

All references disclosed herein are incorporated by reference in their entirety.

We claim:

TABLE 1

SEQ ID NO. 1:

U72994, AC004022, Z68323, AE001160, L34078, AF064863, AC002132, U60440, X66494, N21242, AA678312, W86762, R01605, AA782843, AA275156, W41927, AA874648, AA571241, AA562747, W10480, AA451301, AA866631, AA466667, AA999057, AI029140.

SEQ ID NO. 2:

AC004022, U72994, AC002420, AC004125, AA690961, W41927, AA874648, AC004022, U72994, AC002420, AC004125, AA690961, W41927, AA874648.

SEQ ID NO. 3:

X98371, AL009008, L31790, Z83220, X92946, AC003975, AF008916, U80460, X75544, X66732, X95275, X52177, X07976, AC004451, Z74307, AB000878, AL009179, AF038667, Z78544, Z48008, U23486, J05096, AB000882, Z30213, L11593, U18530, L27325, AC005191, M99579, AA130270, AA158245, AA903098, AI018453, AA436455, AA980593, AA172479, AA637487, AA116588, AA426854, AA050404, AA390025, AI006618, AI048382, C85944, AA673480, AI006510, AA823338, AA413694, W35075, AA015033, AA413584, W29693, AA637069, AA619839, AA125149, AA039004, AA674696, AA871138, AA414747, AA198099, C91478, F071359, AA925957, AA820054, H16496, AI043756, AA892435, AA893551, AA818669, AA892785, AA944026, D33919, N96570, F19798, AI045451, AA800662, D65187, AA944025, AA925731, AA892314, AA945449.

SEQ ID NO. 4:

AA900930, AA925665.

SEQ ID NO. 5:

U58105, Z81485, Z54236, Z48584, U61375, M55267, M59856, X51942, U77302, Z48621, AF032455, Z11866, AB013392, L32792, AA871997, AA084083, AA130829, AA083063, AA666290, N38894, D54459, T28921, AA806015, AA512059, AI043087, AI042894, AA968324, AA238493, AA237462, AI042885, AI046424, AI035670, AA269430, AA250621, AI035540, AA260613, AA106870, AA238658, AA106134, AI042683, AA105958, AA144007, AA986558, AA457910, AA389400, AA673056, AA153254, AA754678, AI021109, AA390813, C36687, T41571, AI011183, AI013356, AI011739, AI030260, AA924384, C44421.

SEQ ID NO. 6:

AF036717, U91327, AF036718, U56248, Z48795, Z99290, M30697, U58204, M24417, AF022983, M33581, AC004619, H64641, AA477478, AA369676, AA088359, AA057574,

AA683066, AA446279, AA332363, T09328, R80982, AA069486, AA410842, C18527, AA293033, H12730, AA287344, AA029631, R83063, AA061290, AA185993, AA880204, AA499308, AA183172, AA242360, AA792388, AA175587, AA277140, AA880395, AA899046, AA859550, C35363, C35702, C32682, F14140, T18049, C83149, T45787, AA924623, D47525, Z30723, AA897884, AA042465, AI009871, AA875198, C83016.

SEQ ID NO. 7:

X74116, AL022148, AC004548, AC000352, Z11664, Z78065, Z74028, AE000163, AE000750, X74229, D90700, R59414, AA176708, W02568, AA354664, R43017, AA973553, F10008, D61827, AA826300, Z41398, T77572, R40189, H85823, W86541, T17276, AA679337, X83357, AA184845, AA416260, AA475603, AA388692, AA764445, AA388689, AA219880, AA290020, AA388507, AA387267, C86741, AA414436, AA451259, AA413796, AA930916, AA793690, AA619447, AA062257, AA522026, AA816247, AA892032, AA817702, H33461, AA925507, AA849449, AI029236, AA247069, AA697975, AA882508, AA893258, AA698410, AA891755, AA698227, AA892782, AA899328, T04373, AA567522, AA698408, AA202615, AA141016, AA697974, AA697998, C61176, D69691, AI030205, AA586054.

SEQ ID NO. 8:

U08218, L38909, Y11095, AC002431, Z23069, S77418, U39060, L38580, AF053367, Z36506, M18102, J03624, AA102264, AA730686, H47968, AA357170, AA130974, C06054, AA626429, F00559, AA604528, AA383348, AA040127, N84965, D54884, D54883, R94309, AA373184, AA128091, W68194, H58283, R76347, AA343938, AA305144, AI049611, AA384516, AA720553, N57395, R97387, D52674, AA169408, H66293, AA456362, T74258, AA730145, AA101952, N86388, AA355003, AA307640, AA385679, AA354542, N99075, N83528, H87678, R84494, R35720, AA670111, AA186452, W32370, D55392, W05161, AA641280, AA120503, C77063, AA146393, AA620177, AA509478, C77481, AA427148, AA474531, W83304, AA207424, AA763436, AA958473, AA799243, AA493061, AA967792, AA145256, AA089338, AA756259, AA789767, AA980112, AA866640, AA914516, AA821675, AA466770, AA015387, AA816036, AA246546, AA941789, AA955779, AA997768, AA997534, T43805, AA956150, T18836, T23333, AA525666, T18787, AA800483, C64685, AA851367, C91730, AA143899, T23399.

SEQ ID NO. 9:

AP000056, U43491, Z74919, L81498, Z94054, AC002503, L81499, AA740188, AA630241, AA974724, AA806907, N88859, N98242, H12649, R06485, R06511, AA546258, C76846, AA208416, AA959219, AA276381, W10055, AA462844, AA444278, W13447, W97802, AA542324, AA137880, AA269331, AA175695, W59029, AA003372, AA146233, AI045761, C93154, C94084, C94208, D68027, C12780, AA687005, AA080598, C12876, C12390, AA848674, AA924440, T15031, AA451569, H35524.

SEQ ID NO. 10:

U25640, AA127328, H24207, H08275, AA283063, AA826096, AA417382, AA464874, W05562, AA453370, N51211, AA495859, R33871, H00927, AA623997, AA220442, AA178568, AA605493, AA394557, AA956116, AA999037, AA818246.

SEQ ID NO. 11:

AB001740, AF039956, AA581972, AA594539, AA236870, AA464410, AA237069, AA694199, AI038896, AA167314, AA577381, AA430117, N23143, R53610, W37647, AA724229, AA313202, AA860618, W16866, AA134966, AA255556, AA305224, R50528, AA844913, W32042, W37383, AA908394, W93357, W31353, R55254, N79251, AA456077, AA477700, AA477701, AA989005, AA455580, N32722, N22935, R50622, AA135047, R51941, T34020, T30416, T32309, AA883332, W93445, AA166984, AA026749, T08224, AA255572, W03768, AA033670, W31880, AA772832, AA230974, AA511207, W82274, AA230365, AA671085, AA511230, AA606681, AA023735, AA444535, W98518, W14718, W85455, AA980318, AA137525, AA035840, AA692158, AA007919, W48013, AA444534, AA981497, AA002566, W48089, W99869, AA960396, AA960580, AA145259, AA145683, AA388960, AA389941, AA266272, AA145124, AA267212, AA959753, AA407991, A175818, AA943997, AA899476, AA899756, AA943998, AA955446, AA012783, AA924956, AA892219, AA955331, AI012225, AA891436.

SEQ ID NO. 12:

U72994, AC004022, AF043493, U43252, U43251, U81830, U58105, U68242, Z93242, AL009029, M29872, U12980, M81118, M30471, Z56258, AF012943, AC004080, AC002563, AF024533, AF002991, Z63771, AP000042, AF064863, U80017, AC004087, Z55235, L05920, AA508139, N90748, AA450240, AA948158, AA828938, AA165115, AI003312, AA436633, AA419100, AA743442, AA961990, AA885286, AA861312, T84801, AI040166, AA494115, AA652324, AA181105, AA095541, R59256, AA503712, AA700364, AA603821, T60326, AA779097, AI023884, AA603785, H79111, W39526, AA506607, W94361, N66078, R01605, H22694, W86762, W99303, AA745640, AA678312, AA431870, W41927, AA874648, C92734, C23102, C53080, C91168, D65098, C32959, C50029, M80125, C34452, C83862, C24659, T21473, AA874720, C06696, W43071, AI043300, C53907.

SEQ ID NO. 13:

X94232, U90437, AC003052, U59809, AC004001, M95396, Z67884, X77486, U70051, X14805, AF022976, Z83823, X77485, J04171, AF036007, U05768, U88315, Z98048, AF036009, AC005179, U41277, U32517, AE001138, D64060, M84387, H29022, AA814221, N26314, AA935912, AA873506, AA608576, AA453605, AA232674, Z38725, AA772022, AA025212, AA318330, R48115, AA234084, H18508, N64543, AA970508, R36933, AA306944, H49559, AA325555, H85834, H89988, AA343974, AA648643, H65664, T62713, H16554, N21122, AA351037, AA484621, AA221492, AA259314, C76383, C76336, AA607924, C76394, AA408562, AA921258, AI006352, W41405, AA153317, AA015435, AA027405, AA794066, AA498038, AA184222, AI011068, AA859614, AA899776, AA955080, AA799674, AA849652, AI009788, AA900928, AI007950, AA109392, AA753592, U92780, AA957632, AA567950, AI009495.

SEQ ID NO. 14:

AC000075, U66140, R14195, AA220229, T31199, R19104, R19148, Z46126, AA417619, Z45284, H14105, R84666, AA090321, AA350108, W52840, R48497, R13097, T66255, W44467, AA247676, AA198489, AA388175, AA261453, AA237111, AA790730, AA162394, AA816498, AI013729, AA684961, AA979759.

SEQ ID NO. 15:

AF069301, D10651, U11419, U11287, M91562, U90278, U72724, X57855, X79424, M16512, M64542, Z14152, AF016667, L01488, Z75955, AF024504, M13968, W67775, AA934587, AA617696, AA913577, AA628682, W74527, AA969876, AA995606, AA622402, AA027090, AA620556, AA085733, AA187157, AI031865, AA972318, AA897169, W79046, AA531124, AA733183, T90909, Z25096, AA721771, AA115089, T49643, R00622, N93780, R00626, AA365494, T71475, N74066, AA027130, T83325, AA115569, AA658299, T55344, T83700, AA426250, AA393863, AA282967, R08138, AI000112, AA807574, AA077926, AA397527, W87761, AA243026, R56368, H16371, AA958697, AA003997, AA008542, AA036229, AA397074, AA250467, AA260498, AA968175, AA253686, AA727785, AI019478, AA474978, AA543461, AA990281, AA245791, AA617042, AA015355, AA983015, AA982200, AA120064, AA462778, AA242574, AA986993, AA986911, AA882490, AA223057, AA543989, W65528, AA848318, AA874979, AA800547, AA945302, AA140994, AA991110, AA851120.

SEQ ID NO. 16:

Z68106, X14199, M14872, Z63497, M31670, AC002123, Z63498, AA280070, AA215687, H93207, AA070367, W95534, AA682436, AA741066, AA173269, AA641255, AA215688, AA724798, N23259, AA442155, AA634563, AA074699, AA642322, AA861347, AA283655, AI002587, W95419, AA357042, AA761253, AA197191, T54480, AA133029, AA378991, AA114599, AA219925, AA174327, AA003800, C86661, AA990433, AA277014, AA445101, AA671205, AI036728, AA241221, AA213304, AI035350, W08919, W36663, AA061406, AA144736, AA240583, AI006563, AA980152, AA250075, AA088967, W17488, AA098269, W10200, AA543712, AA755434, AI012680, AA820868, AA949519, AA391130, AA202576, AA979150, AA012391, AA539472.

SEQ ID NO. 17:

J03592, M24103, AB009386, U44832, J02966, M24102, U27316, U10404, X70847, D12771, D12770, J02683, J03591, U27315, M76669, U39779, M13783, J04982, X74510, X61667, M57424, L78810, AC004000, Z75206, U68723, Z75207, AF009661, X53264, J03320, U66060, AB011800, M77194, AE000021, L07268, AE000936, U03115, AF009663, AA582128, AA916851, AA576667, AA915921, AA916853, N58735, AA428106, AA427849, AI024255, H69807, H11315, N36980, H69597, AA826334, W05080, N37044, AA385873, N48222, AA394173, AA837522, AI002511, AA292870, T96300, AA360716, AA379604, AA862844, AA430455, AA479859, AA133899, AA669954, H92542, AA095298, AA995794, AI003667,

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SEQ ID NO. 20:

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SEQ ID NO. 21:

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SEQ ID NO. 22:

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SEQ ID NO. 23:

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SEQ ID NO. 25:

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SEQ ID NO. 26:

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SEQ ID NO. 27:

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SEQ ID NO. 28:

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SEQ ID NO. 29:

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SEQ ID NO. 30:

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SEQ ID NO. 31:

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SEQ ID NO. 109:

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SEQ ID NO. 111:

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SEQ ID NO. 121:

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SEQ ID NO. 123:

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SEQ ID NO. 127:

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SEQ ID NO. 131:

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SEQ ID NO. 133:

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SEQ ID NO. 135:

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SEQ ID NO. 137:

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SEQ ID NO. 139:

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SEQ ID NO. 141:

S45630, AF007162, X95383, AF029793, M55534, X60351, S77138, S77142, S74229, X60352, M63170, M24906, M28638, J03849, M12016, M73741, U04320, M12014, M24092, L08078, S53164, U26661, M12015, M25770, U16124, X87114, D29960, X14789, X85205, M17247, U05569, U66584, M26142, U47921, U47922, V01219, X95382, AP000007, AE000869, AB009529, AF062537, D10457, S37449, X59541, AA742442, AA704135, AA211774, N35834, AA482745, AA211607, N28898.

SEQ ID NO. 143:

U78082, L78810, U14573, AC004068, U07561, M98511, AC004673, AA613346, AA953216, AA305926, H92800, R98218, AA629543, AA297666, AA302982, AA429481, AA126005, AA837225, AA856961, AA946848, F13749, AA847704, AA833896, AA621381, AA833875, AA459962, H22141, N73060, AA491955, H28477, AA224463, AA708753, AA152253, AI028510, AA483606, AA992126, T54783, AA715075, AA568204, AA715173, N64587, AA570740, AA984258, AA904211, H94979, AA085410, AA599352, AA488620, AA574442, AI049845, AA593471, AA393830, AA610509, AA297145, AA113272, AA835889, AA655005, AA689351, R93919, AA613761, AA550989, AA303054, H07953, AA713815, AA827490, AA865262, AA461308, H73550, AA657835, AA362349, H82679, AA378682, AA577755, AA663472, AA490602, AA857673, AA347114, AI049630, AA086150, AI017251, AA877992, AA084609, AI050760, AA808998, AA503258, AA613138, AA603156, AA513293, R97934, AA610233, AA654874, AA501867, AA604831, N22058, AA492114, T50676, AA757426, AA584482, AA789192, AI004591, T50694, AA862227, AA594145, AA728911, AA847499, AA159978, AA534204.

SEQ ID NO. 145:

Z69030, L42375, U37352, D26445, U38192, U38191, U37770, U38190, U37353, U59418, L76702.

SEQ ID NO. 147:

L07872, L34544, L34543, X17459, S63463, M81871, L08904, U60093, U60094, L07873, L07874.

SEQ ID NO. 149:

U07158, X85784, AJ000541, U76832, L20821, AC003089, AC004504, AF049236, L40609, AF053765, L14677, Z94056, Z18277, AE001073, U85969, X79283, AJ223473, AA632339, AA732931, AA610556, AA973899, AA598896, AA531553, AA826535, AI000209, AA290836, AA642711, AA085920, W22275, D20744, UMGS017, AA487868, AA487869, AA085919, 682 AA833281, AA619252, C77541, AA691960, AA763615, AA164051, AA259589, AA060475, AA254185, AA666705, AA272597, AA152985, AI011416, AA850008, H33152, AA941811.

SEQ ID NO. 151:

M13451, X03445, X03444, M13452, X66870, X76297, X14170, X99257, D14850, D13181, L12399.

SEQ ID NO. 153:

U28918, U17714, X82021, Z98048, D17265, D17092, Z82022, L04270.

SEQ ID NO. 155:

X54859, Z86000, AC003043, X77738, X77737, L35930, AC003084, AC000111, M89651, AP000031, U67588, X03991, AC004660, AL010261, V01515, M86251, L29376, Z71417, L78442, U00921, AC004692, AC003698, AE000742, Z49128, Z73417, Z71418, AA424638, AA442084, AA805748, AA835489, AA713576, AA502343, AA765949, AA812332, AA831755, AA417718, AA776946, AA152295, AA731660, R48791, AA150237, N51650, N52616, N52586, AA533556, AA305755, AA760877, AA729913, AA731659, AA910594, AA904521, AA372550, R48898, N50390, R08712, H83343, AA417867, AA090407, AA009846, AA927286, AA678135, AI033148, AI041408, AA235113, AA398662, M62215, W27276, AA885767, AA460155, AA742433, R19908, AA040696, AA555240, AA043160, AA292844, R53160, AA536080, N70013, N35921, N70096, AA277029, AA560610, AI046716, AA237153, W15784, AA547132, AA231089, AA170968, D46090, C61892, C64408, D34777, D35175, D35914, D37381, AA559708, D37143, C60784, AI008855, AI021808, AI009216, D68214, AA220863, D70434.

SEQ ID NO. 157:

U43195, U58512, U61266, D89493, U36909.

SEQ ID NO. 159:

AF069442, AF001295, M13820, M10081, AB010077, AA491075, AA446881, AA588390, AA479958, N20112, R86178, R97894, T64868, W68074, AA365195, AA928749, AI037069, AA882303, AA791693, AA822133, AI037224, AA404165, AI036575, AA499662, AA864136, AA561223, AA183703, AA647218, AA792208, W48100, D40621, AJ225487, AA294595,

02866, H35041, AA944944, AA597316, D26977, D68334, AA685934, W88345, AA964819.

SEQ ID NO. 161:

K01546, AE000468, X95549, AC004014, Z81584, L19201, X94244, X06932, U39479, X13301, AC000386, U80847, X86737, U39478, AA883211, AA610050, AA774254, AA280736, AA926725, AA459300, N55370, AA233666, H90342, T66839, H91250, AA856968, R92873, AI034196, AI014787, AA910410, AA088535, AA230765, AA467238, AA397279, AA420226, AA396042, AA200070, AA165873, AA762534, AA067133, AA065429, AA185092, AA572057, AA111387, AA175824, AA881071, AA571692, AA104279, AA733670, AI008804, D86670, C67200, D41938, AA141467, D35894, AI001643, AA957220, T37355, T18792, D47809, W21723, AA898504, AA951903, AA661025, AA949796, AA990685, AA661449, AA948837, R04787, D16046, AA439636, AA246769, AA978829, D43523, T02021, AA803212, D22651, AA201227, AA694728, AA891643, D23309, AA820831, D41871, W21774, D16065.

SEQ ID NO. 163:

X15183, AF028832, D87666, J04633, L33676, X07270, U94395, M27024, M30627, X16857, X07265, M36830, M30626, AA669137, AA725103, AA890496, AA314095, AA554815, AA313331, AA730100, AA214035, AA876412, AA121630, AA314010, AA927532, AA968674, AA679253, N66271, AA558907, AA309988, AA587079, AA075436, AA160964, AA205657, AA214083, AA130903, AA917032, AA149623, AA857523, AA889843, AA305037, AA491055, W73240, AA255644, W73295, AA765431, AA178947, N66409, AA074895, AA306976, AA075052, AA075387, AA130892, AA857443, AA405942, AA629891, AA152004, AA129550, W56527, AA513807, AA703828, AA223171, C75280, AA889155, AA854676, AA773063, AA774999, AA152392, AA307057, AA316954, AA657352, AA522607, AA188113, AA026444, AI003623, AA312717, AA312400, T64299, AA178992, AA228992, AI042136, AA457613, AI032857, AA164461, AA625127, AA807763, AA130815, AA054695, AA937097, W93534, N67875, AA526896, W52802, AA527942, N34251, W28646, AA668543, AA496091, W52511, AA070581, AA306826, AA120908, AA699607, AA086423, N72134, AA630369, AA564649, AA046806, AA666249, AA306893, AA225404, AA127417, AA854951.

SEQ ID NO. 165:

M23885, AF047868, AF017732, AB005249, Z83229, AF026483, U97194, Z67884, Z67881, X13481, X07651, AC001226, AC002542, AB002307, AA984684, AA017533, AA306600, AA261957, F08123, R17885, AA282208, H85861, H85836, AA593150, H87276, AA057384, AA243602, AA013399, AA374926, AA721341, R88896, AA021538, AA101740, AA375314, AA090398, H86058, AA984556, AA215816, AA092672, AA034243, AA328017, F11174, AA261777, N40306, W21253, R02386, AA349225, AI038487, H98027, AA385878, AA075431, AA375596, R77638, T73214, AA310841, AA062331, AA919318, AA606883, 373 AA174568, AA790426, AA423321, AA647673, AA109549, AA396473, W16215, AA105538, AA061105, AA066766, AA462773, AA555644, AA499452, AA389523, AA245036, AA475340, AA880992, AA198965, W11981, AA509705, AA237414, AA646230, AA673569,

AA239037, AA672620, AA915168, AA863498, AA123378.

SEQ ID NO. 167:

Y11251, AF030234, AF043945, L40407.

SEQ ID NO. 169:

U33822, X61838, AA572230, AA589570, AA929790, AA104830, C81582, AA271190, AA290278, AA543616, AI043207, AA107832, AA958460, AI020992, AA795905, AA277468, AA475069, AA111610, AA389139, AA154163.

SEQ ID NO. 170:

D32050, D16969, AC004423, S81497.

SEQ ID NO. 172:

D86982, L07131, M14544, AA296228, AA318436, AA296234, H88394, W26642, AF038251, AA394101, N35855, N56791, N35444, AA147382, AA647547, AA939939, AA895989, AA122437, AA277698, W75741, AI036117, AA980469, AA033178, AI006694, AA980625, AA033190, AA175922, AA172918, AA895209, AA028700, AA416048, AA175247, AA217057, AI045760, R64866, D40836, D41873, AA509279, D40089, AA114361, AA751642, AA848690, AA800525, AA802510, C24001, AA841755, AA882663, D40069, AA433358, D40199, AA958134, AA072494, AI008727, AA618978, AA848687, C21884, AA113662, AA945653, AA660093, C58446, AA908068, AA532100, AA264560, AA426658, AA097169, AA751535.

SEQ ID NO. 174:

Z81364, AC003033, AE000665, AA570483, AA532739, AA526905, AA725306, AA134415, AA651838, AA481316, AA600310, C04532, AA004615, H20713, AA913640.

_SEQ ID NO: 176

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SEQ ID NO: 177

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SEQ ID NO: 178

Z50194, U92983, U44088, AC003101, X72892, AF035444, M32474, AF019953, AC001228, Y15443, AF001294, U12418, X06956, M31176, AF015277, AF002708, R43556, AA088367, AA313553, H92530, AA376262, T09403, AA814143, R75643, AA479005, AA773048, AA507143, AA402127, AA430292, AI015600, AA393069, AA463606, AA885498, AA460759,

AA398766, R48359, AA426107, AA909990, AI017459, AA076224, N39533, AI026941, AA412699, AA292828, AI024759, AI016910, AA573306, R48386, AA065307, AA774549, AI016070, AA884918, AA431512, AA306051, AA476440, AA292924, AA621059, AA411830, AA405079, AA596171, AA989987, AA472637, AA690249, AA691927, AA792720, AA637983, AA020137, AA097337, AA117759, W17615, AA285526, AA111347, AA208823, AA879750, AA413058, W33316, AA161891, W41259, AA511152, AA027481, AA020252, AA033106, AA965045, D41048, AI031042, D48020, AA925258, D40853, AA945674, C19585, AI013412, T15040, AA541011, AA990782, AA851306, AA540938, T23386, AA783863, AA979035, AA951002, AA438957, AA979006, AA978995, AA800046, AA556128, C27411, D15562, T20348, AA966363, AA949269, AA785774, AA728671, D16092, N37869, D48782.

SEQ ID NO: 179

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SEQ ID NO: 180

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SEQ ID NO: 181

U52191, D87072, AL022162, AL008710, Z83850, AF055066, AC004254, L25270, AC003013, U53141, AL021728, AC004997, M38703, AC004020, U91321, AP000041, Z69921, AC002551, D87016, X54171, AF055481, X83213, L05489, AC003018, AB009056, AC000069, L81890, AD000685, AC003031, AC003030, Z99715, AF043301, AE000664, AF007544, X15547,

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SEQ ID NO: 507

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SEQ ID NO: 510

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SEQ ID NO: 511

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SEQ ID NO: 512

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SEQ ID NO: 513

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SEQ ID NO: 523

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SEQ ID NO: 524

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AA975130, AA975130 on06f01.s1 NCI_CGAP_Lei2 Homo sapiens cDNA... 579 e-163
AA885226, AA885226 am34e06.s1 Soares NFL T GBC S1 Homo sapien... 559 e-157
AA912472, AA912472 ol96e03.s1 NCI_CGAP_PNS1 Homo sapiens cDNA... 555 e-156
AA320935, AA320935 EST23388 Adipose tissue, white II Homo sap... 553 e-155

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T08932, T08932 EST06824 Homo sapiens cDNA clone HIBBM46 5' end. 537 e-150
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T19350, T19350 h03012t Testis 1 Homo sapiens cDNA clone h0301... 496 e-138
~~H87681, H87681 yw15e04.r1 Homo sapiens cDNA clone 252318 5'. 490 e-136~~
H81522, H81522 yu61h08.r1 Homo sapiens cDNA clone 230655 5'. 466 e-129
T49620, T49620 ya77g03.s1 Homo sapiens cDNA clone 67732 3'. 452 e-125
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N34907, N34907 yy48a09.s1 Homo sapiens cDNA clone 276760 3'. 371 e-100
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AA338831, AA338831 EST43831 Fetal brain I Homo sapiens cDNA 5... 238 2e-60
T07305, T07305 EST05194 Homo sapiens cDNA clone HFBEG86. 230 4e-58
AA159942, AA159942 zo79c05.r1 Stratagene pancreas (#937208) H... 204 3e-50
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AA797488, AA797488 vw28a05.r1 Soares mouse mammary gland NbMM... 519 e-145
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W75918, W75918 me82f05.r1 Soares mouse embryo NbME13.5 14.5 M... 444 e-123
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AA068340, AA068340 mm53f01.r1 Stratagene mouse embryonic carc... 293 1e-77
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AA207496, AA207496 mv78g02.r1 GuayWoodford Beier mouse kidney... 42 0.078
AA120433, AA120433 mp82h11.r1 Soares 2NbMT Mus musculus cDNA ... 42 0.078
W08185, W08185 mb42h02.r1 Soares mouse p3NMF19.5 Mus musculus... 38 1.2
AA065563, AA065563 ml71b06.r1 Stratagene mouse kidney (#93731... 38 1.2
AA288756, AA288756 mr46h07.r1 Life Tech mouse embryo 15 5dpc ... 38 1.2
AA119334, AA119334 mp80e10.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.2
AA163051, AA163051 ms24a10.r1 Stratagene mouse skin (#937313)... 38 1.2
N28074, N28074 MDB1392R Mouse brain, Stratagene Mus musculus ... 38 1.2
AA288757, AA288757 mr46h08.r1 Life Tech mouse embryo 15 5dpc ... 38 1.2
AA122857, AA122857 mq06a02.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.2
AA617519, AA617519 vj77d05.r1 Knowles Solter mouse blastocyst... 38 1.2

W89420, W89420 mf80b03.r1 Soares mouse embryo NbME13.5 14.5 M... 38 1.2
AI047837, AI047837 ud64c11.x1 Sugano mouse liver mlia Mus mus... 38 1.2
AA840310, AA840310 vw91a10.r1 Stratagene mouse skin (#937313)... 36 4.8
AA986428, AA986428 ue13b04.x1 Sugano mouse embryo mewa Mus mu... 36 4.8
~~W47677, W47677 mc89g07.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8~~
AA057996, AA057996 mj56c10.r1 Soares mouse embryo NbME13.5 14... 36 4.8
AA183858, AA183858 mo95h01.r1 Stratagene mouse testis (#93730... 36 4.8
AA212232, AA212232 mu43e08.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8
W41067, W41067 mc39a06.r1 Soares mouse p3NMF19.5 Mus musculus... 36 4.8
AA967594, AA967594 uh01d06.r1 Soares mouse hypothalamus NMHy ... 36 4.8
~~AA414093, AA414093 vc64c07.s1 Knowles Solter mouse 2 cell Mus... 36 4.8~~
AA123833, AA123833 mp93c03.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8
AA432920, AA432920 vd91b11.r1 Soares mouse NbMH Mus musculus ... 36 4.8
AA874496, AA874496 vx03a08.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8
AA000433, AA000433 me76e09.r1 Soares mouse embryo NbME13.5 14... 36 4.8
AA023983, AA023983 mh94a07.r1 Soares mouse placenta 4NbMP13.5... 36 4.8
AA013726, AA013726 mh12e09.r1 Soares mouse placenta 4NbMP13.5... 36 4.8
~~AA274648, AA274648 vb08c01.r1 Soares mouse NML Mus musculus c... 36 4.8~~
AA140347, AA140347 mq89g06.r1 Stratagene mouse heart (#937316... 36 4.8
AA499377, AA499377 vi89c07.r1 Stratagene mouse heart (#937316... 36 4.8
C88747, C88747 Mus musculus early blastocyst cDNA, clone 01B... 36 4.8
AA726125, AA726125 vu88c06.r1 Stratagene mouse skin (#937313)... 36 4.8
AA760311, AA760311 vv71c12.r1 Stratagene mouse skin (#937313)... 36 4.8
AA763007, AA763007 vw60b05.r1 Soares mouse mammary gland NMLM... 36 4.8
AA929878, AA929878 vz44d03.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8
W59064, W59064 md67e10.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8
AA103519, AA103519 mo24b12.r1 Life Tech mouse embryo 13 5dpc ... 36 4.8
AA222310, AA222310 my14d08.r1 Barstead mouse heart MPLRB3 Mus... 36 4.8
W83557, W83557 mf32d02.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8
AA168631, AA168631 ms33c05.r1 Stratagene mouse skin (#937313)... 36 4.8
AA960143, AA960143 vw60b05.s1 Soares mouse mammary gland NMLM... 36 4.8
W34557, W34557 mc58a05.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8
W98818, W98818 mf94e06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8
AA008527, AA008527 mg85h01.r1 Soares mouse embryo NbME13.5 14... 36 4.8
AA008734, AA008734 mg86h03.r1 Soares mouse embryo NbME13.5 14... 36 4.8
AA510568, AA510568 vg33a10.r1 Soares mouse mammary gland NbMM... 36 4.8
AA672524, AA672524 vo59e11.r1 Soares mouse mammary gland NbMM... 36 4.8
AA052773, AA052773 mf24h01.r1 Soares mouse embryo NbME13.5 14... 36 4.8
AA096626, AA096626 mo09h06.r1 Life Tech mouse embryo 10 5dpc ... 36 4.8
AA124880, AA124880 mp73e06.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.8
AA198005, AA198005 mv12b09.r1 GuayWoodford Beier mouse kidney... 36 4.8
AA624213, AA624213 vm98h06.r1 Knowles Solter mouse blastocyst... 36 4.8
AA521863, AA521863 vi08b01.r1 Barstead mouse myotubes MPLRB5.... 36 4.8
AA692113, AA692113 vt19d03.r1 Barstead mouse myotubes MPLRB5 ... 36 4.8
W71551, W71551 me39e11.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.8

AA646501, AA646501 vn12g12.r1 Stratagene mouse heart (#937316... 36 4.8
AA607056, AA607056 vm95e05.r1 Knowles Solter mouse blastocyst... 36 4.8
AA163340, AA163340 ms65b10.r1 Stratagene mouse embryonic carc... 36 4.8
AA110893, AA110893 mm02b04.r1 Stratagene mouse kidney (#93731... 36 4.8

AI030290, AI030290 UI-R-C0-jb-d-01-0-UI.s1 UI-R-C0 Rattus nor... 293 1e-77
C71833, C71833 Rice cDNA, partial sequence (E0428_1A) 44 0.017
AA926551, AA926551 TENS1173 T. cruzi epimastigote normalized ... 42 0.069
AA875699, AA875699 TENU0170 T.cruzi epimastigote normalized c... 42 0.069
AA567661, AA567661 HL01595.5prime HL Drosophila melanogaster ... 40 0.27
C74504, C74504 Rice cDNA, partial sequence (E31753_1A) 40 0.27
AA698333, AA698333 HL04291.5prime HL Drosophila melanogaster ... 38 1.1
AA441429, AA441429 LD16359.5prime LD Drosophila melanogaster ... 38 1.1
N68770, N68770 TgESTzy35b12.r1 TgRH Tachyzoite cDNA Toxoplasm... 38 1.1
AA246440, AA246440 LD05311.5prime LD Drosophila melanogaster ... 38 1.1
AA801776, AA801776 GM12975.5prime GM Drosophila melanogaster ... 38 1.1
N69148, N69148 TgESTzy33d10.r1 TgRH Tachyzoite cDNA Toxoplasm... 38 1.1
AA536484, AA536484 LD17114.5prime LD Drosophila melanogaster ... 38 1.1
AA392544, AA392544 LD11451.5prime LD Drosophila melanogaster ... 38 1.1
AA202696, AA202696 LD03182.5prime LD Drosophila melanogaster ... 38 1.1
AA392367, AA392367 LD11287.5prime LD Drosophila melanogaster ... 38 1.1
AA264629, AA264629 LD08245.5prime LD Drosophila melanogaster ... 38 1.1
AA735318, AA735318 LD21104.5prime LD Drosophila melanogaster ... 38 1.1
AA264558, AA264558 LD08333.5prime LD Drosophila melanogaster ... 38 1.1
AA536476, AA536476 LD17106.5prime LD Drosophila Embryo Drosop... 38 1.1
AA957774, AA957774 UI-R-E1-fv-f-04-0-UI.s1 UI-R-E1 Rattus nor... 38 1.1
AA567991, AA567991 HL02092.5prime HL Drosophila melanogaster ... 38 1.1
AA957876, AA957876 UI-R-E1-fv-f-04-0-UI.s2 UI-R-E1 Rattus nor... 38 1.1
AA892488, AA892488 EST196291 Normalized rat kidney, Bento Soa... 38 1.1
AA699001, AA699001 HL06668.5prime HL Drosophila melanogaster ... 36 4.3
C19706, C19706 Rice cDNA, partial sequence (E10809_1A) 36 4.3
D41773, RICS4574A Rice cDNA, partial sequence (S4574_2A). 36 4.3
C40680, C40680 C.elegans cDNA clone yk247c4 : 5' end, single... 36 4.3
AA698625, AA698625 HL05354.5prime HL Drosophila melanogaster ... 36 4.3
C82819, C82819 Oryctolagus cuniculus corneal endothelial cDN... 36 4.3
D46016, RICS10393A Rice cDNA, partial sequence (S10393_3A). 36 4.3
AA536314, AA536314 LD16858.5prime LD Drosophila melanogaster ... 36 4.3
AA801012, AA801012 EST190509 Normalized rat muscle, Bento Soa... 36 4.3
D46541, RICS11289A Rice cDNA, partial sequence (S11289_1A). 36 4.3
D47315, RICS12612A Rice cDNA, partial sequence (S12612_1A). 36 4.3
AA735857, AA735857 GM09977.5prime GM Drosophila melanogaster ... 36 4.3
AA753921, AA753921 97BS0370 Rice Immature Seed Lambda ZAPII c... 36 4.3
D47243, RICS12505A Rice cDNA, partial sequence (S12505_1A). 36 4.3
AA978395, AA978395 LD28411.5prime LD Drosophila melanogaster ... 36 4.3

D15134, RICC0136A Rice cDNA, partial sequence (C0136A). 36 4.3
D46483, RICS11185A Rice cDNA, partial sequence (S11185_1A). 36 4.3
D46618, RICS11395A Rice cDNA, partial sequence (S11395_1A). 36 4.3
D46659, RICS11457A Rice cDNA, partial sequence (S11457_1A). 36 4.3
D46719, RICS11572A Rice cDNA, partial sequence (S11572_1A). 36 4.3
D48579, RICS14880A Rice cDNA, partial sequence (S14880_2A). 36 4.3
AA802334, AA802334 GM04219.5prime GM Drosophila melanogaster ... 36 4.3
D46066, RICS10470A Rice cDNA, partial sequence (S10470_1A). 36 4.3
D47037, RICS12104A Rice cDNA, partial sequence (S12104_1A). 36 4.3
D46874, RICS11807A Rice cDNA, partial sequence (S11807_2A). 36 4.3
D47174, RICS12340A Rice cDNA, partial sequence (S12340_2A). 36 4.3
T04578, T04578 625 Lambda-PRL2 Arabidopsis thaliana cDNA clon... 36 4.3
C83675, C83675 Oryctolagus cuniculus corneal endothelial cDN... 36 4.3
D47950, RICS13762A Rice cDNA, partial sequence (S13762_1A). 36 4.3
R90044, R90044 16399 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 36 4.3
D46994, RICS12013A Rice cDNA, partial sequence (S12013_2A). 36 4.3
AA440820, AA440820 LD15713.5prime LD Drosophila melanogaster ... 36 4.3
C72089, C72089 Rice cDNA, partial sequence (E0963_1A) 36 4.3
Z84004, SSZ84004 S.scrofa mRNA; expressed sequence tag (5'; ... 36 4.3
D47519, RICS13070A Rice cDNA, partial sequence (S13070_1A). 36 4.3
C19735, C19735 Rice cDNA, partial sequence (E10858_1A) 36 4.3
D47231, RICS12462A Rice cDNA, partial sequence (S12462_1A). 36 4.3
D47147, RICS12293A Rice cDNA, partial sequence (S12293_1A). 36 4.3
AA950198, AA950198 LD30147.5prime LD Drosophila melanogaster ... 36 4.3
Z47624, ATTS4480 A. thaliana transcribed sequence; clone TAI... 36 4.3
D45955, RICS10259A Rice cDNA, partial sequence (S10259_1A). 36 4.3
D47137, RICS12280A Rice cDNA, partial sequence (S12280_1A). 36 4.3
D69927, CELK093H2F C.elegans cDNA clone yk93h2 : 5' end, sin... 36 4.3
AA392275, AA392275 LD11117.5prime LD Drosophila melanogaster ... 36 4.3

SEQ ID NO:546

D87455, D87455 Human mRNA for KIAA0266 gene, complete cds 1164 0.0
Z99129, HS425C14 Human DNA sequence from clone 425C14 on chr... 42 0.20
D90900, D90900 Synechocystis sp. PCC6803 complete genome, 2/... 40 0.80
Z74281, SCYDL233W S.cerevisiae chromosome IV reading frame O... 38 3.1
AL021528, HS394P21 Homo sapiens DNA sequence from PAC 394P21... 38 3.1
Z49155, HSL83D3 Human DNA from cosmid L83d3, Huntington's Di... 38 3.1
U33761, HSU33761 Human cyclin A/CDK2-associated p45 (Skp2) mR... 38 3.1
AF052832, AF052832 Trypanosoma cruzi CL Brener cosmid 1b21 ch... 38 3.1
Z98600, SPAC20G4 S.pombe chromosome I cosmid c20G4 38 3.1

Y09438, SPHUSPLUS S.pombe hus1+ gene 38 3.1
D29951, MUSKIF Mouse mRNA for kinesin family protein KIF1a, ... 38 3.1

HUMAN ESTs

AA151187, AA151187 zo03c11.r1 Stratagene colon (#937204) Homo... 694 0.0
AA824593, AA824593 oc83d10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 670 0.0
AA954862, AA954862 op20c03.s1 NCI_CGAP_Co12 Homo sapiens cDNA... 581 e-164
~~T16360, T16360 NIB1193 Normalized infant brain, Bento Soares ... 517 e-145~~
R54592, R54592 yg81h10.s1 Homo sapiens cDNA clone 40102 3'. 511 e-143
AA373594, AA373594 EST85631 HSC172 cells I Homo sapiens cDNA ... 507 e-142
AA100660, AA100660 zl90a05.r1 Stratagene colon (#937204) Homo... 383 e-104
R42009, R42009 yg05b04.s1 Homo sapiens cDNA clone 31336 3'. 379 e-103
AA249614, AA249614 k3041.seq.F Human fetal heart, Lambda ZAP ... 252 5e-65
AA360633, AA360633 EST69800 T-cell lymphoma Homo sapiens cDNA... 182 4e-44
~~AA053498, AA053498 zl70b11.r1 Stratagene colon (#937204) Homo... 38 1.5~~
AA992442, AA992442 or85h03.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 38 1.5

AA065677, AA065677 mm43c03.r1 Stratagene mouse melanoma (#937... 297 4e-79
AA529728, AA529728 vi38g12.r1 Beddington mouse embryonic regi... 42 0.035
W91608, W91608 MTA.D10.092.A MTA adult mouse thymus library M... 42 0.035
AA177186, AA177186 mt51a11.r1 Stratagene mouse embryonic carc... 42 0.035
AA048008, AA048008 mj26h10.r1 Soares mouse embryo NbME13.5 14... 36 2.2
AA637535, AA637535 vu10c02.r1 Barstead mouse myotubes MPLRB5 ... 36 2.2
AA726355, AA726355 vu90c09.r1 Stratagene mouse skin (#937313)... 36 2.2
AA404025, AA404025 va31c11.r1 GuayWoodford Beier mouse kidney... 36 2.2
AA060014, AA060014 ml34d07.r1 Stratagene mouse testis (#93730... 36 2.2
AA870617, AA870617 vq23h10.r1 Barstead stromal cell line MPLR... 36 2.2
AA414112, AA414112 vc64f08.s1 Knowles Solter mouse 2 cell Mus... 36 2.2
AA764250, AA764250 vv49e09.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.2

H34350, H34350 EST111226 Rat PC-12 cells, NGF-treated (9 days... 36 1.9
C40718, C40718 C.elegans cDNA clone yk247f9 : 5' end, single... 36 1.9
AA817925, AA817925 UI-R-A0-af-g-04-0-UI.s1 UI-R-A0 Rattus nor... 36 1.9
AA955650, AA955650 UI-R-E1-fc-e-10-0-UI.s1 UI-R-E1 Rattus nor... 36 1.9

SEQ ID NO:547

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.35
U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.35
AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.35
U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.4
Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.4
AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 1.4
U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.4

HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0
AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0
AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143
AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 4e-98
AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 3e-95
AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90
AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84
AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84
AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.17
AA888147, AA888147 04h11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.67
AA946650, AA946650 oq38h09.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.67
AA435587, AA435587 zt85d07.s1 Soares testis NHT Homo sapiens ... 40 0.67
AA806381, AA806381 oc22g05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
AA577174, AA577174 nm86e11.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 40 0.67
AA215903, AA215903 hp0042.seq.F Fetal heart, Lambda ZAP Expre... 40 0.67
AA262229, AA262229 zs25b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
AA969632, AA969632 op38h05.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.67
N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.67
AI005324, AI005324 ou13h07.x1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.67
AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.67
AA860208, AA860208 ak48c10.s1 Soares testis NHT Homo sapiens ... 40 0.67
AA814296, AA814296 nz07d08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
AA873216, AA873216 oh70f04.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.67
AA403143, AA403143 zv66d01.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
W45005, W45005 zc05c12.r1 Soares parathyroid tumor NbHPA Homo... 40 0.67
W32428, W32428 zc05c12.s1 Soares parathyroid tumor NbHPA Homo... 40 0.67
AA974988, AA974988 on59b06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.67
AA725024, AA725024 ah97h10.s1 Soares NFL T GBC S1 Homo sapien... 40 0.67
AA757360, AA757360 ah98a01.s1 Soares NFL T GBC S1 Homo sapien... 40 0.67
N72025, N72025 yz96g02.s1 Homo sapiens cDNA clone 290930 3'. 40 0.67
R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.67
AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.67
AA877455, AA877455 ob33g01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.67
AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.67

AA903406, AA903406 ok62c11.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.67
AA461270, AA461270 zx63b07.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
AA927863, AA927863 om18a08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.67
AA587486, AA587486 nn84e09.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.67
~~W47466, W47466 zc34h02.r1 Soares senescent fibroblasts NbHSF ... 40 0.67~~
AA022495, AA022495 ze70e04.s1 Soares fetal heart NbHH19W Homo... 40 0.67
AA460961, AA460961 zx63b07.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
AA393904, AA393904 zt85e06.r1 Soares testis NHT Homo sapiens ... 40 0.67
AA872272, AA872272 oh72a11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.67
W47341, W47341 zc34h02.s1 Soares senescent fibroblasts NbHSF ... 40 0.67
~~N72024, N72024 yz96g01.s1 Homo sapiens cDNA clone 290928 3'. 40 0.67~~
N35076, N35076 yy19b08.s1 Homo sapiens cDNA clone 271671 3'. 40 0.67
AA813115, AA813115 aj44d06.s1 Soares testis NHT Homo sapiens ... 40 0.67
AA826741, AA826741 85f12.s1 NCI_CGAP_Pr24 Homo sapiens cDNA... 40 0.67
AA160827, AA160827 zo62e01.s1 Stratagene pancreas (#937208) H... 40 0.67
AI040354, AI040354 oy33d12.x1 Soares_parathyroid_tumor_NbHPA ... 40 0.67
AA573297, AA573297 nk98d09.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.67
~~AA416559, AA416559 zu18c03.r1 Soares NhHMPu S1 Homo sapiens c... 40 0.67~~
AA401079, AA401079 zv66d01.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
AI005204, AI005204 ou60c12.x1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.67
N21678, N21678 yx63g01.s1 Soares melanocyte 2NbHM Homo sapien... 40 0.67
AA824270, AA824270 aj29f01.s1 Soares testis NHT Homo sapiens ... 40 0.67
AA804907, AA804907 oa89a01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
AA759038, AA759038 ah75h11.s1 Soares testis NHT Homo sapiens ... 40 0.67
AA417295, AA417295 zu18c03.s1 Soares NhHMPu S1 Homo sapiens c... 40 0.67
AA628544, AA628544 af27h12.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.67
AA618498, AA618498 np30a11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 40 0.67
AA503727, AA503727 ne49g02.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.67
AA514777, AA514777 ni24b01.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 40 0.67
AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.67
AA770473, AA770473 ah89h06.s1 Soares NFL T GBC S1 Homo sapien... 40 0.67
AA759377, AA759377 ah54a10.s1 Soares testis NHT Homo sapiens ... 40 0.67
AA629243, AA629243 zu77e03.s1 Soares testis NHT Homo sapiens ... 40 0.67
AA262162, AA262162 zs25b12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.67
AA161105, AA161105 zo58c05.s1 Stratagene pancreas (#937208) H... 38 2.6
AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.6
AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 2.6
AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.6
N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.6
AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.6
AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.6
H30248, H30248 yp42a01.s1 Homo sapiens cDNA clone 190056 3'. 38 2.6
R82551, R82551 yj19d06.r1 Homo sapiens cDNA clone 149195 5'. 38 2.6

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43
AA014223, AA014223 mh20a03.r1 Soares mouse placenta 4NbMP13.5... 40 0.24
AA014768, AA014768 mi66h04.r1 Soares mouse embryo NbME13.5 14... 40 0.24
AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.24
AA103139, AA103139 mo17f05.r1 Life Tech mouse embryo 13 5dpc ... 40 0.24
AI048515, AI048515 uh61e08.r1 Soares mouse embryonic stem cel... 40 0.24
AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 40 0.24
AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 40 0.24
AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.24
AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 40 0.24
AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.24
AA790448, AA790448 vw04f09.r1 Soares mouse mammary gland NbMM... 40 0.24
AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 40 0.24
AA007762, AA007762 mg76b03.r1 Soares mouse embryo NbME13.5 14... 40 0.24
W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 40 0.24
AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.24
AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 40 0.24
AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 40 0.24
AA543280, AA543280 vj80h05.r1 Soares mouse mammary gland NbMM... 40 0.24
AA106301, AA106301 ml81a09.r1 Stratagene mouse kidney (#93731... 40 0.24
AA467482, AA467482 ve01a10.r1 Soares mouse NbMH Mus musculus ... 40 0.24
AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 40 0.24
W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.24
AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 40 0.24
AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.24
AA138067, AA138067 mq37c11.r1 Barstead MPLRB1 Mus musculus cD... 40 0.24
AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 40 0.24
AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.24
AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 40 0.24
AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.24
AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 40 0.24
W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.24
AA033481, AA033481 mi42b07.r1 Soares mouse embryo NbME13.5 14... 40 0.24
AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.94
AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 3.7
C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 3.7
AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 3.7
W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.7
AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 3.7
AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 3.7
W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.7
AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 3.7
AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 3.7
AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 3.7

AI047609, AI047609 uh63g07.r1 Soares mouse embryonic stem cel... 36 3.7
AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 3.7
AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 3.7
AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.7
W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.7
AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.7
AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.7
AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 3.7
AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 3.7
AI035925, AI035925 ub49e05.r1 Soares mouse mammary gland NbMM... 36 3.7
AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 3.7
AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 3.7
AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 3.7
AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.7
AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 3.7

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.053
C83463, C83463 Oryctolagus cuniculus corneal endothelial cDN... 38 0.84
AA859448, AA859448 UI-R-A0-bf-b-01-0-UI.s1 UI-R-A0 Rattus nor... 38 0.84
AA874930, AA874930 UI-R-E0-ci-b-05-0-UI.s1 UI-R-E0 Rattus nor... 38 0.84
C82607, C82607 Oryctolagus cuniculus corneal endothelial cDN... 38 0.84
AI009631, AI009631 EST204082 Normalized rat lung, Bento Soare... 38 0.84
AA801145, AA801145 EST190642 Normalized rat ovary, Bento Soar... 38 0.84
AI012760, AI012760 EST207211 Normalized rat placenta, Bento S... 38 0.84
AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.84
AA801144, AA801144 EST190641 Normalized rat ovary, Bento Soar... 38 0.84
AA660819, AA660819 00713 MtRHE Medicago truncatula cDNA 5' 38 0.84
AA859865, AA859865 UI-R-E0-cc-b-04-0-UI.s1 UI-R-E0 Rattus nor... 38 0.84
AI009035, AI009035 EST203486 Normalized rat embryo, Bento Soa... 38 0.84
AA859542, AA859542 UI-R-E0-br-d-03-0-UI.s1 UI-R-E0 Rattus nor... 38 0.84
T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.84
H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.3
AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.3
D45997, RICS10346A Rice cDNA, partial sequence (S10346_1A). 36 3.3
AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.3
C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.3
AA785775, AA785775 h4b05a1.f1 Aspergillus nidulans 24hr asexu... 36 3.3
D46069, RICS10475A Rice cDNA, partial sequence (S10475_1A). 36 3.3
AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 3.3
Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.3
Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.3
AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.3
AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.3
Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.3

SEQ ID NO:548

U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.34
AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.34
U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.34
Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.3
~~AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 1.3~~
U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.3
U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.3

HUMAN ESTs

~~W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0~~
AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0
AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143
AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 3e-98
AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 3e-95
AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90
AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84
AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84
AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.16
AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.64
AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.64
AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.64
AA573297, AA573297 nk98d09.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.64
N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.64
AA888147, AA888147 04h11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.64
AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.64
AA877455, AA877455 ob33g01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.64
R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.64
AA514777, AA514777 ni24b01.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 40 0.64
AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.5
N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.5
AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.5
AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.5
AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 2.5
AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.5

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43
AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.23
AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.23
AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.23
AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.23
AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.23
AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.23
AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.23
AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.91
AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.6
AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.6
W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.6
AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 3.6
AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 3.6
AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 3.6
W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.6
AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 3.6
AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.6
AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 3.6
AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 3.6
AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 3.6
AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.6
AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 3.6
C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 3.6
AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 3.6
AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 3.6
AI035925, AI035925 ub49e05.r1 Soares mouse mammary gland NbMM... 36 3.6
AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 3.6
AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 3.6
W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.6
AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 3.6
AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 3.6
AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 3.6

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.052
T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.81
AA660819, AA660819 00713 MtRHE Medicago truncatula cDNA 5' 38 0.81
AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.81
D46069, RICS10475A Rice cDNA, partial sequence (S10475_1A). 36 3.2
AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.2
AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.2
Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.2
H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.2
AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 3.2

D45997, RICS10346A Rice cDNA, partial sequence (S10346_1A). 36 3.2
Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.2
AA785775, AA785775 h4b05a1.f1 Aspergillus nidulans 24hr asexu... 36 3.2
C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.2
AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.2
AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.2
Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.2

SEQ ID NO:549

U79271, HSU79271 Human clones 23920 and 23921 mRNA sequence 650 0.0
AC000395, AC000395 Genomic sequence from Human 9q34, complete... 42 0.28
AC004636, AC004636 Homo sapiens chromosome 5, P1 clone 1268h6... 42 0.28
M94579, HUMCEL Human carboxyl ester lipase (CEL) gene, comple... 42 0.28
AC002097, AC002097 Homo sapiens chromosome 9q34, clone 246H5,... 42 0.28
AB006709, AB006709 Vibrio alginolyticus rpoN gene for RNA po... 42 0.28
Z47074, CEK07C10 Caenorhabditis elegans cosmid K07C10, compl... 40 1.1
AC004755, AC004755 Homo sapiens chromosome 19, fosmid 37502,... 40 1.1
Z28051, SCYKL051W S.cerevisiae chromosome XI reading frame O... 40 1.1
AF022655, AF022655 Homo sapiens cep250 centrosome associated... 40 1.1
AB006708, AB006708 Arabidopsis thaliana genomic DNA, chromos... 40 1.1
AF049105, AF049105 Homo sapiens centrosomal Nek2-associated p... 40 1.1
Z28050, SCYKL050C S.cerevisiae chromosome XI reading frame O... 40 1.1
X75781, SCXI286K S.cerevisiae chromosome XI (28.6 kb) DNA fo... 40 1.1
Y16899, DMY16899 Drosophila melanogaster mRNA for optomotor-... 38 4.3
M87854, RATBARK1 Rattus norvegicus beta-adrenergic receptor k... 38 4.3
M74822, RATMHTLL Rat MHC class I TL-like protein gene, comple... 38 4.3
M80776, HUMBARK1A Human beta-adrenergic receptor kinase 1 mRN... 38 4.3
D84549, YSACA Candida tropicalis DNA for carnitine acetyltra... 38 4.3
L23127, RATRMCI Rattus norvegicus germline MHC class I gene, ... 38 4.3
AC004257, AC004257 Homo sapiens chromosome 19, cosmid R33209,... 38 4.3
U70850, CELF28F9 Caenorhabditis elegans cosmid F28F9 38 4.3
U88309, CELT23B3 Caenorhabditis elegans cosmid T23B3 38 4.3
X53421, DVCHOS18 D. virilis s18, s15, s19, s16 chorion prote... 38 4.3
D89245, D89245 Schizosaccharomyces pombe mRNA, partial cds, ... 38 4.3
AF009623, AF009623 Parascaris univalens PUMA1 (puma1) mRNA, c... 38 4.3
S48813, S48813 beta-adrenergic receptor kinase [rats, brain, ... 38 4.3
Z67883, CEK02A4 Caenorhabditis elegans cosmid K02A4, complet... 38 4.3
U90567, GGU90567 Gallus gallus glutamine rich protein mRNA, p... 38 4.3
M98498, BOVEZRINA Bos taurus ezrin mRNA, complete cds. 38 4.3
M34073, MUSMHT10C Mus musculus (clone T10-c) MHC class I cell... 38 4.3

S81843, S81843 beta-adrenergic receptor kinase 1 [Syrian hams... 38 4.3
X61157, HSBARK H.sapiens mRNA for beta-adrenergic receptor k... 38 4.3
U08438, HSNBARKS4 Human beta-adrenergic receptor kinase (ADRB... 38 4.3
U39674, CELC06E2 Caenorhabditis elegans cosmid C06E2. 38 4.3

HUMAN ESTs

W29097, W29097 56d11 Human retina cDNA randomly primed sublib... 1045 0.0
AA886109, AA886109 ny44f05.s1 NCI_CGAP_Pr12 Homo sapiens cDNA... 656 0.0
~~AA829894, AA829894 oe51e12.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 650 0.0~~
AA879456, AA879456 oj91g03.s1 Soares_NFL_T_GBC_S1 Homo sapien... 650 0.0
AA029201, AA029201 zk12f08.s1 Soares pregnant uterus NbHPU Ho... 650 0.0
AA102109, AA102109 zk87g11.s1 Soares pregnant uterus NbHPU Ho... 650 0.0
AA843811, AA843811 ak09c08.s1 Soares parathyroid tumor NbHPA ... 650 0.0
W72147, W72147 zd70f08.s1 Soares fetal heart NbHH19W Homo sap... 650 0.0
N51485, N51485 yz04e06.s1 Homo sapiens cDNA clone 282082 3'. 650 0.0
AI033069, AI033069 ow93f02.s1 Soares_fetal_liver_spleen_1NFLS... 642 0.0
AA161465, AA161465 zo73a06.s1 Stratagene pancreas (#937208) H... 638 0.0
N51277, N51277 yz14d07.s1 Homo sapiens cDNA clone 283021 3'. 636 e-180
N64528, N64528 yz91e06.s1 Homo sapiens cDNA clone 290434 3'. 636 e-180
H99906, H99906 yx32h10.s1 Homo sapiens cDNA clone 263491 3'. 636 e-180
AA812519, AA812519 ai79b03.s1 Soares testis NHT Homo sapiens ... 636 e-180
R71679, R71679 yj85e08.s1 Homo sapiens cDNA clone 155558 3'. 628 e-178
AA744290, AA744290 ny51d02.s1 NCI_CGAP_Pr18 Homo sapiens cDNA... 626 e-177
AI038590, AI038590 ox34e03.s1 Soares_total_fetus_Nb2HF8_9w Ho... 624 e-177
AA099913, AA099913 zk87g11.r1 Soares pregnant uterus NbHPU Ho... 624 e-177
AA083859, AA083859 zn16d06.s1 Stratagene neuroepithelium NT2R... 622 e-176
AA883684, AA883684 al58a05.s1 Soares NFL T GBC S1 Homo sapien... 613 e-173
R39448, R39448 yc95d03.s1 Homo sapiens cDNA clone 23921 3'. 593 e-167
R36854, R36854 yf52c07.s1 Homo sapiens cDNA clone 25899 3'. 591 e-167
H98684, H98684 yx17g01.s1 Homo sapiens cDNA clone 262032 3'. 585 e-165
R07471, R07471 ye97a06.s1 Homo sapiens cDNA clone 125650 3'. 581 e-164
AA910762, AA910762 ol25h06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 559 e-157
AA083954, AA083954 zn17d06.s1 Stratagene neuroepithelium NT2R... 555 e-156
AA346369, AA346369 EST52776 Fetal heart II Homo sapiens cDNA ... 545 e-153
R54092, R54092 yg98d07.s1 Homo sapiens cDNA clone 41818 3'. 539 e-151
H09074, H09074 yl97a06.s1 Homo sapiens cDNA clone 46164 3'. 535 e-150
N21975, N21975 yw30c10.s1 Homo sapiens cDNA clone 253746 3'. 533 e-149
D59844, HUM070E11A Human fetal brain cDNA 3'-end GEN-070E11. 466 e-129
H11525, H11525 ym15h07.s1 Homo sapiens cDNA clone 48232 3'. 442 e-122
AA971254, AA971254 op73c08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 442 e-122
W77907, W77907 zd70f08.r1 Soares fetal heart NbHH19W Homo sap... 428 e-118
AA878973, AA878973 oj26d11.s1 NCI_CGAP_Kid3 Homo sapiens cDNA... 389 e-106
AA715235, AA715235 nv10g01.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 357 2e-96

AA328928, AA328928 EST32475 Embryo, 12 week I Homo sapiens cD... 355 7e-96
AA860455, AA860455 aj80f02.s1 Soares parathyroid tumor NbHPA ... 283 2e-74
AA026096, AA026096 ze97a04.r1 Soares fetal heart NbHH19W Homo... 268 1e-69
AA026516, AA026516 ze97a04.s1 Soares fetal heart NbHH19W Homo... 172 6e-41
T26899, T26899 ESTDIR509 Homo sapiens cDNA clone CDDIR509 3'. 170 2e-40
N71178, N71178 yw30c10.r1 Homo sapiens cDNA clone 253746 5'. 165 1e-38
AA372290, AA372290 EST84170 Raji cells, cyclohexamide treated... 98 3e-18
AI038890, AI038890 ox84g12.x1 Soares_senescent_fibroblasts_Nb... 40 0.53
D81647, HUM180D08B Human fetal brain cDNA 5'-end GEN-180D08. 38 2.1
AA452630, AA452630 zx33f08.r1 Soares total fetus Nb2HF8 9w Ho... 38 2.1
AA682624, AA682624 zi19g01.s1 Soares fetal liver spleen 1NFLS... 38 2.1
AA742364, AA742364 ny89c12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.1
AA907234, AA907234 ol03h08.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 38 2.1
T09391, T09391 EST07284 Homo sapiens cDNA clone HIBBT71 5' en... 38 2.1
AA161236, AA161236 zo59h07.s1 Stratagene pancreas (#937208) H... 38 2.1
AA252941, AA252941 zr50g09.r1 Soares NhHMPu S1 Homo sapiens c... 38 2.1
AA252245, AA252245 zr64g07.s1 Soares NhHMPu S1 Homo sapiens c... 38 2.1
AA780678, AA780678 ac70h01.s1 Stratagene fetal retina 937202 ... 38 2.1
W05501, W05501 za84a12.r1 Soares fetal lung NbHL19W Homo sapi... 38 2.1
AI039908, AI039908 ox25f07.x1 Soares_total_fetus_Nb2HF8_9w Ho... 38 2.1
AA280664, AA280664 zs99f09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.1
AA973566, AA973566 oo46f09.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 38 2.1
N27253, N27253 yx17g01.r1 Homo sapiens cDNA clone 262032 5'. 38 2.1
AA995707, AA995707 os29c09.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 38 2.1
AI016407, AI016407 ot72e09.s1 Soares_total_fetus_Nb2HF8_9w Ho... 38 2.1
N70619, N70619 za84a12.s1 Homo sapiens cDNA clone 299230 3'. 38 2.1
AA242923, AA242923 zr64g07.r1 Soares NhHMPu S1 Homo sapiens c... 38 2.1
AA938631, AA938631 oo96f07.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 38 2.1
AA985290, AA985290 am74g03.s1 Stratagene schizo brain S11 Hom... 38 2.1

AA690806, AA690806 vt25h10.r1 Barstead mouse myotubes MPLRB5 ... 377 e-103
AA155014, AA155014 mr99h05.r1 Stratagene mouse embryonic carc... 180 8e-44
AA269966, AA269966 va57d06.r1 Soares mouse 3NME12 5 Mus muscu... 172 2e-41
AA089195, AA089195 mo05h11.r1 Stratagene mouse lung 937302 Mu... 163 2e-38
AA466212, AA466212 vg86g02.r1 Barstead mouse pooled organs MP... 68 8e-10
AA423476, AA423476 ve76d07.r1 Soares mouse mammary gland NbMM... 60 2e-07
AA597213, AA597213 vo28a05.r1 Barstead mouse irradiated colon... 40 0.19
AA396266, AA396266 vb45c01.r1 Soares mouse lymph node NbMLN M... 40 0.19
AA967806, AA967806 uh05d06.r1 Soares mouse hypothalamus NMHy ... 38 0.75
AA591111, AA591111 vm12c06.r1 Knowles Solter mouse blastocyst... 38 0.75
W65797, W65797 me14g02.r1 Soares mouse embryo NbME13.5 14.5 M... 38 0.75
AA153891, AA153891 mq56e05.r1 Soares 2NbMT Mus musculus cDNA ... 38 0.75

AI019772, AI019772 ua90h02.r1 Soares mouse mammary gland NbMM... 36 3.0
AA472253, AA472253 vh10g05.r1 Soares mouse mammary gland NbMM... 36 3.0
AA230895, AA230895 mw14g07.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.0
W18052, W18052 mb83g03.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.0
AA797681, AA797681 vx66c12.r1 Stratagene mouse skin (#937313)... 36 3.0
W66734, W66734 me26g05.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.0
AA968020, AA968020 uh07g01.r1 Soares mouse hypothalamus NMHy ... 36 3.0
AA051644, AA051644 mj55d12.r1 Soares mouse embryo NbME13.5 14... 36 3.0
AA162797, AA162797 mr29g09.r1 Soares mouse 3NbMS Mus musculus... 36 3.0
AA549644, AA549644 vk80f08.s1 Knowles Solter mouse 2 cell Mus... 36 3.0
AA273295, AA273295 vc01e01.r1 Soares mouse lymph node NbMLN M... 36 3.0
AA048480, AA048480 mj33d08.r1 Soares mouse embryo NbME13.5 14... 36 3.0
AA098207, AA098207 mn83d01.r1 Stratagene mouse Tcell 937311 M... 36 3.0
AA027381, AA027381 mi05c06.r1 Soares mouse placenta 4NbMP13.5... 36 3.0
AA544474, AA544474 vk33h06.r1 Soares mouse mammary gland NbMM... 36 3.0
AA416466, AA416466 vd15c09.s1 Knowles Solter mouse 2 cell Mus... 36 3.0
AA285999, AA285999 vb88h08.r1 Soares mouse 3NbMS Mus musculus... 36 3.0
AA175025, AA175025 ms85f06.r1 Soares mouse 3NbMS Mus musculus... 36 3.0
AA544386, AA544386 vk33f06.r1 Soares mouse mammary gland NbMM... 36 3.0
AA175557, AA175557 ms96g04.r1 Soares mouse 3NbMS Mus musculus... 36 3.0
AA711924, AA711924 vu59f09.r1 Soares mouse mammary gland NbMM... 36 3.0
AA734052, AA734052 vv22c10.r1 Stratagene mouse heart (#937316... 36 3.0
W53738, W53738 md12a12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.0
AA611837, AA611837 vo82a06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.0
AA879531, AA879531 vv96f06.r1 Soares mouse mammary gland NbMM... 36 3.0
AA288625, AA288625 vb23g09.r1 Soares mouse 3NbMS Mus musculus... 36 3.0

AA784124, AA784124 d2b06a1.f1 Aspergillus nidulans 24hr asexu... 38 0.67
AI044911, AI044911 UI-R-C1-kk-e-05-0-UI.s1 UI-R-C1 Rattus nor... 36 2.6
AA550452, AA550452 1605m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 36 2.6
F20017, ATTS6056 A. thaliana transcribed sequence; clone TAP... 36 2.6
AA786697, AA786697 k5d01a1.f1 Aspergillus nidulans 24hr asexu... 36 2.6
AA433457, AA433457 SW3ICA2345SK Brugia malayi infective larva... 36 2.6

SEQ ID NO:550

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.20
AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.20
U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.20
Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 0.80

AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 0.80
U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 0.80
Y14330, HSY14330 Homo sapiens partial mRNA for jagged2 protein 38 3.2
AF003521, AF003521 Homo sapiens Jagged 2 mRNA, complete cds 38 3.2
AF029778, AF029778 Homo sapiens Jagged2 (JAG2) mRNA, complete... 38 3.2
AF020201, AF020201 Homo sapiens Jagged 2 mRNA, complete cds 38 3.2
Z71523, SCYNL247W S.cerevisiae chromosome XIV reading frame ... 38 3.2
AF029779, AF029779 Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alt... 38 3.2
U70049, RNU70049 Rattus norvegicus jagged2 precursor gene, pa... 38 3.2
X96722, SCCHXIVL S.cerevisiae DNA region from chromosome XIV... 38 3.2
AF005938, AF005938 Cavia porcellus L-type voltage-dependent c... 38 3.2
X78972, SBSTRBF S.bluensis ISP 5564 genes strB and strF 38 3.2
X94912, HSPR22 H.sapiens Pr22 gene 38 3.2

HUMAN ESTs

AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0
AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-144
AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 2e-98
AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 2e-95
AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 1e-90
AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 1e-84
AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 1e-84
AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.098
AI005204, AI005204 ou60c12.x1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.39
AA757360, AA757360 ah98a01.s1 Soares NFL T GBC S1 Homo sapien... 40 0.39
AI005324, AI005324 ou13h07.x1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.39
AA416559, AA416559 zu18c03.r1 Soares NhHMPu S1 Homo sapiens c... 40 0.39
AA262162, AA262162 zs25b12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.39
AA824270, AA824270 aj29f01.s1 Soares testis NHT Homo sapiens ... 40 0.39
AA826741, AA826741 85f12.s1 NCI_CGAP_Pr24 Homo sapiens cDNA... 40 0.39
AA813115, AA813115 aj44d06.s1 Soares testis NHT Homo sapiens ... 40 0.39
AA403143, AA403143 zv66d01.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
AA725024, AA725024 ah97h10.s1 Soares NFL T GBC S1 Homo sapien... 40 0.39
AA804907, AA804907 oa89a01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.39
AA628544, AA628544 af27h12.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
AA618498, AA618498 np30a11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 40 0.39
AA503727, AA503727 ne49g02.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.39
AA460961, AA460961 zx63b07.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
AA770473, AA770473 ah89h06.s1 Soares NFL T GBC S1 Homo sapien... 40 0.39
AA759377, AA759377 ah54a10.s1 Soares testis NHT Homo sapiens ... 40 0.39
AA629243, AA629243 zu77e03.s1 Soares testis NHT Homo sapiens ... 40 0.39
AA903406, AA903406 ok62c11.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.39
AA215903, AA215903 hp0042.seq.F Fetal heart, Lambda ZAP Expre... 40 0.39

AA160827, AA160827 zo62e01.s1 Stratagene pancreas (#937208) H... 40 0.39
AA577174, AA577174 nm86e11.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 40 0.39
AA969632, AA969632 op38h05.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.39
N72025, N72025 yz96g02.s1 Homo sapiens cDNA clone 290930 3'. 40 0.39
AA974988, AA974988 on59b06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.39
W32428, W32428 zc05c12.s1 Soares parathyroid tumor NbHPA Homo... 40 0.39
N21678, N21678 yx63g01.s1 Soares melanocyte 2NbHM Homo sapien... 40 0.39
AA860208, AA860208 ak48c10.s1 Soares testis NHT Homo sapiens ... 40 0.39
AA814296, AA814296 nz07d08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.39
AA806381, AA806381 oc22g05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.39
AA435587, AA435587 zt85d07.s1 Soares testis NHT Homo sapiens ... 40 0.39
W45005, W45005 zc05c12.r1 Soares parathyroid tumor NbHPA Homo... 40 0.39
AA393904, AA393904 zt85e06.r1 Soares testis NHT Homo sapiens ... 40 0.39
AA759038, AA759038 ah75h11.s1 Soares testis NHT Homo sapiens ... 40 0.39
AA927863, AA927863 om18a08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 40 0.39
AA461270, AA461270 zx63b07.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
AA417295, AA417295 zu18c03.s1 Soares NhHMPu S1 Homo sapiens c... 40 0.39
W47466, W47466 zc34h02.r1 Soares senescent fibroblasts NbHSF ... 40 0.39
AA262229, AA262229 zs25b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.39
AA587486, AA587486 nn84e09.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.39
AA401079, AA401079 zv66d01.s1 Soares total fetus Nb2HF8 9w Ho... 40 0.39
AA872272, AA872272 oh72a11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.39
W47341, W47341 zc34h02.s1 Soares senescent fibroblasts NbHSF ... 40 0.39
N72024, N72024 yz96g01.s1 Homo sapiens cDNA clone 290928 3'. 40 0.39
N35076, N35076 yy19b08.s1 Homo sapiens cDNA clone 271671 3'. 40 0.39
AI040354, AI040354 oy33d12.x1 Soares_parathyroid_tumor_NbHPA ... 40 0.39
AA946650, AA946650 oq38h09.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.39
AA022495, AA022495 ze70e04.s1 Soares fetal heart NbHH19W Homo... 40 0.39
AA873216, AA873216 oh70f04.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.39
R82551, R82551 yj19d06.r1 Homo sapiens cDNA clone 149195 5'. 38 1.5
H30248, H30248 yp42a01.s1 Homo sapiens cDNA clone 190056 3'. 38 1.5
AA161105, AA161105 zo58c05.s1 Stratagene pancreas (#937208) H... 38 1.5
AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 1.5
AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 1.5
AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 1.5
AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 1.5

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 6e-44
AA467482, AA467482 ve01a10.r1 Soares mouse NbMH Mus musculus ... 40 0.14
AA543280, AA543280 vj80h05.r1 Soares mouse mammary gland NbMM... 40 0.14
AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 40 0.14
AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.14

AA014768, AA014768 mi66h04.r1 Soares mouse embryo NbME13.5 14... 40 0.14
AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 40 0.14
AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 40 0.14
AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.14
AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.14
AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 40 0.14
AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 40 0.14
AA790448, AA790448 vw04f09.r1 Soares mouse mammary gland NbMM... 40 0.14
AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 40 0.14
AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.14
AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.14
AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 40 0.14
AA138067, AA138067 mq37c11.r1 Barstead MPLRB1 Mus musculus cD... 40 0.14
AA103139, AA103139 mo17f05.r1 Life Tech mouse embryo 13 5dpc ... 40 0.14
AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 40 0.14
AI048515, AI048515 uh61e08.r1 Soares mouse embryonic stem cel... 40 0.14
W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.14
AA007762, AA007762 mg76b03.r1 Soares mouse embryo NbME13.5 14... 40 0.14
AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 40 0.14
AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 40 0.14
AA014223, AA014223 mh20a03.r1 Soares mouse placenta 4NbMP13.5... 40 0.14
AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 40 0.14
AA106301, AA106301 ml81a09.r1 Stratagene mouse kidney (#93731... 40 0.14
AA033481, AA033481 mi42b07.r1 Soares mouse embryo NbME13.5 14... 40 0.14
W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.14
W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 40 0.14
AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.14
AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 0.55
AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.2
AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 2.2
AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 2.2
AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 2.2
C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 2.2
AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 2.2
AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 2.2
AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 2.2
AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 2.2
AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 2.2
W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 2.2
AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 2.2
AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 2.2
AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 2.2
AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 2.2
AI047609, AI047609 uh63g07.r1 Soares mouse embryonic stem cel... 36 2.2
AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 2.2

AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.2
AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 2.2

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.031
AA801145, AA801145 EST190642 Normalized rat ovary, Bento Soar... 38 0.48
AI012760, AI012760 EST207211 Normalized rat placenta, Bento S... 38 0.48
AA874930, AA874930 UI-R-E0-ci-b-05-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48
C82607, C82607 Oryctolagus cuniculus corneal endothelial cDN... 38 0.48
AA859865, AA859865 UI-R-E0-cc-b-04-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48
C83463, C83463 Oryctolagus cuniculus corneal endothelial cDN... 38 0.48
AA801144, AA801144 EST190641 Normalized rat ovary, Bento Soar... 38 0.48
AA859448, AA859448 UI-R-A0-bf-b-01-0-UI.s1 UI-R-A0 Rattus nor... 38 0.48
AI009631, AI009631 EST204082 Normalized rat lung, Bento Soare... 38 0.48
AI009035, AI009035 EST203486 Normalized rat embryo, Bento Soa... 38 0.48
AA859542, AA859542 UI-R-E0-br-d-03-0-UI.s1 UI-R-E0 Rattus nor... 38 0.48
H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 1.9
AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 1.9
Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 1.9
Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 1.9
Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 1.9
AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 1.9
AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 1.9
AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 1.9
AA785775, AA785775 h4b05a1.f1 Aspergillus nidulans 24hr asexu... 36 1.9

SEQ ID NO:551

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.36
AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.36
U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.36
U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.4
U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.4
Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.4
AC004301, AC004301 Drosophila melanogaster DNA sequence (P1 D... 40 1.4

HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0
AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0

AA348243, AA348243	EST54707 Hippocampus I Homo sapiens cDNA 5...	513	e-143
AA551799, AA551799	nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ...	363	4e-98
AA327309, AA327309	EST30621 Colon I Homo sapiens cDNA 5' end	353	4e-95
AA344913, AA344913	EST50856 Gall bladder II Homo sapiens cDNA...	337	2e-90
AA121174, AA121174	zl88g08.s1 Stratagene colon (#937204) Homo...	317	2e-84
AA121198, AA121198	zl88g08.r1 Stratagene colon (#937204) Homo...	317	2e-84
AA001561, AA001561	ze46e07.s1 Soares retina N2b4HR Homo sapie...	42	0.17
AA877455, AA877455	ob33g01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA...	40	0.68
N35888, N35888	yy28b05.s1 Homo sapiens cDNA clone 272529 3'.	40	0.68
~~AA040802, AA040802~~	~~zf07g05.s1 Soares fetal heart NbHH19W Homo...~~	~~40~~	~~0.68~~
AA573297, AA573297	nk98d09.s1 NCI_CGAP_Co3 Homo sapiens cDNA ...	40	0.68
AA041240, AA041240	zf07g05.r1 Soares fetal heart NbHH19W Homo...	40	0.68
AA514777, AA514777	ni24b01.s1 NCI_CGAP_Co4 Homo sapiens cDNA ...	40	0.68
R02514, R02514	ye70b08.r1 Homo sapiens cDNA clone 123063 5'.	40	0.68
AA039536, AA039536	zk39h10.s1 Soares pregnant uterus NbHPU Ho...	40	0.68
AA888147, AA888147	04h11.s1 NCI_CGAP_Co10 Homo sapiens cDNA...	40	0.68
~~AA172158, AA172158~~	~~zp29a01.s1 Stratagene neuroepithelium (#93...~~	~~40~~	~~0.68~~
AA416734, AA416734	zu08c01.s1 Soares testis NHT Homo sapiens ...	38	2.7
N98472, N98472	yy65a04.r1 Homo sapiens cDNA clone 278382 5'.	38	2.7
AA416815, AA416815	zu08c01.r1 Soares testis NHT Homo sapiens ...	38	2.7
AA852281, AA852281	NHTBCae11g05r1 Normal Human Trabecular Bon...	38	2.7
AA948291, AA948291	oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ...	38	2.7
R14449, R14449	yf81h09.r1 Homo sapiens cDNA clone 29034 5'.	38	2.7
AA431486, AA431486	zw72g01.s1 Soares testis NHT Homo sapiens ...	38	2.7

AA616807, AA616807	vn68c05.r1 Barstead mouse irradiated colon...	180	1e-43
AA469884, AA469884	vf71g10.r1 Barstead mouse pooled organs MP...	40	0.24
AA038869, AA038869	mi95b10.r1 Soares mouse p3NMF19.5 Mus musc...	40	0.24
AA185487, AA185487	mt62c07.r1 Soares 2NbMT Mus musculus cDNA ...	40	0.24
AA230758, AA230758	my32g10.r1 Barstead mouse pooled organs MP...	40	0.24
AA276740, AA276740	vc42a12.r1 Soares mouse 3NbMS Mus musculus...	40	0.24
AA763419, AA763419	vw54a12.r1 Soares mouse mammary gland NMLM...	40	0.24
AA106439, AA106439	ml59a08.r1 Stratagene mouse testis (#93730...	40	0.24
AA250010, AA250010	mz59b12.r1 Soares mouse lymph node NbMLN M...	38	0.97
AA068686, AA068686	mm59a03.r1 Stratagene mouse embryonic carc...	38	0.97
AA139459, AA139459	mq86a03.r1 Stratagene mouse melanoma (#937...	38	0.97
AA881111, AA881111	vz06e09.r1 Soares mouse mammary gland NbMM...	36	3.8
AA692425, AA692425	vt59b05.r1 Barstead mouse irradiated colon...	36	3.8
AA049011, AA049011	mj48c09.r1 Soares mouse embryo NbME13.5 14...	36	3.8
AA966976, AA966976	ua38f11.r1 Soares mouse mammary gland NbMM...	36	3.8
AI047077, AI047077	uh61g06.r1 Soares mouse embryonic stem cel...	36	3.8
AA103139, AA103139	mo17f05.r1 Life Tech mouse embryo 13 5dpc ...	36	3.8

AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 3.8
AA543280, AA543280 vj80h05.r1 Soares mouse mammary gland NbMM... 36 3.8
AA007762, AA007762 mg76b03.r1 Soares mouse embryo NbME13.5 14... 36 3.8
AA014223, AA014223 mh20a03.r1 Soares mouse placenta 4NbMP13.5... 36 3.8
AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 3.8
AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 3.8
W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.8
AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 3.8
AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.8
AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 36 3.8
~~AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 3.8~~
AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 3.8
AI047609, AI047609 uh63g07.r1 Soares mouse embryonic stem cel... 36 3.8
AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 36 3.8
AA138067, AA138067 mq37c11.r1 Barstead MPLRB1 Mus musculus cD... 36 3.8
W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 36 3.8
AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 3.8
AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 3.8
AI035925, AI035925 ub49e05.r1 Soares mouse mammary gland NbMM... 36 3.8
AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 36 3.8
W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.8
AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 36 3.8
AA467482, AA467482 ve01a10.r1 Soares mouse NbMH Mus musculus ... 36 3.8
AA014768, AA014768 mi66h04.r1 Soares mouse embryo NbME13.5 14... 36 3.8
AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 36 3.8
AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 3.8
AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 36 3.8
AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 3.8
AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 3.8
AA106301, AA106301 ml81a09.r1 Stratagene mouse kidney (#93731... 36 3.8
AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 3.8
C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 3.8
AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 3.8
AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 3.8
AA033481, AA033481 mi42b07.r1 Soares mouse embryo NbME13.5 14... 36 3.8
AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 36 3.8
AI048515, AI048515 uh61e08.r1 Soares mouse embryonic stem cel... 36 3.8
W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.8
AA790448, AA790448 vw04f09.r1 Soares mouse mammary gland NbMM... 36 3.8
AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 3.8
AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 36 3.8
W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.8
W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.8
AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 3.8

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.055
AA891284, AA891284 EST195087 Normalized rat heart, Bento Soar... 40 0.22
Z83055, RNZ83055 R.norvegicus mRNA; expressed sequence tag; ... 40 0.22
AI010967, AI010967 EST205418 Normalized rat muscle, Bento Soa... 40 0.22
AA852049, AA852049 EST194818 Normalized rat spleen, Bento Soa... 40 0.22
H33489, H33489 EST109542 Rat PC-12 cells, NGF-treated (9 days... 40 0.22
AA799616, AA799616 EST189113 Normalized rat heart, Bento Soar... 40 0.22
Z83044, RNZ83044 R.norvegicus mRNA; expressed sequence tag; ... 40 0.22
AA660819, AA660819 00713 MtRHE Medicago truncatula cDNA 5' 38 0.86
AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.86
T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.86
AA785775, AA785775 h4b05a1.f1 Aspergillus nidulans 24hr asexu... 36 3.4
AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 3.4
AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.4
C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.4
AA800635, AA800635 EST190132 Normalized rat lung, Bento Soare... 36 3.4
Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.4
Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.4
AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.4
AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.4
H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.4
Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.4
D45997, RICS10346A Rice cDNA, partial sequence (S10346_1A). 36 3.4
AA125602, AA125602 JM00M011 QM3 Miracidia Sjc 3/96 Schistosom... 36 3.4
AA800634, AA800634 EST190131 Normalized rat lung, Bento Soare... 36 3.4
D46069, RICS10475A Rice cDNA, partial sequence (S10475_1A). 36 3.4

SEQ ID NO:552

U66201, MMU66201 Mus musculus fibroblast growth factor homolo... 42 0.38
AF020738, AF020738 Mus musculus fibroblast growth factor-rela... 42 0.38
U66197, HSU66197 Human fibroblast growth factor homologous fa... 42 0.38
Z46966, MMIMOGN44 M.musculus mRNA for imogen 44. 40 1.5
U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 40 1.5
U85773, HSU85773 Human phosphomannomutase (PMM2) mRNA, comple... 40 1.5

HUMAN ESTs

W22160, W22160 63A6 Human retina cDNA Tsp509I-cleaved sublibr... 791 0.0
AA860926, AA860926 ak22d06.s1 Soares testis NHT Homo sapiens ... 650 0.0

AA348243, AA348243 EST54707 Hippocampus I Homo sapiens cDNA 5... 513 e-143
AA551799, AA551799 nk04a11.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 363 4e-98
AA327309, AA327309 EST30621 Colon I Homo sapiens cDNA 5' end 353 4e-95
AA344913, AA344913 EST50856 Gall bladder II Homo sapiens cDNA... 337 2e-90
AA121198, AA121198 zl88g08.r1 Stratagene colon (#937204) Homo... 317 2e-84
AA121174, AA121174 zl88g08.s1 Stratagene colon (#937204) Homo... 317 2e-84
AA001561, AA001561 ze46e07.s1 Soares retina N2b4HR Homo sapie... 42 0.18
AA172158, AA172158 zp29a01.s1 Stratagene neuroepithelium (#93... 40 0.72
N35888, N35888 yy28b05.s1 Homo sapiens cDNA clone 272529 3'. 40 0.72
~~AA877455, AA877455 ob33g01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.72~~
AA573297, AA573297 nk98d09.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.72
AA040802, AA040802 zf07g05.s1 Soares fetal heart NbHH19W Homo... 40 0.72
R02514, R02514 ye70b08.r1 Homo sapiens cDNA clone 123063 5'. 40 0.72
AA514777, AA514777 ni24b01.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 40 0.72
AA041240, AA041240 zf07g05.r1 Soares fetal heart NbHH19W Homo... 40 0.72
AA888147, AA888147 04h11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.72
~~AA039536, AA039536 zk39h10.s1 Soares pregnant uterus NbHPU Ho... 40 0.72~~
AA416734, AA416734 zu08c01.s1 Soares testis NHT Homo sapiens ... 38 2.8
N25839, N25839 yx22e05.r1 Homo sapiens cDNA clone 262496 5'. 38 2.8
AA431486, AA431486 zw72g01.s1 Soares testis NHT Homo sapiens ... 38 2.8
N98472, N98472 yy65a04.r1 Homo sapiens cDNA clone 278382 5'. 38 2.8
AA416815, AA416815 zu08c01.r1 Soares testis NHT Homo sapiens ... 38 2.8
AA852281, AA852281 NHTBCae11g05r1 Normal Human Trabecular Bon... 38 2.8
AA948291, AA948291 oq34d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 38 2.8

AA616807, AA616807 vn68c05.r1 Barstead mouse irradiated colon... 180 1e-43
AA185487, AA185487 mt62c07.r1 Soares 2NbMT Mus musculus cDNA ... 40 0.26
AA276740, AA276740 vc42a12.r1 Soares mouse 3NbMS Mus musculus... 40 0.26
AA469884, AA469884 vf71g10.r1 Barstead mouse pooled organs MP... 40 0.26
AA230758, AA230758 my32g10.r1 Barstead mouse pooled organs MP... 40 0.26
AA038869, AA038869 mi95b10.r1 Soares mouse p3NMF19.5 Mus musc... 40 0.26
AA106439, AA106439 ml59a08.r1 Stratagene mouse testis (#93730... 40 0.26
AA763419, AA763419 vw54a12.r1 Soares mouse mammary gland NMLM... 40 0.26
AA139459, AA139459 mq86a03.r1 Stratagene mouse melanoma (#937... 38 1.0
AA068686, AA068686 mm59a03.r1 Stratagene mouse embryonic carc... 38 1.0
AA218431, AA218431 my07e05.r1 Barstead mouse lung MPLRB2 Mus ... 36 4.0
AI047077, AI047077 uh61g06.r1 Soares mouse embryonic stem cel... 36 4.0
C87249, C87249 Mus musculus fertilized egg cDNA 3'-end seque... 36 4.0
AI035925, AI035925 ub49e05.r1 Soares mouse mammary gland NbMM... 36 4.0
AA111190, AA111190 mp66b11.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.0
AA645119, AA645119 vs72d03.r1 Stratagene mouse skin (#937313)... 36 4.0
AA530735, AA530735 vj32g11.r1 Stratagene mouse diaphragm (#93... 36 4.0

AA000268, AA000268 mg32e09.r1 Soares mouse embryo NbME13.5 14... 36 4.0
AA793845, AA793845 vr35e12.r1 Barstead mouse myotubes MPLRB5 ... 36 4.0
AA840087, AA840087 uc99h12.r1 Soares mouse uterus NMPu Mus mu... 36 4.0
AA711873, AA711873 vu28e06.r1 Barstead mouse myotubes MPLRB5 ... 36 4.0
AA790448, AA790448 vw04f09.r1 Soares mouse mammary gland NbMM... 36 4.0
AA106301, AA106301 ml81a09.r1 Stratagene mouse kidney (#93731... 36 4.0
AA543280, AA543280 vj80h05.r1 Soares mouse mammary gland NbMM... 36 4.0
AA007762, AA007762 mg76b03.r1 Soares mouse embryo NbME13.5 14... 36 4.0
AA921560, AA921560 vy52c06.r1 Stratagene mouse lung 937302 Mu... 36 4.0
~~AA692425, AA692425 vt59b05.r1 Barstead mouse irradiated colon... 36 4.0~~
AA833479, AA833479 uc91c03.r1 Soares mouse uterus NMPu Mus mu... 36 4.0
AA824205, AA824205 vy20g08.r1 Stratagene mouse macrophage (#9... 36 4.0
AA033481, AA033481 mi42b07.r1 Soares mouse embryo NbME13.5 14... 36 4.0
W61547, W61547 md57a02.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.0
AA796056, AA796056 vo65d01.r1 Soares mouse mammary gland NbMM... 36 4.0
AA467482, AA467482 ve01a10.r1 Soares mouse NbMH Mus musculus ... 36 4.0
~~AA239210, AA239210 mx89e02.r1 Soares mouse NML Mus musculus c... 36 4.0~~
AA881111, AA881111 vz06e09.r1 Soares mouse mammary gland NbMM... 36 4.0
AA542324, AA542324 vk53e07.r1 Stratagene mouse Tcell 937311 M... 36 4.0
AA089210, AA089210 mo05d10.r1 Stratagene mouse lung 937302 Mu... 36 4.0
W77724, W77724 me84h06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.0
AI048515, AI048515 uh61e08.r1 Soares mouse embryonic stem cel... 36 4.0
AA009071, AA009071 mg87b11.r1 Soares mouse embryo NbME13.5 14... 36 4.0
AA475425, AA475425 vh20g09.r1 Soares mouse mammary gland NbMM... 36 4.0
AA230661, AA230661 mw15f08.r1 Soares mouse 3NME12 5 Mus muscu... 36 4.0
AA138067, AA138067 mq37c11.r1 Barstead MPLRB1 Mus musculus cD... 36 4.0
W83172, W83172 mf09a06.r1 Soares mouse p3NMF19.5 Mus musculus... 36 4.0
AA797372, AA797372 vw27b08.r1 Soares mouse mammary gland NbMM... 36 4.0
AA711859, AA711859 vu59c10.r1 Soares mouse mammary gland NbMM... 36 4.0
AA967316, AA967316 vj47a03.r1 Stratagene mouse skin (#937313)... 36 4.0
W87202, W87202 mf55g08.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.0
AA103139, AA103139 mo17f05.r1 Life Tech mouse embryo 13 5dpc ... 36 4.0
AA014223, AA014223 mh20a03.r1 Soares mouse placenta 4NbMP13.5... 36 4.0
W62989, W62989 md88h12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.0
W20935, W20935 mb96c07.r1 Soares mouse p3NMF19.5 Mus musculus... 36 4.0
AA966976, AA966976 ua38f11.r1 Soares mouse mammary gland NbMM... 36 4.0
AA856298, AA856298 vw99b01.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.0
AA014768, AA014768 mi66h04.r1 Soares mouse embryo NbME13.5 14... 36 4.0
AA497479, AA497479 vh29b12.r1 Soares mouse mammary gland NbMM... 36 4.0
AA049011, AA049011 mj48c09.r1 Soares mouse embryo NbME13.5 14... 36 4.0
AA016868, AA016868 mh36e12.r1 Soares mouse placenta 4NbMP13.5... 36 4.0
AI047609, AI047609 uh63g07.r1 Soares mouse embryonic stem cel... 36 4.0
AA591243, AA591243 vm18c04.r1 Knowles Solter mouse blastocyst... 36 4.0

AA957268, AA957268 UI-R-E1-fq-e-06-0-UI.s1 UI-R-E1 Rattus nor... 42 0.058
T00613, T00613 wEST01334 Caenorhabditis elegans cDNA clone CE... 38 0.90
AA956139, AA956139 UI-R-E1-fi-h-08-0-UI.s1 UI-R-E1 Rattus nor... 38 0.90
AA660819, AA660819 00713 MtRHE Medicago truncatula cDNA 5' 38 0.90
AA125602, AA125602 JM00M011.QM3 Miracidia Sjc 3/96 Schistosom... 36 3.6
Z33974, ATTS3035 A. thaliana transcribed sequence; clone PAP... 36 3.6
C68472, C68472 C.elegans cDNA clone yk305a12 : 5' end, singl... 36 3.6
AA785775, AA785775 h4b05a1.f1 Aspergillus nidulans 24hr asexu... 36 3.6
Z32602, ATTS2730 A. thaliana transcribed sequence; clone PAP... 36 3.6
AA943364, AA943364 EST198863 Normalized rat brain, Bento Soar... 36 3.6
Z32603, ATTS2731 A. thaliana transcribed sequence; clone PAP... 36 3.6
AA842765, AA842765 M-EST080 Sugarcane mature stalk Saccharum ... 36 3.6
D45997, RICS10346A Rice cDNA, partial sequence (S10346_1A). 36 3.6
AA955567, AA955567 UI-R-E1-fa-a-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.6
AA800634, AA800634 EST190131 Normalized rat lung, Bento Soare... 36 3.6
AA660859, AA660859 00754 MtRHE Medicago truncatula cDNA 5' si... 36 3.6
AA800635, AA800635 EST190132 Normalized rat lung, Bento Soare... 36 3.6
D46069, RICS10475A Rice cDNA, partial sequence (S10475_1A). 36 3.6
H32878, H32878 EST108396 Rat PC-12 cells, untreated Rattus sp... 36 3.6

SEQ ID NO:553

Z99297, HS262D12 Homo sapiens DNA sequence from PAC 262D12 o... 1963 0.0
Z81540, CEF46B3 Caenorhabditis elegans cosmid F46B3, complet... 40 0.89
U67488, U67488 Methanococcus jannaschii section 30 of 150 of ... 38 3.5
AE000786, AE000786 Borrelia burgdorferi plasmid lp28-2, compl... 38 3.5
L02053, OMMGSHTR1 Ommastrephes sloani glutathione transferase... 38 3.5
AC004521, ATAC004521 Arabidopsis thaliana chromosome II BAC F... 38 3.5
L41250, DROGPDHN Drosophila nebulosa glycerol-3-phosphate deh... 38 3.5
AE000619, HPAE000619 Helicobacter pylori section 97 of 134 of... 38 3.5
U39720, Mycoplasma genitalium ackA, licA, mucB, rpL10, rpL32... 38 3.5
AC004533, HUAC004533 Homo sapiens Chromosome 16 BAC clone CIT... 38 3.5
U62292, HSU62292 Human elastin (ELN) gene, partial cds 38 3.5

HUMAN ESTs

W02630, W02630 za52c02.r1 Soares fetal liver spleen 1NFLS Hom... 1009 0.0
AA557183, AA557183 nl74f12.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 874 0.0
AA761171, AA761171 nz09e11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 866 0.0
AA976975, AA976975 oq26g11.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 854 0.0
AA449515, AA449515 zx06b11.r1 Soares total fetus Nb2HF8 9w Ho... 848 0.0

AA678392, AA678392 zi26h10.s1 Soares fetal liver spleen 1NFLS... 848 0.0
AA909198, AA909198 ol12d06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 831 0.0
W79208, W79208 zd79g05.r1 Soares fetal heart NbHH19W Homo sap... 813 0.0
W03125, W03125 za53c02.r1 Soares fetal liver spleen 1NFLS Hom... 807 0.0
W94750, W94750 ze13h08.r1 Soares fetal heart NbHH19W Homo sap... 785 0.0
AA354894, AA354894 EST63217 Jurkat T-cells V Homo sapiens cDN... 771 0.0
H70075, H70075 yr92b03.r1 Homo sapiens cDNA clone 212717 5'. 745 0.0
W77859, W77859 zd70b08.r1 Soares fetal heart NbHH19W Homo sap... 728 0.0
AA425424, AA425424 zw48f03.s1 Soares total fetus Nb2HF8 9w Ho... 718 0.0
AA476893, AA476893 zu29f09.r1 Soares ovary tumor NbHOT Homo s... 688 0.0
AA456676, AA456676 aa01h02.s1 Soares NhHMPu S1 Homo sapiens c... 688 0.0
AA662309, AA662309 nu97c11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 668 0.0
W72135, W72135 zd70b08.s1 Soares fetal heart NbHH19W Homo sap... 650 0.0
N74362, N74362 za52c02.s1 Homo sapiens cDNA clone 296162 3'. 622 e-176
N66917, N66917 za47d09.s1 Homo sapiens cDNA clone 295697 3'. 585 e-165
AA251287, AA251287 zs04c06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 583 e-164
AA971082, AA971082 op70h01.s1 Soares_NFL_T_GBC_S1 Homo sapien... 567 e-160
W78165, W78165 zd79g05.s1 Soares fetal heart NbHH19W Homo sap... 565 e-159
AA253290, AA253290 zr71g03.r1 Soares NhHMPu S1 Homo sapiens c... 559 e-157
AA729063, AA729063 nw22f08.s1 NCI_CGAP_GCB0 Homo sapiens cDNA... 557 e-157
AA987313, AA987313 or81h06.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 553 e-155
AA300954, AA300954 EST13832 Testis tumor Homo sapiens cDNA 5'... 541 e-152
AA425594, AA425594 zw48f03.r1 Soares total fetus Nb2HF8 9w Ho... 529 e-148
N24014, N24014 yx87g10.s1 Homo sapiens cDNA clone 268770 3'. 523 e-146
AA947355, AA947355 od86e12.s1 NCI_CGAP_Ov2 Homo sapiens cDNA ... 504 e-140
AA121074, AA121074 zl88b06.s1 Stratagene colon (#937204) Homo... 460 e-127
AA742964, AA742964 ny15d01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 454 e-126
AA306814, AA306814 EST177885 Colon carcinoma (HCC) cell line ... 452 e-125
W87699, W87699 zh65b11.r1 Soares fetal liver spleen 1NFLS S1 ... 446 e-123
W87700, W87700 zh65b11.s1 Soares fetal liver spleen 1NFLS S1 ... 438 e-121
AA449084, AA449084 zx06b11.s1 Soares total fetus Nb2HF8 9w Ho... 398 e-109
N99231, N99231 zb76f11.s1 Soares senescent fibroblasts NbHSF ... 391 e-106
N49900, N49900 yv24d04.s1 Homo sapiens cDNA clone 243655 3'. 383 e-104
AA782911, AA782911 ai62a10.s1 Soares testis NHT Homo sapiens ... 365 6e-99
AA936553, AA936553 on23g11.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 361 9e-98
N74414, N74414 za53c02.s1 Homo sapiens cDNA clone 296258 3'. 353 2e-95
AA834628, AA834628 od98a10.s1 NCI_CGAP_Ov2 Homo sapiens cDNA ... 341 8e-92
AA693756, AA693756 zi55f11.s1 Soares fetal liver spleen 1NFLS... 341 8e-92
AA909616, AA909616 ol09d06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 341 8e-92
H69662, H69662 yr92b03.s1 Homo sapiens cDNA clone 212717 3'. 321 8e-86
AA249558, AA249558 jj7521.seq.F Human fetal heart, Lambda ZAP... 317 1e-84
AA911960, AA911960 oh88g08.s1 NCI_CGAP_Co8 Homo sapiens cDNA ... 317 1e-84
AA969099, AA969099 op55e06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 303 2e-80
AA766191, AA766191 oa12g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 212 5e-53
AA689312, AA689312 nx05e10.s1 NCI_CGAP_GC3 Homo sapiens cDNA ... 200 2e-49

AA418586, AA418586	zv93e05.r1 Soares NhHMPu S1 Homo sapiens c...	182	5e-44
AA418570, AA418570	zv93e05.s1 Soares NhHMPu S1 Homo sapiens c...	182	5e-44
AA534939, AA534939	nf82f03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ...	167	3e-39
AA888430, AA888430	nw74e05.s1 NCI_CGAP_Pr12 Homo sapiens cDNA...	167	3e-39
N50003, N50003	yv24d04.r1 Homo sapiens cDNA clone 243655 5' s...	149	6e-34
AA535102, AA535102	nf84f06.s1 NCI_CGAP_Co3 Homo sapiens cDNA ...	135	1e-29
AA262335, AA262335	zr71g03.s1 Soares NhHMPu S1 Homo sapiens c...	129	6e-28
AA766681, AA766681	oa34c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA...	105	9e-21
AA761492, AA761492	nz27a05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA...	101	1e-19
AA688350, AA688350	nv15a05.s1 NCI_CGAP_Pr22 Homo sapiens cDNA...	90	5e-16
AA347041, AA347041	EST53285 Fetal heart II Homo sapiens cDNA ...	76	8e-12
T94395, T94395	ye35e02.s1 Homo sapiens cDNA clone 119738 3'.	46	0.007
AA833565, AA833565	aj46a02.s1 Soares testis NHT Homo sapiens ...	46	0.007
AA095460, AA095460	l4630.seq.F Fetal heart, Lambda ZAP Expres...	40	0.43
AA904415, AA904415	ok07e06.s1 Soares_NFL_T_GBC_S1 Homo sapien...	40	0.43
AI018800, AI018800	ov32h04.x1 Soares_testis_NHT Homo sapiens ...	38	1.7
AA631083, AA631083	nq77e07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA...	38	1.7

AA399772, AA399772	vd70g05.r1 Beddington mouse embryonic regi...	347	5e-94
AA467106, AA467106	vd98b04.r1 Soares mouse NbMH Mus musculus ...	309	1e-82
AI046844, AI046844	uh55c11.r1 Soares mouse embryonic stem cel...	208	3e-52
AA475075, AA475075	vh11g05.r1 Soares mouse mammary gland NbMM...	194	4e-48
AA646094, AA646094	vs31e06.r1 Stratagene mouse Tcell 937311 M...	186	1e-45
AA390020, AA390020	vb30e07.r1 Soares mouse lymph node NbMLN M...	170	6e-41
AA245553, AA245553	my52g04.r1 Barstead mouse pooled organs MP...	170	6e-41
AA930741, AA930741	vs57b02.r1 Stratagene mouse skin (#937313)...	155	4e-36
W62610, W62610	md58c06.r1 Soares mouse embryo NbME13.5 14.5 M...	117	8e-25
AA239270, AA239270	my40e01.r1 Barstead mouse pooled organs MP...	109	2e-22
AA015148, AA015148	mh16e01.r1 Soares mouse placenta 4NbMP13.5...	54	1e-05
AA764095, AA764095	vw09h02.r1 Soares 2NbMT Mus musculus cDNA ...	38	0.61
AA238570, AA238570	my35h02.r1 Barstead mouse pooled organs MP...	38	0.61
AA600576, AA600576	vm75f08.r1 Knowles Solter mouse blastocyst...	38	0.61
AA636273, AA636273	vq76a10.s1 Knowles Solter mouse 2 cell Mus...	36	2.4
AA051407, AA051407	mj41f08.r1 Soares mouse embryo NbME13.5 14...	36	2.4
AA823136, AA823136	vw41b03.r1 Soares mouse mammary gland NbMM...	36	2.4
W83831, W83831	mf26a06.r1 Soares mouse embryo NbME13.5 14.5 M...	36	2.4
D77944, MUSC0D06	Mouse embryonal carcinoma F9 cell cDNA, C0D06	36	2.4
AA915408, AA915408	vz29h04.r1 Soares 2NbMT Mus musculus cDNA ...	36	2.4
AI047229, AI047229	uh63a09.r1 Soares mouse embryonic stem cel...	36	2.4
AA271880, AA271880	va73d01.r1 Soares mouse 3NME12 5 Mus muscu...	36	2.4
AA475165, AA475165	vg95f01.r1 Barstead mouse pooled organs MP...	36	2.4
AA619774, AA619774	vl58a05.s1 Knowles Solter mouse 2 cell Mus...	36	2.4

AA673116, AA673116 vn49g11.r1 Barstead mouse myotubes MPLRB5 ... 36 2.4
AA870623, AA870623 vq24a07.r1 Barstead stromal cell line MPLR... 36 2.4
W58907, W58907 md52f12.r1 Soares mouse embryo NbME13.5 14.5 M... 36 2.4
AA690593, AA690593 vu53d05.r1 Soares mouse mammary gland NbMM... 36 2.4
AA754801, AA754801 vu21f03.r1 Barstead mouse myotubes MPLRB5 ... 36 2.4
AA271607, AA271607 va72a12.r1 Soares mouse 3NME12 5 Mus muscu... 36 2.4
AA064256, AA064256 mj66a03.r1 Soares mouse p3NMF19.5 Mus musc... 36 2.4
AA475144, AA475144 vg95d01.r1 Barstead mouse pooled organs MP... 36 2.4
AA197736, AA197736 mv02g08.r1 GuayWoodford Beier mouse kidney... 36 2.4

AA817944, AA817944 UI-R-A0-ag-e-01-0-UI.s1 UI-R-A0 Rattus nor... 40 0.14
F14714, SSC8B01 S.scrofa mRNA; expressed sequence tag (5'; c... 38 0.54
H91505, H91505 SWMFCA089SK Brugia malayi microfilaria cDNA (S... 36 2.1
AA998610, AA998610 UI-R-C0-if-c-04-0-UI.s1 UI-R-C0 Rattus nor... 36 2.1
AA893562, AA893562 EST197365 Normalized rat liver, Bento Soar... 36 2.1
AI008397, AI008397 EST202848 Normalized rat embryo, Bento Soa... 36 2.1

SEQ ID NO:554

Z92544, HS313D11 Human DNA sequence from cosmid 313D11 from ... 700 0.0
Z46940, HSPRMTNP2 H.sapiens PRM1 gene, PRM2 gene and TNP2 gene 44 0.048
U85039, TMU85039 Theileria mutans 32 kDa immunodominant pirop... 42 0.19
U85251, TMU85251 Theileria mutans 32 kDa immunodominant pirop... 42 0.19
AF003630, AF003630 Theileria mutans clone 15, 32 kDa immunodo... 42 0.19
AF003629, AF003629 Theileria mutans clone 9, 32 kDa immunodom... 42 0.19
AB007884, AB007884 Homo sapiens KIAA0424 mRNA, partial cds 42 0.19
U85040, TMU85040 Theileria mutans 32 kDa immunodominant pirop... 42 0.19
Z97343, ATFCA8 Arabidopsis thaliana DNA chromosome 4, ESSA I... 40 0.75
L19655, TOSRNA1X Tomato ringspot virus polyprotein (RNA-1) ge... 40 0.75
M73822, TOSRNA1A Tomato ringspot virus RNA1 gene, 5' end. 40 0.75
L02543, BOVMTNNT Bos taurus nicotinamide nucleotide transhydr... 40 0.75
J03534, BOVNAD Bovine mitochondrial nicotinamide nucleotide t... 40 0.75
M62862, TRBRTE Trypanosoma cruzi retrotransposon encoding gag... 40 0.75
X72711, MMREPCFC M.musculus mRNA for replication factor C, l... 38 3.0
M88489, MUSNBP Mus musculus nonamer binding protein mRNA, com... 38 3.0
U36441, MMU36441 Mus musculus differentiation specific elemen... 38 3.0
AB002354, AB002354 Human mRNA for KIAA0356 gene, complete cds 38 3.0
J03149, CATFMSC Cat (F.domesticus) c-fms proto-oncogene mRNA ... 38 3.0
J05475, CHKVICOLL Chicken type VI collagen alpha 2 (VI) subun... 38 3.0

AF038163, AF038163 Homo sapiens interleukin-15 (IL-15) gene, ... 38 3.0
X75917, HSFBMBF H.sapiens mRNA for fetal beta-MHC binding fa... 38 3.0
X06542, DMHSPG3 Drosophila heat shock gene 3 from 67B locus 38 3.0
D17315, DRODAGK Fruit fly mRNA for diacylglycerol kinase, co... 38 3.0
Z58600, HS45E3F H.sapiens CpG DNA, clone 45e3, forward read ... 38 3.0
D78638, D78638 Xenopus laevis mRNA for DNA (cytosine-5-)-met... 38 3.0
Z49204, MMNADPTRH M.musculus mRNA for NADP transhydrogenase. 38 3.0
L10425, BPEMETC Bordetella avium beta-cystathionase-lyase (me... 38 3.0
U01222, U01222 Mus musculus activator 1 large subunit (A1-p14... 38 3.0
U15037, MMU15037 Mus musculus replication factor C large subu... 38 3.0
K01643, FCSSMONC Feline sarcoma virus (McDonough strain) tran... 38 3.0
Z57538, HS183C6F H.sapiens CpG DNA, clone 183c6, forward rea... 38 3.0
U07157, MMU07157 Mus musculus ISRE-binding protein (IBF-1) mR... 38 3.0
Z64961, HS183F7R H.sapiens CpG DNA, clone 183f7, reverse rea... 38 3.0

HUMAN ESTs

SEQ ID NO:555

AF039693, AF039693 Homo sapiens unknown protein mRNA, complet... 916 0.0
S51239, S51239 calreticulin [Aplysia californica=marine snail... 48 0.005
Z74035, CEF47G9 Caenorhabditis elegans cosmid F47G9, complet... 46 0.019
AF022814, AF022814 Fugu rubripes transcription factor (SLP-1)... 44 0.073
X82638, CSCYTOX C.sordelii cytotoxin gene 42 0.29
U63063, SCU63063 Saccharomyces cerevisiae something about sil... 42 0.29
X63501, SCRPC53 S.cerevisiae RPC53 gene for RNA polymerase C... 42 0.29
U67572, U67572 Methanococcus jannaschii section 114 of 150 of... 42 0.29
Z74201, SCYDL153C S.cerevisiae chromosome IV reading frame O... 42 0.29
U66032, MTU66032 Methanosarcina thermophila CO dehydrogenase/... 42 0.29
Z95620, SPBC3D6 S.pombe chromosome II cosmid c3D6 42 0.29
X97751, SCIV23 S.cerevisiae chrIV genes STE7, CLB3, MSH5, RP... 42 0.29
X65541, ATCAN A.thaliana mRNA for carbonic anhydrase 42 0.29
L14750, ATHCARANHY Arabidopsis thaliana carbonic anhydrase ge... 42 0.29
U00995, U00995 Rattus norvegicus TA1 mRNA, complete cds. 40 1.1
S73876, S73876 FPR3=FKBP-70 [Saccharomyces cerevisiae, Genomi... 40 1.1
U12825, SCU12825 Saccharomyces cerevisiae transcription facto... 40 1.1
Z74237, SCYDL189W S.cerevisiae chromosome IV reading frame O... 40 1.1
U76906, REU76906 Rhizobium etli FixK (fixK), FixN (fixN), mon... 40 1.1

AF050157, MMHC135G15 Mus musculus major histocompatibility lo... 40 1.1
X58857, SCPPH22 S.cerevisiae PPH22 gene for protein phosphat... 40 1.1
X79379, SCPROIS S.cerevisiae gene for proline isomerase 40 1.1
Z68341, CEF01G4 Caenorhabditis elegans cosmid F01G4, complet... 40 1.1
M17192, MUSHOX1 Mouse homeodomain protein (Hox1.1) mRNA, comp... 40 1.1
U50307, CELF43H9 Caenorhabditis elegans cosmid F43H9. 40 1.1
S73144, S73144 bone sialoprotein [cattle, fetal bone cells, m... 40 1.1
L34569, YSCFPR3A Saccharomyces cerevisiae (clone pBYNG1) prol... 40 1.1
D78303, D78303 Rattus norvegicus YT521 mRNA for RNA splicing... 40 1.1
X83276, SCDNAIV S.cerevisiae DNA for ORFs from chromosome IV 40 1.1
U54558, HSU54558 Human translation initiation factor eIF3 p66... 40 1.1
Z50109, CEC09H10 Caenorhabditis elegans cosmid C09H10, compl... 40 1.1
X56983, EAVATP1 E.arvense gene for catalytic 70kDa V-ATPase ... 40 1.1
AB011125, AB011125 Homo sapiens mRNA for KIAA0553 protein, p... 40 1.1
Z46373, SC8248 S.cerevisiae chromosome XIII cosmid 8248 40 1.1
AF039042, CELZK697 Caenorhabditis elegans cosmid ZK697 40 1.1
Z28028, SCYKL028W S.cerevisiae chromosome XI reading frame O... 40 1.1
AC005266, AC005266 Homo sapiens chromosome 19, cosmid F23465,... 38 4.5
U60822, HSU60822 Human dystrophin (DMD) gene, exons 7, 8 and ... 38 4.5
AJ003141, HVAJ3141 Hordeum vulgare mRNA for stress-related p... 38 4.5
M26250, CRAGAP43 Goldfish (C.auratus) growth-associated prote... 38 4.5
X95267, GGRYR3 G.gallus mRNA for ryanodine receptor type 3 38 4.5
L37092, MUSCDPK Mus musculus cyclin-dependent kinase homologu... 38 4.5
Z72507, CEF17C11 Caenorhabditis elegans cosmid F17C11, compl... 38 4.5
U29608, DMU29608 Drosophila melanogaster large tumor suppress... 38 4.5
Z49072, CET24A11 Caenorhabditis elegans cosmid T24A11, compl... 38 4.5
M83142, RATBGASTR Rattus norvegicus beta-galactoside-alpha 2,... 38 4.5
Z20656, HSCAMHCA Homo sapiens of cardiac alpha-myosin heavy ... 38 4.5
M82937, YSACS2A Candida albicans chitin synthase 2 (CHS2) gen... 38 4.5
U28888, MMU28888 Mus musculus neurogenic differentiation fact... 38 4.5
S66408, S66408 c-erbB=proto-oncogene {exon 1, promoter} [chic... 38 4.5
AC002396, AC002396 Arabidopsis thaliana chromosome I BAC F3I6... 38 4.5
AE000665, MMAE000665 Mus musculus TCR beta locus from bases 5... 38 4.5
L39837, DROWARTS Drosophila melanogaster tumor supressor (war... 38 4.5
AG000377, AG000377 Homo sapiens genomic DNA, 21q region, clo... 38 4.5
X05632, HSMHCAG1 Human alpha-MHC gene for myosin heavy chain... 38 4.5
AC002108, AC002108 Genomic sequence from Mouse 4, complete se... 38 4.5
U37219, HSU37219 Human cyclophilin-like protein CyP-60 mRNA, ... 38 4.5
M58633, MUSP58GTA Mouse p58/GTA protein kinase mRNA, complete... 38 4.5
M25162, HUMMYHC08 Human cardiac alpha-myosin heavy chain (MYH... 38 4.5
Z46259, SCRPD3COS S.cerevisiae FY1676 RPD3 gene. 38 4.5
U09558, LJU09558 Lactobacillus johnsonii ATCC 11506 insertion... 38 4.5
U66160, MMUSC104 Mus musculus extracellular matrix associated... 38 4.5
Z73126, SCYLL021W S.cerevisiae chromosome XII reading frame ... 38 4.5
U83981, HSU83981 Homo sapiens apoptosis associated protein (G... 38 4.5

U59897, MRU59897 Macropus robustus hypoxanthine phosphoribosy... 38 4.5
D38256, YSCSCT1 Yeast gene for suppressor of ctr mutation 38 4.5
X69838, HSG9A H.sapiens mRNA for G9a 38 4.5
X52952, RNCMOSO Rat mRNA for c-mos 38 4.5
U37221, HSU37221 Human cyclophilin-like protein mRNA, partial... 38 4.5
X65880, DPRH4OP1 D.pseudoobscura rh4 opsin gene, exon 1 38 4.5
U58971, NTU58971 Nicotiana tabacum calmodulin-binding protein... 38 4.5
Z35773, SCYBL012C S.cerevisiae chromosome II reading frame O... 38 4.5
X67668, MMHMG2 M.musculus mRNA for high mobility group 2 pro... 38 4.5
L81727, HSL81727 Homo sapiens (subclone 1_d5 from P1 H69) DNA... 38 4.5
AL023800, HS833B2 Human DNA sequence *** SEQUENCING IN PROGR... 38 4.5
X62438, HVPERO H.vulgare mRNA for peroxidase 38 4.5
AC004096, AC004096 Mouse Cosmid ma66a100 from 14D1-D2, comple... 38 4.5
AL008980, PFSC03050 Plasmodium falciparum DNA *** SEQUENCING... 38 4.5
U64827, MMU64827 Mus musculus extracellular matrix associated... 38 4.5
AC003010, HUAC003010 Homo sapiens Chromosome 16 BAC clone CIT... 38 4.5
AE001002, AE001002 Archaeoglobus fulgidus section 105 of 172 ... 38 4.5
U86662, LEU86662 Lycopersicon esculentum VPS41 (tVPS41) mRNA,... 38 4.5
M20386, CHKEGFR Chicken epidermal growth factor receptor (CER... 38 4.5
M77637, CHKEGF Gallus gallus EGF/TGF-alpha receptor (c-erbB) ... 38 4.5
U08185, MMU08185 Mus musculus BALB/c zinc-finger protein Blim... 38 4.5
AC004231, AC004231 Homo sapiens chromosome 17, clone hRPC.111... 38 4.5
Z50100, HVC39SAT H.vulgare GAA-satellite DNA 38 4.5
X53731, SCSPA2G S.cerevisiae SPA2 gene 38 4.5
U37220, HSU37220 Human cyclophilin-like protein mRNA, partial... 38 4.5
X97560, SC32KBF S.cerevisiae 32kb DNA fragment of chromosome... 38 4.5
AB011479, AB011479 Arabidopsis thaliana genomic DNA, chromos... 38 4.5
U89340, LVU89340 Lytechinus variegtus Endo16 homolog (LvEndo1... 38 4.5
U73850, TCU73850 Trypanosoma cruzi 29 kDa proteasome subunit ... 38 4.5
AB006698, AB006698 Arabidopsis thaliana genomic DNA, chromos... 38 4.5
D37888, CYIMYC2 Cyprinus carpio c-myc gene for c-Myc, comple... 38 4.5
AF017349, MMDSGIII 7 Mus musculus desmoglein 3 (Dsg3) gene, i... 38 4.5
X91807, OSTA136 O.sativa mRNA for alpha-tubulin (clone OSTA-... 38 4.5
Z71587, SCYNL311C S.cerevisiae chromosome XIV reading frame ... 38 4.5
AE000742, AE000742 Aquifex aeolicus section 74 of 109 of the ... 38 4.5

HUMAN ESTs

AA324311, AA324311 EST27136 Cerebellum II Homo sapiens cDNA 5... 593 e-167
AA639190, AA639190 ns04a01.r1 NCI_CGAP_Ew1 Homo sapiens cDNA ... 513 e-143
AA172199, AA172199 zo96a06.r1 Stratagene ovarian cancer (#937... 505 e-141
AA588066, AA588066 nk10d08.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 502 e-140
AA412036, AA412036 zt68d09.s1 Soares testis NHT Homo sapiens ... 502 e-140
AA508745, AA508745 ni23a03.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 502 e-140

AA480337, AA480337 ne33a03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 502 e-140
AA902270, AA902270 ok69e04.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 502 e-140
AA947303, AA947303 ok20d04.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Hom... 502 e-140
R23642, R23642 yh35e03.r1 Homo sapiens cDNA clone 131740 5'. 490 e-136
AA811913, AA811913 ob51d06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 464 e-128
AA172083, AA172083 zo96a06.s1 Stratagene ovarian cancer (#937... 464 e-128
AA725458, AA725458 ai16g01.s1 Soares parathyroid tumor NbHPA ... 400 e-109
R26558, R26558 yh35e02.s1 Homo sapiens cDNA clone 131738 3'. 359 5e-97
AA402403, AA402403 zt68d09.r1 Soares testis NHT Homo sapiens ... 315 6e-84
R58372, R58372 G3243 Fetal heart Homo sapiens cDNA clone G324... 262 8e-68
AA389703, AA389703 M421 Fetal heart, Lambda ZAP Express Homo ... 202 6e-50
W25749, W25749 11b4 Human retina cDNA randomly primed sublibr... 103 4e-20
W27158, W27158 22h9 Human retina cDNA randomly primed sublibr... 66 1e-08
T65784, T65784 yc11f10.s1 Homo sapiens cDNA clone 80395 3' si... 42 0.14
AA179601, AA179601 zp49f10.r1 Stratagene HeLa cell s3 937216 ... 42 0.14
AA928679, AA928679 on48e08.s1 NCI_CGAP_Co8 Homo sapiens cDNA ... 40 0.55
AA887972, AA887972 nq95g11.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.55
W46946, W46946 zc40c05.s1 Soares senescent fibroblasts NbHSF ... 40 0.55
AA887862, AA887862 nq99b08.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 40 0.55
AA554819, AA554819 ni34d08.s1 NCI_CGAP_Lu1 Homo sapiens cDNA ... 40 0.55
AA557362, AA557362 nl81d12.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.55
AA252258, AA252258 zr29e04.s1 Stratagene NT2 neuronal precurs... 40 0.55
N34310, N34310 yy52b10.s1 Homo sapiens cDNA clone 277147 3' s... 40 0.55
AA552228, AA552228 nk06b04.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 40 0.55
AI017648, AI017648 ou99b02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA... 40 0.55
T17395, T17395 NIB846 Normalized infant brain, Bento Soares H... 40 0.55
AA219659, AA219659 zr05e10.s1 Stratagene NT2 neuronal precurs... 40 0.55
AA463841, AA463841 zx67f06.r1 Soares total fetus Nb2HF8 9w Ho... 40 0.55
N66817, N66817 za09b11.s1 Homo sapiens cDNA clone 292029 3' s... 40 0.55
AA167358, AA167358 zp06f12.s1 Stratagene ovarian cancer (#937... 40 0.55
AA063505, AA063505 zf70d02.r1 Soares pineal gland N3HPG Homo ... 40 0.55
AA731625, AA731625 nw64a04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.55
AA100119, AA100119 zl80g04.s1 Stratagene colon (#937204) Homo... 40 0.55
AA181572, AA181572 zp51d04.s1 Stratagene HeLa cell s3 937216 ... 40 0.55
AA327182, AA327182 EST30459 Colon I Homo sapiens cDNA 5' end ... 40 0.55
R48608, R48608 yj65f07.s1 Homo sapiens cDNA clone 153637 3' s... 40 0.55
AA678485, AA678485 ah06e04.s1 Gessler Wilms tumor Homo sapien... 40 0.55
AA082353, AA082353 zn38c11.r1 Stratagene endothelial cell 937... 40 0.55
AA633213, AA633213 nq57c06.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 40 0.55
W38410, W38410 zc77g09.s1 Pancreatic Islet Homo sapiens cDNA ... 40 0.55
AA345893, AA345893 EST51967 Gall bladder I Homo sapiens cDNA ... 40 0.55
N26876, N26876 yx97f06.s1 Homo sapiens cDNA clone 269699 3' s... 40 0.55
N95279, N95279 zb60c09.s1 Soares fetal lung NbHL19W Homo sapi... 40 0.55
AI041637, AI041637 ox92h08.x1 Soares_senescent_fibroblasts_Nb... 40 0.55
N67830, N67830 za05d12.s1 Homo sapiens cDNA clone 291671 3' s... 40 0.55

AA535094, AA535094 nf84e06.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
AA514414, AA514414 nf57d11.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
T56802, T56802 ya71h07.s2 Homo sapiens cDNA clone 67165 3' co... 40 0.55
N68147, N68147 yz55f12.s1 Homo sapiens cDNA clone 286991 3' s... 40 0.55
AA535811, AA535811 nf93g10.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
AA115591, AA115591 zl05g09.s1 Soares pregnant uterus NbHPU Ho... 40 0.55
N75851, N75851 za96g11.s1 Homo sapiens cDNA clone 300452 3'. 40 0.55
AA534433, AA534433 nf80a08.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
H99778, H99778 yx36g01.s1 Homo sapiens cDNA clone 263856 3' s... 40 0.55
AA970859, AA970859 oo81h03.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 40 0.55
F02131, HSC0PF092 H. sapiens partial cDNA sequence; clone c-... 40 0.55
AA810279, AA810279 od14g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.55
AA595146, AA595146 nl84b01.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.55
AA632386, AA632386 np67e06.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.55
AA135124, AA135124 zo24c04.s1 Stratagene colon (#937204) Homo... 40 0.55
AA143500, AA143500 zo31b10.s1 Stratagene colon (#937204) Homo... 40 0.55
AA854992, AA854992 aj53g12.s1 Soares testis NHT Homo sapiens ... 40 0.55
AA156872, AA156872 zl20h07.s1 Soares pregnant uterus NbHPU Ho... 40 0.55
AA160994, AA160994 zq41c12.s1 Stratagene hNT neuron (#937233)... 40 0.55
AA961724, AA961724 or60a10.s1 NCI_CGAP_GC3 Homo sapiens cDNA ... 40 0.55
AA551210, AA551210 nj27e09.s1 NCI_CGAP_AA1 Homo sapiens cDNA ... 40 0.55
R44103, R44103 yg27c10.s1 Homo sapiens cDNA clone 33636 3'. 40 0.55
AA938086, AA938086 oj08h08.s1 NCI_CGAP_Mel3 Homo sapiens cDNA... 40 0.55
AA576021, AA576021 nm57d11.s1 NCI_CGAP_Br3 Homo sapiens cDNA ... 40 0.55
AA722725, AA722725 zg86b09.s1 Soares fetal heart NbHH19W Homo... 40 0.55
AA678948, AA678948 ah08h11.s1 Gessler Wilms tumor Homo sapien... 40 0.55
W07435, W07435 za96g11.r1 Soares fetal lung NbHL19W Homo sapi... 40 0.55
T34639, T34639 EST72167 Homo sapiens cDNA 5' end similar to s... 40 0.55
AA632245, AA632245 np67b09.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 40 0.55
R98701, R98701 yr31f08.s1 Homo sapiens cDNA clone 206919 3'. 40 0.55
R76418, R76418 yi58a10.s1 Homo sapiens cDNA clone 143418 3'. 40 0.55
AI028447, AI028447 ow08b09.x1 Soares_parathyroid_tumor_NbHPA ... 40 0.55
AI002929, AI002929 an15e12.s1 Gessler Wilms tumor Homo sapien... 40 0.55
AA779388, AA779388 ae26a03.s1 Soares NbHFB Homo sapiens cDNA ... 40 0.55
AA776220, AA776220 ah10f02.s1 Gessler Wilms tumor Homo sapien... 40 0.55
AA815223, AA815223 oc05c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.55
W60807, W60807 zd27b08.s1 Soares fetal heart NbHH19W Homo sap... 40 0.55
AA666007, AA666007 ag71g01.s1 Gessler Wilms tumor Homo sapien... 40 0.55
AA643849, AA643849 np26f07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 40 0.55
AA846740, AA846740 aj99b12.s1 Soares parathyroid tumor NbHPA ... 40 0.55
AA598498, AA598498 ae38h01.s1 Gessler Wilms tumor Homo sapien... 40 0.55
AA535972, AA535972 nf95a01.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 40 0.55
AA488544, AA488544 ab37g06.r1 Stratagene HeLa cell s3 937216 ... 40 0.55
AA866044, AA866044 oh52g07.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.55
C14370, C14370 Human fetal brain cDNA 5'-end GEN-050F01 40 0.55

AA237204, AA237204	mx18d02.r1 Soares mouse NML Mus musculus c...	167	1e-39
AA563402, AA563402	vl75d08.r1 Knowles Solter mouse blastocyst...	38	0.78
AA413261, AA413261	ve52f04.r1 Beddington mouse embryonic regi...	38	0.78
AA097645, AA097645	mm36f09.r1 Stratagene mouse skin (#937313)...	38	0.78
AA122578, AA122578	mn25b08.r1 Beddington mouse embryonic regi...	38	0.78
AA122581, AA122581	mn25c08.r1 Beddington mouse embryonic regi...	38	0.78
AA646168, AA646168	vn11e06.r1 Stratagene mouse Tcell 937311 M...	36	3.1
~~AA200881, AA200881~~	~~mu03c09.r1 Soares mouse 3NbMS Mus musculus...~~	~~36~~	~~3.1~~
AI048938, AI048938	uc84h06.y1 Sugano mouse kidney mkia Mus mu...	36	3.1
AA217675, AA217675	mv01b09.r1 Soares mouse lymph node NbMLN M...	36	3.1
AI006387, AI006387	ua71d09.r1 Soares 2NbMT Mus musculus cDNA ...	36	3.1
AA162722, AA162722	mn42b07.r1 Beddington mouse embryonic regi...	36	3.1
AA207387, AA207387	mv89a11.r1 GuayWoodford Beier mouse kidney...	36	3.1
AA511382, AA511382	vg14b04.r1 Soares mouse NbMH Mus musculus ...	36	3.1
AA123112, AA123112	mn30g01.r1 Beddington mouse embryonic regi...	36	3.1
AA106683, AA106683	ml83h06.r1 Stratagene mouse kidney (#93731...	36	3.1
AA105882, AA105882	ml84h07.r1 Stratagene mouse kidney (#93731...	36	3.1
W12171, W12171	ma59a10.r1 Soares mouse p3NMF19.5 Mus musculus...	36	3.1
AA208446, AA208446	mv85e01.r1 GuayWoodford Beier mouse kidney...	36	3.1
AA451370, AA451370	vf84h02.r1 Soares mouse mammary gland NbMM...	36	3.1
AA244639, AA244639	mx02g12.r1 Soares mouse NML Mus musculus c...	36	3.1
AA267119, AA267119	mz74d07.r1 Soares mouse lymph node NbMLN M...	36	3.1
AA561847, AA561847	vl27a12.r1 Stratagene mouse Tcell 937311 M...	36	3.1
AA237313, AA237313	mx17b11.r1 Soares mouse NML Mus musculus c...	36	3.1
AA145817, AA145817	mq68a12.r1 Soares 2NbMT Mus musculus cDNA ...	36	3.1
AA052080, AA052080	mf69f12.r1 Soares mouse embryo NbME13.5 14...	36	3.1
AA000646, AA000646	mg23f09.r1 Soares mouse embryo NbME13.5 14...	36	3.1
AA510521, AA510521	vh59a05.r1 Soares mouse mammary gland NbMM...	36	3.1
AI006122, AI006122	ua86h01.r1 Soares mouse mammary gland NbMM...	36	3.1
AA987039, AA987039	uc74e05.x1 Sugano mouse liver mlia Mus mus...	36	3.1
W77413, W77413	me64d06.r1 Soares mouse embryo NbME13.5 14.5 M...	36	3.1
AA114809, AA114809	mn17e09.r1 Beddington mouse embryonic regi...	36	3.1
AA793564, AA793564	vn54c05.r1 Barstead mouse myotubes MPLRB5 ...	36	3.1
AA174537, AA174537	mt10f09.r1 Soares mouse 3NbMS Mus musculus...	36	3.1
W62181, W62181	md87d08.r1 Soares mouse embryo NbME13.5 14.5 M...	36	3.1
AA272905, AA272905	va39d01.r1 Soares mouse 3NME12 5 Mus muscu...	36	3.1
AA286005, AA286005	va30e05.r1 GuayWoodford Beier mouse kidney...	36	3.1
AA212823, AA212823	mw81c07.r1 Soares mouse NML Mus musculus c...	36	3.1
AA125061, AA125061	mq83d10.r1 Stratagene mouse melanoma (#937...	36	3.1

AA519228, AA519228	TgESTzz39h02.s1 TgME49 invivo Bradyzoite c...	44	0.011

AA520185, AA520185 TgESTzz39d03.s1 TgME49 invivo Bradyzoite c... 44 0.011
AA531917, AA531917 TgESTzz48f01.r1 TgME49 invivo Bradyzoite c... 44 0.011
AA519997, AA519997 TgESTzz36h03.r1 TgME49 invivo Bradyzoite c... 44 0.011
AA520811, AA520811 TgESTzz64d05.r1 TgME49 invivo Bradyzoite c... 44 0.011
AA520866, AA520866 TgESTzz68e05.r1 TgME49 invivo Bradyzoite c... 44 0.011
AA519844, AA519844 TgESTzz36c03.r1 TgME49 invivo Bradyzoite c... 44 0.011
AA274295, AA274295 TgESTzz24c11.s1 TgME49 invivo Bradyzoite c... 44 0.011
AA520901, AA520901 TgESTzz65a05.r1 TgME49 invivo Bradyzoite c... 44 0.011
AA519829, AA519829 TgESTzz36a02.r1 TgME49 invivo Bradyzoite c... 44 0.011
AA531839, AA531839 TgESTzz47h05.r1 TgME49 invivo Bradyzoite c... 44 0.011
C70525, C70525 C.elegans cDNA clone yk409g6 : 5' end, single... 44 0.011
AA520235, AA520235 TgESTzz53c06.r1 TgME49 invivo Bradyzoite c... 42 0.044
T42800, T42800 6063 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 42 0.044
R29976, R29976 12581 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 42 0.044
H32045, H32045 EST106774 Rat PC-12 cells, untreated Rattus sp... 40 0.18
AA819924, AA819924 MF5MA171.AE3 S. mansoni female adult Lambd... 40 0.18
H37128, H37128 15257 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 40 0.18
T04367, T04367 414 Lambda-PRL2 Arabidopsis thaliana cDNA clon... 40 0.18
R90528, R90528 16883 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 40 0.18
AA660422, AA660422 00298 MtRHE Medicago truncatula cDNA 5' 40 0.18
U94861, RRU94861 Rattus norvegicus clone HCY3 mRNA sequence 40 0.18
F14275, ATTS5197 A. thaliana transcribed sequence; clone YBY... 38 0.69
W43730, W43730 23107 CD4-16 Arabidopsis thaliana cDNA clone H... 38 0.69
N65025, N65025 20065 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 38 0.69
AI001628, AI001628 EST0210 Tilapia brain cDNA library in pUC1... 38 0.69
H74687, H74687 383 Brassica napus cDNA clone R25R... 38 0.69
AA395597, AA395597 27394 Lambda-PRL2 Arabidopsis thaliana cDN... 38 0.69
AA753070, AA753070 97AS2091 Rice Immature Seed Lambda ZAPII c... 38 0.69
D41274, RICS3647A Rice cDNA, partial sequence (S3647_1A). 38 0.69
Z25731, ATTS1208 A. thaliana transcribed sequence; clone VCV... 38 0.69
N82780, N82780 TgESTzy34e03.r1 TgRH Tachyzoite cDNA Toxoplasm... 38 0.69
AA597822, AA597822 29889 Lambda-PRL2 Arabidopsis thaliana cDN... 38 0.69
AA948906, AA948906 LD27590.5prime LD Drosophila melanogaster ... 38 0.69
AI013695, AI013695 EST208370 Normalized rat spleen, Bento Soa... 38 0.69
AA753263, AA753263 96BS0294 Rice Immature Seed Lambda ZAPII c... 38 0.69
F14402, ATTS5324 A. thaliana transcribed sequence; clone TAP... 36 2.7
T46158, T46158 9421 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 2.7
C91400, C91400 Dictyostelium discoideum slug cDNA, clone SSK169 36 2.7
T46009, T46009 9272 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 2.7
AA440655, AA440655 LD15510.5prime LD Drosophila melanogaster ... 36 2.7
AA559374, AA559374 MU002092.NH3 York-Harrop-lung-A Schistosom... 36 2.7
Z32623, ATTS2751 A. thaliana transcribed sequence; clone YAP... 36 2.7
T43683, T43683 6946 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 2.7
AA263535, AA263535 LD06645.5prime LD Drosophila melanogaster ... 36 2.7
C37095, C37095 C.elegans cDNA clone yk482c11 : 3' end, singl... 36 2.7

C57017, C57017 C.elegans cDNA clone yk308h9 : 3' end, single... 36 2.7
C93857, C93857 Dictyostelium discoideum slug cDNA, clone SSL794 36 2.7
C92242, C92242 Dictyostelium discoideum slug cDNA, clone SSD283 36 2.7
Z33976, ATTS3037 A. thaliana transcribed sequence; clone YAP... 36 2.7
R62091, R62091 EST351 Strongylocentrotus purpuratus cDNA 5' end. 36 2.7
AA567455, AA567455 HL01288.5prime HL Drosophila melanogaster ... 36 2.7
C74456, C74456 Rice cDNA, partial sequence (E31357_1A) 36 2.7
AA753227, AA753227 97AS2316 Rice Immature Seed Lambda ZAPII c... 36 2.7
C92456, C92456 Dictyostelium discoideum slug cDNA, clone SSE569 36 2.7
~~T20458, T20458 2466 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 2.7~~
R29905, R29905 12510 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 36 2.7
M79841, M79841 wEST00378 Caenorhabditis elegans cDNA clone CE... 36 2.7
Z17562, ATTS0136 A. thaliana transcribed sequence; clone TAT... 36 2.7
D71983, CELK084H2R C.elegans cDNA clone yk84h2 : 3' end, sin... 36 2.7
T20404, T20404 2412 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 2.7
AI012789, AI012789 EST207240 Normalized rat placenta, Bento S... 36 2.7
~~U83048, BTU83048 Bos taurus clone 0429 mRNA sequence 36 2.7~~
AA660182, AA660182 00022 MtRHE Medicago truncatula cDNA 5' si... 36 2.7
D48514, RICS14740A Rice cDNA, partial sequence (S14740_1A). 36 2.7
C90110, C90110 Dictyostelium discoideum slug cDNA, clone SSI103 36 2.7
H36880, H36880 15009 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 36 2.7
AA699152, AA699152 HL07807.5prime HL Drosophila melanogaster ... 36 2.7
C11922, C11922 C.elegans cDNA clone yk144a11 : 5' end, singl... 36 2.7
AA816691, AA816691 LD03795.5prime LD Drosophila melanogaster ... 36 2.7

SEQ ID NO:556

X99668, MM22A3 M.musculus mRNA for exon from unknown gene 22A3 260 5e-67
Z83760, CICOS41 Ciona intestinalis DNA sequence from cosmid ... 40 0.94
Z75710, CED1081 Caenorhabditis elegans cosmid D1081, complet... 40 0.94
U73628, HSU73628 Human chromosome 11 101h11 cosmid, complete ... 40 0.94
X99757, DMDYDTRO D.melanogaster mRNA for dystrophin 38 3.7
U51189, HIVU51189 HIV-1 clone 93th253 from Thailand, complete... 38 3.7
AC004118, AC004118 Drosophila melanogaster (P1 DS06238 (D26))... 38 3.7
U50313, CELF44C4 Caenorhabditis elegans cosmid F44C4. 38 3.7
AC004503, AC004503 Homo sapiens chromosome 5, P1 clone 1354A7... 38 3.7
M16840, WHTCPCA2 Wheat Asp-tRNA gene. 38 3.7
Y13381, RNAMPH1 Rattus norvegicus mRNA for amphiphysin, amph1 38 3.7
AC002994, AC002994 Homo sapiens chromosome 17, clone HRPC987K... 38 3.7
AB008271, AB008271 Arabidopsis thaliana genomic DNA, chromos... 38 3.7
D49701, ASNNIAD Aspergillus oryzae niaD gene for nitrate red... 38 3.7

X59422, HSPLD1 H.sapiens Pl d1 repetitive DNA 38 3.7
Z98555, PFSC03027 Plasmodium falciparum DNA *** SEQUENCING I... 38 3.7

HUMAN ESTs

AA315671, AA315671 EST187451 Colon carcinoma (HCC) cell line ... 932 0.0
U56653, HSU56653 Human heat shock inducible mRNA 769 0.0
AA487685, AA487685 ab23b09.r1 Stratagene lung (#937210) Homo ... 751 0.0
AA044797, AA044797 zk67g12.r1 Soares pregnant uterus NbHPU Ho... 749 0.0
AA314922, AA314922 EST186735 HCC cell line (matastasis to liv... 698 0.0
AA082278, AA082278 zn42d12.r1 Stratagene endothelial cell 937... 668 0.0
H22613, H22613 yn64f03.r1 Homo sapiens cDNA clone 173213 5'. 624 e-177
AA044743, AA044743 zk67g12.s1 Soares pregnant uterus NbHPU Ho... 622 e-176
AA487470, AA487470 ab23b09.s1 Stratagene lung (#937210) Homo ... 601 e-170
AA121057, AA121057 zm22b03.r1 Stratagene pancreas (#937208) H... 581 e-164
AA194396, AA194396 zq05g05.s1 Stratagene muscle 937209 Homo s... 535 e-150
AA384283, AA384283 EST97787 Thyroid Homo sapiens cDNA 5' end 535 e-150
AA669015, AA669015 ab88f01.s1 Stratagene lung (#937210) Homo ... 535 e-150
AA194336, AA194336 zq05g05.r1 Stratagene muscle 937209 Homo s... 505 e-141
R96173, R96173 yt84e09.r1 Homo sapiens cDNA clone 231016 5'. 486 e-135
AA028934, AA028934 zk08b09.s1 Soares pregnant uterus NbHPU Ho... 484 e-134
AA564849, AA564849 nj22c04.s1 NCI_CGAP_AA1 Homo sapiens cDNA ... 442 e-122
AA932576, AA932576 oo57g10.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 440 e-121
AA876265, AA876265 oi12g09.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 434 e-120
AA025525, AA025525 ze86a11.s1 Soares fetal heart NbHH19W Homo... 430 e-118
U56654, HSU56654 Human heat shock inducible mRNA 426 e-117
AA746600, AA746600 nx18c02.s1 NCI_CGAP_GC3 Homo sapiens cDNA ... 406 e-111
AA876346, AA876346 oj24a11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 406 e-111
W23082, W23082 78D1 Human retina cDNA Tsp509I-cleaved sublibr... 402 e-110
AI034059, AI034059 ow14h11.x1 Soares_parathyroid_tumor_NbHPA ... 357 2e-96
AA662934, AA662934 nu92d09.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 323 2e-86
AA844331, AA844331 ai95f01.s1 Soares parathyroid tumor NbHPA ... 301 8e-80
AA249866, AA249866 y0761.seq.F Human fetal heart, Lambda ZAP ... 297 1e-78
R19215, R19215 yg24b07.r1 Homo sapiens cDNA clone 33126 5'. 280 3e-73
T39355, T39355 ya04g08.r1 Homo sapiens cDNA clone 60542 5'. 254 2e-65
AA731264, AA731264 nw57c08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 220 2e-55
AA768549, AA768549 oa67c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 220 2e-55
AA668506, AA668506 ac49a11.s1 Stratagene hNT neuron (#937233)... 216 4e-54
T55337, T55337 yb79b05.s1 Homo sapiens cDNA clone 77361 3'. 198 8e-49
AA860575, AA860575 aj86a09.s1 Soares parathyroid tumor NbHPA ... 198 8e-49
AA335548, AA335548 EST39962 Epididymus Homo sapiens cDNA 5' end 109 6e-22
R13183, R13183 yf73f02.r1 Homo sapiens cDNA clone 27960 5'. 58 2e-06
T80034, T80034 yd04c06.r1 Homo sapiens cDNA clone 24672 5'. 38 1.8
AA595230, AA595230 nl84g02.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 38 1.8

AA871935, AA871935 vq42h02.r1 Barstead bowel MPLRB9 Mus muscu... 664 0.0
AA062330, AA062330 ml35e10.r1 Stratagene mouse testis (#93730... 589 e-167
AI048164, AI048164 ud71b09.y1 Sugano mouse liver mlia Mus mus... 537 e-151
W08037, W08037 mb37h01.r1 Soares mouse p3NMF19.5 Mus musculus... 462 e-128
AA387311, AA387311 vc19a03.r1 Ko mouse embryo 11 5dpc Mus mus... 264 6e-69
AA163072, AA163072 ms31a11.r1 Stratagene mouse skin (#937313)... 212 2e-53
AA596763, AA596763 vm60a10.r1 Stratagene mouse Tcell 937311 M... 178 3e-43
~~AA562549, AA562549 vl63a11.r1 Knowles Solter mouse blastocyst... 143 2e-32~~
AA212378, AA212378 mu44c03.r1 Soares 2NbMT Mus musculus cDNA ... 113 1e-23
AA450862, AA450862 vg55h12.r1 Beddington mouse embryonic regi... 111 5e-23
AA990073, AA990073 ua59a01.r1 Soares 2NbMT Mus musculus cDNA ... 86 3e-15
AA921175, AA921175 vy54b10.r1 Stratagene mouse lung 937302 Mu... 78 8e-13
AA261119, AA261119 mz89e01.r1 Soares mouse NML Mus musculus c... 38 0.65
AI005952, AI005952 ua80f06.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.6
AA123274, AA123274 mn23a08.r1 Beddington mouse embryonic regi... 36 2.6
AI036828, AI036828 vw96c02.r1 Stratagene mouse skin (#937313)... 36 2.6

H35787, H35787 EST109178 Rat PC-12 cells, NGF-treated (9 days... 105 3e-21
AA686082, AA686082 EST109179 Rat PC-12 cells, NGF-treated (9 ... 86 3e-15
C23464, C23464 Japanese flounder liver cDNA, LE5(10) 72 4e-11
C23465, C23465 Japanese flounder liver cDNA, LE5(10) 56 2e-06
AA520314, AA520314 TgESTzz38h12.r1 TgME49 invivo Bradyzoite c... 38 0.57
AA520085, AA520085 TgESTzz37g05.r1 TgME49 invivo Bradyzoite c... 38 0.57
AA520033, AA520033 TgESTzz36f10.r1 TgME49 invivo Bradyzoite c... 38 0.57
AA012516, AA012516 TgESTzz23f04.r1 TgME49cDNA Toxoplasma gond... 38 0.57
AA274286, AA274286 TgESTzz24c01.s1 TgME49 invivo Bradyzoite c... 38 0.57
AA660585, AA660585 00471 MtRHE Medicago truncatula cDNA 5' si... 38 0.57
L35828, BNAESTBD Brassica rapa (clone F0621) expressed sequen... 38 0.57
AA520070, AA520070 TgESTzz37e05.r1 TgME49 invivo Bradyzoite c... 38 0.57
C30080, C30080 C.elegans cDNA clone yk236c3 : 3' end, single... 36 2.3
C39044, C39044 C.elegans cDNA clone yk505a4 : 3' end, single... 36 2.3
C55023, C55023 C.elegans cDNA clone yk422a3 : 3' end, single... 36 2.3
AA542589, AA542589 fa08d06.s1 Zebrafish ICRFzfls Danio rerio ... 36 2.3
N25370, N25370 EST000480 Schistosoma mansoni cDNA clone SMTBA... 36 2.3
AA820625, AA820625 LD24443.5prime LD Drosophila melanogaster ... 36 2.3
AA494922, AA494922 fa12g10.r1 Zebrafish ICRFzfls Danio rerio ... 36 2.3
AA495181, AA495181 fa04d06.s1 Zebrafish ICRFzfls Danio rerio ... 36 2.3
D73287, CELK116G6R C.elegans cDNA clone yk116g6 : 3' end, si... 36 2.3
C28238, C28238 Rice cDNA, partial sequence (C60429_1A) 36 2.3

SEQ ID NO:557

AF039693, AF039693 Homo sapiens unknown protein mRNA, complet... 948 0.0
S51239, S51239 calreticulin [Aplysia californica=marine snail... 56 1e-05
Z74035, CEF47G9 Caenorhabditis elegans cosmid F47G9, complet... 46 0.012
U25723, CPU25723 Cavia porcellus alpha-2B adrenoceptor gene, ... 44 0.047
AL021407, HS13D10 Homo sapiens DNA sequence from PAC 13D10 o... 42 0.19
U67572, U67572 Methanococcus jannaschii section 114 of 150 of... 42 0.19
V01470, ZMZE01 Zea mays gene encoding a zein gene (clone lam... 42 0.19
U06631, HSU06631 Human (H326) mRNA, complete cds. 42 0.19
X82638, CSCYTOX C.sordelii cytotoxin gene 42 0.19
AE000926, AE000926 Methanobacterium thermoautotrophicum from ... 42 0.19
AC004135, AC004135 Genomic sequence for Arabidopsis thaliana ... 42 0.19
AC003010, HUAC003010 Homo sapiens Chromosome 16 BAC clone CIT... 40 0.74
AF050157, MMHC135G15 Mus musculus major histocompatibility lo... 40 0.74
AC002352, AC002352 Homo sapiens 12q24 PAC P256D10 complete se... 40 0.74
X07699, MMNUCLEO Mouse nucleolin gene 40 0.74
X02399, MMHOM6 Mouse embryonal carcinoma DNA fragment contai... 40 0.74
M93661, RATNOTCHX Rat notch 2 mRNA. 40 0.74
M17440, MUSMHC4H2S Mouse MHC (H-2) S region complement compon... 40 0.74
U15972, MMU15972 Mus musculus homeobox (Hoxa7) gene, complete... 40 0.74
AB001601, AB001601 Homo sapiens DBP2 mRNA for ATP-dependent ... 40 0.74
U09820, HSU09820 Human helicase II (RAD54L) mRNA, complete cds. 40 0.74
AB011149, AB011149 Homo sapiens mRNA for KIAA0577 protein, c... 40 0.74
U26259, MMU26259 Mus musculus C2-H2 zinc finger protein mRNA,... 40 0.74
L48363, MUSZFPTR Mus musculus zinc finger protein gene, compl... 40 0.74
AC003113, AC003113 Arabidopsis thaliana BAC F24O1 chromosome ... 40 0.74
D76432, D76432 Mouse mRNA for transcriptional repressor delt... 40 0.74
U72937, HSU72937 Human putative DNA dependent ATPase and heli... 40 0.74
U72915, HSATRX16 Human putative DNA dependent ATPase and heli... 40 0.74
U00995, U00995 Rattus norvegicus TA1 mRNA, complete cds. 40 0.74
Z48618, SCCHVII35 S.cerevisiae genes for RAD54, ACE1(CUP2), ... 40 0.74
U75653, HSU75653 Human zinc finger helicase (Znf-HX) mRNA, co... 40 0.74
Z72672, SCYGL150C S.cerevisiae chromosome VII reading frame ... 40 0.74
Z50109, CEC09H10 Caenorhabditis elegans cosmid C09H10, compl... 40 0.74
AF013969, AF013969 Mus musculus antigen containing epitope to... 40 0.74
M95627, HUMAAMP1X Homo sapiens angio-associated migratory cel... 40 0.74
U72936, HSU72936 Human putative DNA dependent ATPase and heli... 40 0.74
M88753, DROHTCHRPI Fruitfly heterochromatin protein-1 gene, c... 40 0.74
U76906, REU76906 Rhizobium etli FixK (fixK), FixN (fixN), mon... 40 0.74
U97085, HSXNP14 Homo sapiens X-linked nuclear protein (ATRX) ... 40 0.74
L34363, HUMNUCPRO Human X-linked nuclear protein (XNP) gene, ... 40 0.74
U72938, HSU72938 Human putative DNA dependent ATPase and heli... 40 0.74

X56983, EAVATP1 E.arvense gene for catalytic 70kDa V-ATPase ... 40 0.74
U88539, MMU88539 Mus musculus chromatin structural protein ho... 40 0.74
U07704, HSU07704 Human protein kinase PITSLRE isoform PBETA21... 38 2.9
U07705, HSU07705 Human protein kinase PITSLRE isoform PBETA22... 38 2.9
AF019612, AF019612 Homo sapiens S2P mRNA, complete cds 38 2.9
U04818, HSU04818 Human protein kinase PITSLRE alpha 2-4 mRNA,... 38 2.9
AB002381, AB002381 Human mRNA for KIAA0383 gene, partial cds 38 2.9
AB009520, AB009520 Pyrococcus horikoshii OT3 genomic DNA, 13... 38 2.9
Z83848, HS57A13 Human DNA sequence from PAC 57A13 between ma... 38 2.9
AC004592, AC004592 Homo sapiens PAC clone DJ0244J05 from 5q31... 38 2.9
L11710, ZEFZCMYC Brachydanio rerio c-myc oncoprotein mRNA, co... 38 2.9
D43920, CHKMETASE Chicken mRNA for DNA (cytosine-5-)-methylt... 38 2.9
U49056, RNU49056 Rattus norvegicus CTD-binding SR-like protei... 38 2.9
U04824, HSU04824 Human protein kinase PITSLRE alpha 2-1 mRNA,... 38 2.9
U78045, HSU78045 Human collagenase and stromelysin genes, com... 38 2.9
U04816, HSU04816 Human protein kinase PITSLRE alpha 2-2 mRNA,... 38 2.9
U04817, HSU04817 Human protein kinase PITSLRE alpha 2-3 mRNA,... 38 2.9

HUMAN ESTs

AA639190, AA639190 ns04a01.r1 NCI_CGAP_Ew1 Homo sapiens cDNA ... 519 e-145
AA172199, AA172199 zo96a06.r1 Stratagene ovarian cancer (#937... 513 e-144
R23642, R23642 yh35e03.r1 Homo sapiens cDNA clone 131740 5'... 490 e-136
AA902270, AA902270 ok69e04.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 450 e-124
AA947303, AA947303 ok20d04.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Hom... 402 e-110
AA588066, AA588066 nk10d08.s1 NCI_CGAP_Co2 Homo sapiens cDNA ... 347 1e-93
AA412036, AA412036 zt68d09.s1 Soares testis NHT Homo sapiens ... 347 1e-93
AA480337, AA480337 ne33a03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 347 1e-93
AA508745, AA508745 ni23a03.s1 NCI_CGAP_Co4 Homo sapiens cDNA ... 347 1e-93
AA172083, AA172083 zo96a06.s1 Stratagene ovarian cancer (#937... 315 4e-84
AA811913, AA811913 ob51d06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 299 2e-79
AA402403, AA402403 zt68d09.r1 Soares testis NHT Homo sapiens ... 299 2e-79
AA725458, AA725458 ai16g01.s1 Soares parathyroid tumor NbHPA ... 250 2e-64
R26558, R26558 yh35e02.s1 Homo sapiens cDNA clone 131738 3'. 250 2e-64
W25749, W25749 11b4 Human retina cDNA randomly primed sublibr... 103 3e-20
W27158, W27158 22h9 Human retina cDNA randomly primed sublibr... 66 6e-09
AA737681, AA737681 nw63c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 42 0.090
T65784, T65784 yc11f10.s1 Homo sapiens cDNA clone 80395 3' si... 42 0.090
R52021, R52021 yg84h09.r1 Homo sapiens cDNA clone 40181 5' si... 42 0.090
AA569993, AA569993 nm47h04.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 42 0.090
R50149, R50149 yj61c05.s1 Homo sapiens cDNA clone 153224 3' s... 42 0.090
R87930, R87930 yo47a11.s1 Homo sapiens cDNA clone 181052 3' s... 42 0.090
AA812204, AA812204 ob84f01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 42 0.090
AA770224, AA770224 ah82e12.s1 Soares testis NHT Homo sapiens ... 42 0.090

D29591, HUMNK752 Human keratinocyte cDNA, clone 752 40 0.36
AA324325, AA324325 EST27219 Cerebellum II Homo sapiens cDNA 5... 40 0.36
AA053063, AA053063 zl71c03.r1 Stratagene colon (#937204) Homo... 40 0.36
T35539, T35539 EST86964 Homo sapiens cDNA 5' end similar to N... 40 0.36
AA974278, AA974278 oq14d03.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.36
W26196, W26196 22b5 Human retina cDNA randomly primed sublibr... 40 0.36
H92585, H92585 yt89c03.s1 Homo sapiens cDNA clone 231460 3'. 40 0.36
AA232334, AA232334 zr27b04.r1 Stratagene NT2 neuronal precurs... 40 0.36
N55775, N55775 J2481F Homo sapiens cDNA clone J2481 5'. 40 0.36
R98701, R98701 yr31f08.s1 Homo sapiens cDNA clone 206919 3'. 40 0.36
C14370, C14370 Human fetal brain cDNA 5'-end GEN-050F01 40 0.36
H19156, H19156 yn50c01.r1 Homo sapiens cDNA clone 171840 5'. 40 0.36
AA299557, AA299557 EST12080 Uterus tumor I Homo sapiens cDNA ... 40 0.36
W84460, W84460 zd89d12.r1 Soares fetal heart NbHH19W Homo sap... 40 0.36
T54194, T54194 ya90a02.r2 Homo sapiens cDNA clone 68906 5'. 40 0.36
AA100203, AA100203 zm16f12.r1 Stratagene pancreas (#937208) H... 38 1.4
AA993061, AA993061 ot92h08.s1 Soares_total_fetus_Nb2HF8_9w Ho... 38 1.4
R53406, R53406 yj70d07.r1 Homo sapiens cDNA clone 154093 5' s... 38 1.4
H99671, H99671 yx35b03.s1 Homo sapiens cDNA clone 263693 3'. 38 1.4
W03410, W03410 za07c09.r1 Soares melanocyte 2NbHM Homo sapien... 38 1.4
N35475, N35475 yy24b03.s1 Homo sapiens cDNA clone 272141 3'. 38 1.4
AA630851, AA630851 nt57f04.s1 NCI_CGAP_Pr3 Homo sapiens cDNA ... 38 1.4
N66458, N66458 yz41b08.s1 Homo sapiens cDNA clone 285591 3'. 38 1.4
AA736438, AA736438 zh31b09.s1 Soares pineal gland N3HPG Homo ... 38 1.4
AA911761, AA911761 og19b01.s1 NCI_CGAP_PNS1 Homo sapiens cDNA... 38 1.4
AA085513, AA085513 zn43a10.r1 Stratagene HeLa cell s3 937216 ... 38 1.4
AA678530, AA678530 ah02e05.s1 Gessler Wilms tumor Homo sapien... 38 1.4
AA782011, AA782011 ai75b12.s1 Soares testis NHT Homo sapiens ... 38 1.4
F12352, HSC38H091 H. sapiens partial cDNA sequence; clone c-... 38 1.4
AA861288, AA861288 ak33g01.s1 Soares testis NHT Homo sapiens ... 38 1.4
AA908705, AA908705 ol01b09.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 38 1.4
AA298850, AA298850 EST114450 Thyroid Homo sapiens cDNA 5' end 38 1.4

AA237204, AA237204 mx18d02.r1 Soares mouse NML Mus musculus c... 172 1e-41
AI047347, AI047347 ud65c01.y1 Sugano mouse liver mlia Mus mus... 42 0.032
AA832736, AA832736 vw45g10.r1 Soares mouse mammary gland NbMM... 42 0.032
AA960471, AA960471 vw63a05.s1 Soares mouse mammary gland NMLM... 40 0.13
AA880584, AA880584 vw92e01.r1 Stratagene mouse skin (#937313)... 40 0.13
AA107508, AA107508 mp05e07.r1 Life Tech mouse embryo 8 5dpc 1... 40 0.13
AA116682, AA116682 mn28c06.r1 Beddington mouse embryonic regi... 40 0.13
AA522310, AA522310 vi45b02.r1 Beddington mouse embryonic regi... 40 0.13
AA162231, AA162231 mn44h02.r1 Beddington mouse embryonic regi... 40 0.13

AA414037, AA414037 vc68g03.s1 Knowles Solter mouse 2 cell Mus... 40 0.13
AA596585, AA596585 vm58e12.r1 Stratagene mouse Tcell 937311 M... 38 0.51
AA863563, AA863563 vx05a10.r1 Soares 2NbMT Mus musculus cDNA ... 38 0.51
AA795177, AA795177 vq94g04.r1 Knowles Solter mouse blastocyst... 38 0.51
AA914764, AA914764 vy92h04.r1 Soares mouse mammary gland NbMM... 38 0.51
AA590440, AA590440 vm20c04.r1 Knowles Solter mouse blastocyst... 38 0.51
AA563402, AA563402 vl75d08.r1 Knowles Solter mouse blastocyst... 38 0.51
AA260352, AA260352 va93c10.r1 Soares mouse 3NME12 5 Mus muscu... 38 0.51
AA444734, AA444734 ve75d10.r1 Soares mouse mammary gland NbMM... 38 0.51
C85885, C85885 Mus musculus fertilized egg cDNA 3'-end seque... 38 0.51
AA794590, AA794590 vu78h12.r1 Stratagene mouse skin (#937313)... 38 0.51
AA529643, AA529643 vi38a09.r1 Beddington mouse embryonic regi... 38 0.51
AA607084, AA607084 vm84a09.r1 Knowles Solter mouse blastocyst... 38 0.51
AA636994, AA636994 vn05g06.r1 Knowles Solter mouse blastocyst... 38 0.51
AA675676, AA675676 vr73h08.s1 Knowles Solter mouse 2 cell Mus... 38 0.51
AA163890, AA163890 ms52f09.r1 Life Tech mouse embryo 13 5dpc ... 38 0.51
C80539, C80539 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 38 0.51
AA051352, AA051352 mj53a09.r1 Soares mouse embryo NbME13.5 14... 38 0.51
W36885, W36885 mb64f09.r1 Soares mouse p3NMF19.5 Mus musculus... 38 0.51
AA930627, AA930627 vy67c05.r1 Stratagene mouse macrophage (#9... 38 0.51
AA244639, AA244639 mx02g12.r1 Soares mouse NML Mus musculus c... 36 2.0
AA967267, AA967267 vz70e08.r1 Soares mouse mammary gland NbMM... 36 2.0
AI048938, AI048938 uc84h06.y1 Sugano mouse kidney mkia Mus mu... 36 2.0
AA162722, AA162722 mn42b07.r1 Beddington mouse embryonic regi... 36 2.0
AA170036, AA170036 ms52d01.r1 Life Tech mouse embryo 13 5dpc ... 36 2.0
AA511382, AA511382 vg14b04.r1 Soares mouse NbMH Mus musculus ... 36 2.0
AA555634, AA555634 vk49f08.r1 Stratagene mouse Tcell 937311 M... 36 2.0
AA212823, AA212823 mw81c07.r1 Soares mouse NML Mus musculus c... 36 2.0
AA606813, AA606813 vm90h12.r1 Knowles Solter mouse blastocyst... 36 2.0
AA591610, AA591610 vk49d08.r1 Stratagene mouse Tcell 937311 M... 36 2.0
AA987039, AA987039 uc74e05.x1 Sugano mouse liver mlia Mus mus... 36 2.0
AA105882, AA105882 ml84h07.r1 Stratagene mouse kidney (#93731... 36 2.0
AA451370, AA451370 vf84h02.r1 Soares mouse mammary gland NbMM... 36 2.0
AA612185, AA612185 vo03d05.r1 Stratagene mouse skin (#937313)... 36 2.0
AA103424, AA103424 mo21e05.r1 Life Tech mouse embryo 13 5dpc ... 36 2.0
AA145817, AA145817 mq68a12.r1 Soares 2NbMT Mus musculus cDNA ... 36 2.0
AA272905, AA272905 va39d01.r1 Soares mouse 3NME12 5 Mus muscu... 36 2.0
AA237313, AA237313 mx17b11.r1 Soares mouse NML Mus musculus c... 36 2.0
AA267119, AA267119 mz74d07.r1 Soares mouse lymph node NbMLN M... 36 2.0
AA106683, AA106683 ml83h06.r1 Stratagene mouse kidney (#93731... 36 2.0
AA125061, AA125061 mq83d10.r1 Stratagene mouse melanoma (#937... 36 2.0
AA655241, AA655241 vq84c07.s1 Knowles Solter mouse 2 cell Mus... 36 2.0
AA512835, AA512835 vg13f11.r1 Soares mouse NbMH Mus musculus ... 36 2.0

C70525, C70525	C.elegans cDNA clone yk409g6 : 5' end, single...	44	0.007
F15112, SSO4D09	S.scrofa mRNA; expressed sequence tag (5'; c...	42	0.029
AA684640, AA684640	EST104989 Rat PC-12 cells, untreated Rattu...	40	0.11
H32045, H32045	EST106774 Rat PC-12 cells, untreated Rattus sp...	40	0.11
AA660422, AA660422	00298 MtRHE Medicago truncatula cDNA 5'	40	0.11
C59696, C59696	C.elegans cDNA clone yk440e1 : 3' end, single...	38	0.45
AI008699, AI008699	EST203150 Normalized rat embryo, Bento Soa...	38	0.45
AA753263, AA753263	96BS0294 Rice Immature Seed Lambda ZAPII c...	38	0.45
T38461, T38461	EST103957 Saccharomyces cerevisiae cDNA 3' end.	38	0.45
~~C59257, C59257~~	~~C.elegans cDNA clone yk386b12 : 3' end, singl...~~	~~38~~	~~0.45~~
AA948906, AA948906	LD27590.5prime LD Drosophila melanogaster ...	38	0.45
AI001628, AI001628	EST0210 Tilapia brain cDNA library in pUC1...	38	0.45
H31962, H31962	EST106545 Rat PC-12 cells, untreated Rattus sp...	38	0.45
AA979509, AA979509	LD34118.5prime LD Drosophila melanogaster ...	38	0.45
D41274, RICS3647A	Rice cDNA, partial sequence (S3647_1A).	38	0.45
C58362, C58362	C.elegans cDNA clone yk366a8 : 3' end, single...	38	0.45
~~C57756, C57756~~	~~C.elegans cDNA clone yk298b9 : 3' end, single...~~	~~38~~	~~0.45~~
AA753070, AA753070	97AS2091 Rice Immature Seed Lambda ZAPII c...	38	0.45
H74687, H74687	383 Brassica napus cDNA clone R25R.	38	0.45
C10513, C10513	C.elegans cDNA clone yk147e9 : 3' end, single...	38	0.45
C55569, C55569	C.elegans cDNA clone yk191d1 : 3' end, single...	38	0.45
C94819, C94819	Sus scrofa mRNA; expressed sequence tag (5'...	38	0.45
C32982, C32982	C.elegans cDNA clone yk338a12 : 3' end, singl...	38	0.45
AA816691, AA816691	LD03795.5prime LD Drosophila melanogaster ...	36	1.8
AA519844, AA519844	TgESTzz36c03.r1 TgME49 invivo Bradyzoite c...	36	1.8
AA531839, AA531839	TgESTzz47h05.r1 TgME49 invivo Bradyzoite c...	36	1.8
AA660182, AA660182	00022 MtRHE Medicago truncatula cDNA 5' si...	36	1.8
D71983, CELK084H2R	C.elegans cDNA clone yk84h2 : 3' end, sin...	36	1.8
R29905, R29905	12510 Lambda-PRL2 Arabidopsis thaliana cDNA cl...	36	1.8
AA519997, AA519997	TgESTzz36h03.r1 TgME49 invivo Bradyzoite c...	36	1.8
U83048, BTU83048	Bos taurus clone 0429 mRNA sequence	36	1.8
AA440655, AA440655	LD15510.5prime LD Drosophila melanogaster ...	36	1.8
AA559374, AA559374	MU002092.NH3 York-Harrop-lung-A Schistosom...	36	1.8
C93857, C93857	Dictyostelium discoideum slug cDNA, clone SSL794	36	1.8
AA520901, AA520901	TgESTzz65a05.r1 TgME49 invivo Bradyzoite c...	36	1.8
T46158, T46158	9421 Lambda-PRL2 Arabidopsis thaliana cDNA clo...	36	1.8
AA520866, AA520866	TgESTzz68e05.r1 TgME49 invivo Bradyzoite c...	36	1.8
Z17562, ATTS0136	A. thaliana transcribed sequence; clone TAT...	36	1.8
AA520811, AA520811	TgESTzz64d05.r1 TgME49 invivo Bradyzoite c...	36	1.8
AA567455, AA567455	HL01288.5prime HL Drosophila melanogaster ...	36	1.8
AA519228, AA519228	TgESTzz39h02.s1 TgME49 invivo Bradyzoite c...	36	1.8
AA531917, AA531917	TgESTzz48f01.r1 TgME49 invivo Bradyzoite c...	36	1.8
AA519829, AA519829	TgESTzz36a02.r1 TgME49 invivo Bradyzoite c...	36	1.8
AA520185, AA520185	TgESTzz39d03.s1 TgME49 invivo Bradyzoite c...	36	1.8
C37095, C37095	C.elegans cDNA clone yk482c11 : 3' end, singl...	36	1.8

T46009, T46009 9272 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8
T20458, T20458 2466 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8
F14402, ATTS5324 A. thaliana transcribed sequence; clone TAP... 36 1.8
T20404, T20404 2412 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.8
AA274295, AA274295 TgESTzz24c11.s1 TgME49 invivo Bradyzoite c... 36 1.8
AA699152, AA699152 HL07807.5prime HL Drosophila melanogaster ... 36 1.8
AA902065, AA902065 NCM1A12T3 Mycelial Neurospora crassa cDNA ... 36 1.8

SEQ ID NO:558

AF016585, AF016585 Streptomyces caelestis cytochrome P-450 hy... 42 0.092
U50719, MSU50719 Manduca sexta neuroglian mRNA, complete cds 40 0.36
~~Z97208, SPAC15A10 S.pombe chromosome I cosmid c15A10 40 0.36~~
AC003063, AC003063 Mus musculus Chromosome 16 BAC Clone b40-o... 40 0.36
X66455, MMFGFR2 M.musculus promoter region of fibroblast gro... 40 0.36
D83785, D83785 Human mRNA for KIAA0200 gene, complete cds 40 0.36
AC000398, AC000398 Genomic sequence from Mouse 11, complete s... 38 1.4
AF062345, AF062345 Caulobacter crescentus Sts1 (sts1), S-laye... 38 1.4
X12359, RCNIFR12 Rhodobacter capsulatus nifR1 and nifR2 gene... 38 1.4
X72382, RCNIFR3 R.capsulatus nifR3 DNA 38 1.4

HUMAN ESTs

R36714, R36714 yh93g06.s1 Homo sapiens cDNA clone 137338 3'. 775 0.0
D61030, HUM149A04B Human fetal brain cDNA 5'-end GEN-149A04. 666 0.0
D60944, HUM141D02B Human fetal brain cDNA 5'-end GEN-141D02. 656 0.0
H03308, H03308 yj47d09.s1 Homo sapiens cDNA clone 151889 3'. 609 e-172
AA435561, AA435561 zt73d09.s1 Soares testis NHT Homo sapiens ... 587 e-166
AA977877, AA977877 oq56d03.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 571 e-161
AA846787, AA846787 aj41h03.s1 Soares testis NHT Homo sapiens ... 563 e-159
AA972542, AA972542 oo82e01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 561 e-158
AA954270, AA954270 on72e06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 557 e-157
AA740333, AA740333 ob23c02.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 557 e-157
AA999722, AA999722 ov04c06.s1 NCI_CGAP_Kid3 Homo sapiens cDNA... 555 e-156
AA970621, AA970621 op40h08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 551 e-155
AA932930, AA932930 oo04g11.s1 Soares_NFL_T_GBC_S1 Homo sapien... 541 e-152
AA725406, AA725406 ai13b11.s1 Soares parathyroid tumor NbHPA ... 539 e-152
W74439, W74439 zd75d10.s1 Soares fetal heart NbHH19W Homo sap... 539 e-152
AA868538, AA868538 ak43e08.s1 Soares testis NHT Homo sapiens ... 539 e-152
R79832, R79832 yi89b08.s1 Homo sapiens cDNA clone 146391 3' s... 537 e-151

R63227, R63227 yi07e06.s1 Homo sapiens cDNA clone 138562 3'. 535 e-150
AI027967, AI027967 ov84d04.x1 Soares_testis_NHT Homo sapiens ... 535 e-150
AA776717, AA776717 ah49d07.s1 Soares testis NHT Homo sapiens ... 535 e-150
AI040961, AI040961 ov53d06.x1 Soares_testis_NHT Homo sapiens ... 533 e-150
AI024835, AI024835 ov35h09.x1 Soares_testis_NHT Homo sapiens ... 533 e-150
AA740667, AA740667 ob01g12.s1 NCI_CGAP_Kid3 Homo sapiens cDNA... 531 e-149
AA994527, AA994527 ou42h06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 531 e-149
AA932728, AA932728 oo31g06.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 529 e-149
AI001978, AI001978 ot39f03.s1 Soares_testis_NHT Homo sapiens ... 529 e-149
N37092, N37092 yy41g08.s1 Homo sapiens cDNA clone 273854 3'. 529 e-149
N27547, N27547 yy01e05.s1 Homo sapiens cDNA clone 269984 3'. 527 e-148
AA883578, AA883578 al46b08.s1 Soares NFL T GBC S1 Homo sapien... 527 e-148
AA890154, AA890154 al53f07.s1 Soares_NFL_T_GBC_S1 Homo sapien... 525 e-147
AA757222, AA757222 ah56f11.s1 Soares testis NHT Homo sapiens ... 525 e-147
AA456074, AA456074 aa17b07.s1 Soares NhHMPu S1 Homo sapiens c... 523 e-147
AA884285, AA884285 am32f04.s1 Soares NFL T GBC S1 Homo sapien... 523 e-147
AA969436, AA969436 op53e12.s1 Soares_NFL_T_GBC_S1 Homo sapien... 521 e-146
AA952918, AA952918 on55h11.s1 Soares_NFL_T_GBC_S1 Homo sapien... 521 e-146
AA971938, AA971938 op88b01.s1 Soares_NFL_T_GBC_S1 Homo sapien... 521 e-146
R25112, R25112 yh36b12.s1 Homo sapiens cDNA clone 131807 3'. 519 e-146
AA865258, AA865258 og87d08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 519 e-146
AA758323, AA758323 ah65e11.s1 Soares testis NHT Homo sapiens ... 519 e-146
AA972041, AA972041 op88e06.s1 Soares_NFL_T_GBC_S1 Homo sapien... 519 e-146
R76443, R76443 yi58e11.s1 Homo sapiens cDNA clone 143468 3'. 519 e-146
AA917965, AA917965 om37e04.s1 Soares_NFL_T_GBC_S1 Homo sapien... 517 e-145
AA505880, AA505880 ni01a09.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 517 e-145
AA906270, AA906270 oj98e12.s1 Soares_NFL_T_GBC_S1 Homo sapien... 517 e-145
AA758549, AA758549 ah70b04.s1 Soares testis NHT Homo sapiens ... 517 e-145
AA927156, AA927156 om20f05.s1 Soares_NFL_T_GBC_S1 Homo sapien... 515 e-144
AA976254, AA976254 oo30f08.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 515 e-144
R23891, R23891 yh28a12.s1 Homo sapiens cDNA clone 131038 3'. 515 e-144
AA938552, AA938552 oo78g11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 513 e-144
AA483809, AA483809 ne41c08.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 513 e-144
AA962659, AA962659 or31f10.s1 NCI_CGAP_GC3 Homo sapiens cDNA ... 511 e-143
AA724803, AA724803 ai05f02.s1 Soares parathyroid tumor NbHPA ... 511 e-143
AA410432, AA410432 zv12c09.s1 Soares NhHMPu S1 Homo sapiens c... 511 e-143
AA775373, AA775373 ad19c07.s1 Soares NbHFB Homo sapiens cDNA ... 511 e-143
AA758038, AA758038 ah67h09.s1 Soares testis NHT Homo sapiens ... 509 e-143
AA904368, AA904368 ol15d02.s1 Soares_NFL_T_GBC_S1 Homo sapien... 509 e-143
AA861386, AA861386 ak37b11.s1 Soares testis NHT Homo sapiens ... 507 e-142
R31547, R31547 yh72g03.s1 Homo sapiens cDNA clone 135316 3'. 505 e-141
AA843421, AA843421 ak07f11.s1 Soares parathyroid tumor NbHPA ... 504 e-141
H02479, H02479 yj35e10.s1 Homo sapiens cDNA clone 150762 3'. 504 e-141
N29346, N29346 yw85c12.s1 Homo sapiens cDNA clone 259030 3'. 504 e-141
AA815351, AA815351 ai63g05.s1 Soares testis NHT Homo sapiens ... 504 e-141

AA923373, AA923373 ol46e03.s1 Soares_NFL_T_GBC_S1 Homo sapien... 502 e-140
H01218, H01218 yj31c08.s1 Homo sapiens cDNA clone 150350 3'. 500 e-140
AA988977, AA988977 or87e11.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 500 e-140
AA628621, AA628621 af40c02.s1 Soares total fetus Nb2HF8 9w Ho... 500 e-140
AA442745, AA442745 zv60a07.s1 Soares testis NHT Homo sapiens ... 498 e-139
AA777492, AA777492 zj02e07.s1 Soares fetal liver spleen 1NFLS... 498 e-139
R73670, R73670 yi55f03.s1 Homo sapiens cDNA clone 143165 3'. 498 e-139
H12460, H12460 yj12d05.s1 Homo sapiens cDNA clone 148521 3'. 498 e-139
AA875917, AA875917 oj15a08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 496 e-138
~~R76230, R76230 yi71g11.s1 Homo sapiens cDNA clone 144740 3'. 494 e-138~~
AA970616, AA970616 op40h03.s1 Soares_NFL_T_GBC_S1 Homo sapien... 494 e-138
AA912408, AA912408 ol23a05.s1 Soares_NFL_T_GBC_S1 Homo sapien... 492 e-137
AA910051, AA910051 ol40e08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 492 e-137
AA815444, AA815444 ai65b11.s1 Soares testis NHT Homo sapiens ... 492 e-137
R76814, R76814 yi62f06.s1 Homo sapiens cDNA clone 143843 3'. 488 e-136
AA954722, AA954722 oo84c12.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 488 e-136
~~R65987, R65987 yi23e10.s1 Homo sapiens cDNA clone 140106 3'. 486 e-136~~
R63480, R63480 yi08e11.s1 Homo sapiens cDNA clone 138668 3'. 486 e-136
AA885425, AA885425 am12h09.s1 Soares NFL T GBC S1 Homo sapien... 486 e-136
AA884231, AA884231 am32a01.s1 Soares NFL T GBC S1 Homo sapien... 484 e-135
AA885048, AA885048 am11a12.s1 Soares NFL T GBC S1 Homo sapien... 482 e-134
AA996162, AA996162 os14f10.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 482 e-134
AA748637, AA748637 ny10a02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 482 e-134
AI031908, AI031908 ow47e12.x1 Soares_parathyroid_tumor_NbHPA ... 482 e-134
AA884703, AA884703 am18e02.s1 Soares NFL T GBC S1 Homo sapien... 480 e-134
AA928243, AA928243 on87c10.s1 Soares_NFL_T_GBC_S1 Homo sapien... 480 e-134
AI025986, AI025986 ow03a09.s1 Soares_parathyroid_tumor_NbHPA ... 478 e-133
AA897637, AA897637 oj72g07.s1 Soares_NFL_T_GBC_S1 Homo sapien... 472 e-131
AA877346, AA877346 01c07.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 472 e-131
AA833569, AA833569 aj46b02.s1 Soares testis NHT Homo sapiens ... 472 e-131
AA832163, AA832163 oc91b02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 470 e-131
R89052, R89052 ym99e08.s1 Homo sapiens cDNA clone 167078 3'. 470 e-131
N26589, N26589 yx91f03.s1 Homo sapiens cDNA clone 269117 3'. 460 e-128
R73883, R73883 yi56c03.s1 Homo sapiens cDNA clone 143236 3'. 454 e-126
AA579968, AA579968 ng51c03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 444 e-123
AA843427, AA843427 ak07g06.s1 Soares parathyroid tumor NbHPA ... 438 e-121
AA705903, AA705903 ah42g12.s1 Soares testis NHT Homo sapiens ... 436 e-121
AA835882, AA835882 oc81d05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 434 e-120
AA812583, AA812583 aj43b02.s1 Soares testis NHT Homo sapiens ... 432 e-119
AA512970, AA512970 nj16b08.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 432 e-119
R26664, R26664 yh35g10.s1 Homo sapiens cDNA clone 131778 3'. 428 e-118
AA429715, AA429715 zv60a07.r1 Soares testis NHT Homo sapiens ... 414 e-114
H17430, H17430 ym40f09.s1 Homo sapiens cDNA clone 50607 3'. 404 e-111
AA436117, AA436117 zu03d10.r1 Soares testis NHT Homo sapiens ... 402 e-110
AA099077, AA099077 zl77a09.s1 Stratagene colon (#937204) Homo... 400 e-110

R72440, R72440 yj90h02.s1 Homo sapiens cDNA clone 156051 3'. 379 e-103
AA577436, AA577436 nm96h06.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 351 4e-95
AA516390, AA516390 nf55e03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 347 6e-94
AA534533, AA534533 nf80h06.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 341 3e-92
AA541583, AA541583 ni89f05.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 311 3e-83
N72191, N72191 yz99f07.s1 Homo sapiens cDNA clone 291205 3'. 303 8e-81
AA905015, AA905015 ok09b08.s1 Soares_NFL_T_GBC_S1 Homo sapien... 303 8e-81
AA393148, AA393148 zt73d09.r1 Soares testis NHT Homo sapiens ... 287 4e-76
AA939048, AA939048 op56h04.s1 Soares_NFL_T_GBC_S1 Homo sapien... 256 2e-66
AA412317, AA412317 zt97c05.r1 Soares testis NHT Homo sapiens ... 246 2e-63
R65986, R65986 yi23e10.r1 Homo sapiens cDNA clone 140106 5'. 238 4e-61
AA400827, AA400827 zt76c07.s1 Soares testis NHT Homo sapiens ... 232 2e-59
W00472, W00472 yz99f07.r1 Homo sapiens cDNA clone 291205 5'. 180 8e-44
AA860558, AA860558 aj81e09.s1 Soares parathyroid tumor NbHPA ... 180 8e-44
AA455577, AA455577 aa17b07.r1 Soares NhHMPu S1 Homo sapiens c... 176 1e-42
AA583931, AA583931 nn64e04.s1 NCI_CGAP_Lar1 Homo sapiens cDNA... 172 2e-41
AA907332, AA907332 ol22g11.s1 Soares_NFL_T_GBC_S1 Homo sapien... 168 3e-40
R71169, R71169 yi53a12.r1 Homo sapiens cDNA clone 142942 5'. 159 3e-37
W79084, W79084 zd75d10.r1 Soares fetal heart NbHH19W Homo sap... 155 4e-36
AA295914, AA295914 EST101137 Thymus III Homo sapiens cDNA 5' end 135 4e-30
AA860415, AA860415 aj60d10.s1 Soares testis NHT Homo sapiens ... 100 2e-19
H01351, H01351 yi99a07.r1 Homo sapiens cDNA clone 147348 5'. 98 9e-19
AA709286, AA709286 ai21g07.s1 Soares testis NHT Homo sapiens ... 96 3e-18
AA931370, AA931370 oo03d01.s1 Soares_NFL_T_GBC_S1 Homo sapien... 96 3e-18
AA501911, AA501911 ng54a08.s1 NCI_CGAP_Li2 Homo sapiens cDNA ... 94 1e-17
AA548419, AA548419 nj14g09.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 92 5e-17
AA588892, AA588892 no23b06.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 92 5e-17
AI025228, AI025228 ov40h08.x1 Soares_testis_NHT Homo sapiens ... 76 3e-12
R73757, R73757 yi55f03.r1 Homo sapiens cDNA clone 143165 5'. 74 1e-11
R23710, R23710 yh35g10.r1 Homo sapiens cDNA clone 131778 5'. 56 3e-06
N40362, N40362 yy01e05.r1 Homo sapiens cDNA clone 269984 5'. 50 2e-04
H59895, H59895 yr04c12.r1 Homo sapiens cDNA clone 204310 5'. 48 7e-04
H12509, H12509 yj12d05.r1 Homo sapiens cDNA clone 148521 5'. 44 0.011
N20344, N20344 yx38d02.s1 Homo sapiens cDNA clone 264003 3'. 38 0.70
AA614692, AA614692 np52b10.s1 NCI_CGAP_Br1.1 Homo sapiens cDN... 38 0.70
H30707, H30707 yo78f07.r1 Homo sapiens cDNA clone 184069 5'. 36 2.7
H52973, H52973 yq82e04.r1 Homo sapiens cDNA clone 202302 5'. 36 2.7
AA218550, AA218550 zq96b02.r1 Stratagene NT2 neuronal precurs... 36 2.7
AA312481, AA312481 EST183215 Jurkat T-cells VI Homo sapiens c... 36 2.7
AA632009, AA632009 np74c07.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 36 2.7
H13363, H13363 yl71b10.r1 Homo sapiens cDNA clone 43343 5'. 36 2.7
AI022018, AI022018 ow64d01.x1 Soares_senescent_fibroblasts_Nb... 36 2.7
AA781996, AA781996 ai75a06.s1 Soares testis NHT Homo sapiens ... 36 2.7
N21623, N21623 yx60a09.s1 Homo sapiens cDNA clone 266104 3'. 36 2.7
AA326194, AA326194 EST29340 Cerebellum II Homo sapiens cDNA 5... 36 2.7

C76071, C76071 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 250 4e-65
AA051612, AA051612 mj52c07.r1 Soares mouse embryo NbME13.5 14... 238 1e-61
AA561635, AA561635 vl01h07.r1 Knowles Solter mouse blastocyst.... 234 2e-60
AA288419, AA288419 vb14h01.r1 Soares mouse NML Mus musculus c... 220 3e-56
AA212883, AA212883 mw78e10.r1 Soares mouse NML Mus musculus c... 220 3e-56
AA268018, AA268018 vb08e07.r1 Soares mouse NML Mus musculus c... 212 8e-54
AA692427, AA692427 vt59b07.r1 Barstead mouse irradiated colon... 200 3e-50
~~W18566, W18566 mb98h02.r1 Soares mouse p3NMF19.5 Mus musculus... 192 7e-48~~
AA543948, AA543948 vj69b08.r1 Knowles Solter mouse blastocyst... 147 4e-34
W41070, W41070 mc39b06.r1 Soares mouse p3NMF19.5 Mus musculus... 123 5e-27
Z31174, MMTEST52 M.musculus expressed sequence tag MTEST52 117 3e-25
AA530723, AA530723 vj32f07.r1 Stratagene mouse diaphragm (#93... 74 5e-12
AA966940, AA966940 ua38c01.r1 Soares mouse mammary gland NbMM... 72 2e-11
AA111079, AA111079 mp50e01.r1 Barstead MPLRB1 Mus musculus cD... 44 0.004
AA049187, AA049187 mj51a02.r1 Soares mouse embryo NbME13.5 14... 36 0.99
AA058246, AA058246 mg74e12.r1 Soares mouse embryo NbME13.5 14... 36 0.99
AA153730, AA153730 mq60a02.r1 Soares 2NbMT Mus musculus cDNA ... 36 0.99
AA473959, AA473959 vd02b12.s1 Knowles Solter mouse 2 cell Mus... 36 0.99
W47887, W47887 mc83h09.r1 Soares mouse embryo NbME13.5 14.5 M... 36 0.99
AA033312, AA033312 mi43g01.r1 Soares mouse embryo NbME13.5 14... 36 0.99
AA980820, AA980820 ua46a04.r1 Soares mouse mammary gland NbMM... 36 0.99
Z31139, MMTEST427 M.musculus expressed sequence tag MTEST427 36 0.99
C76637, C76637 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 34 3.9
AI049314, AI049314 uc87b10.y1 Sugano mouse kidney mkia Mus mu... 34 3.9
AA670807, AA670807 vs70b02.r1 Stratagene mouse skin (#937313)... 34 3.9
AA727571, AA727571 vv01h11.r1 Stratagene mouse skin (#937313)... 34 3.9
AA571966, AA571966 vg12f07.r1 Soares mouse NbMH Mus musculus ... 34 3.9
W37059, W37059 mb73f10.r1 Soares mouse p3NMF19.5 Mus musculus... 34 3.9
AA760280, AA760280 vv74h11.r1 Stratagene mouse skin (#937313)... 34 3.9
AA799036, AA799036 vn40c12.r1 Stratagene mouse skin (#937313)... 34 3.9
AA432831, AA432831 vf28g07.r1 Knowles Solter mouse 8 cell Mus... 34 3.9
AA562435, AA562435 vk98c01.r1 Knowles Solter mouse blastocyst... 34 3.9
AA726680, AA726680 vu93g12.r1 Stratagene mouse skin (#937313)... 34 3.9
AA217464, AA217464 mu87d11.r1 Soares mouse lymph node NbMLN M... 34 3.9
AA790564, AA790564 vx71e06.r1 Stratagene mouse skin (#937313)... 34 3.9
AA033172, AA033172 mi37f06.r1 Soares mouse embryo NbME13.5 14... 34 3.9
AA616204, AA616204 vo96h02.r1 Soares mouse mammary gland NbMM... 34 3.9
AA982055, AA982055 ua37h05.r1 Soares mouse mammary gland NbMM... 34 3.9
W47850, W47850 mc82h10.r1 Soares mouse embryo NbME13.5 14.5 M... 34 3.9
AA537538, AA537538 vk48c12.r1 Soares mouse mammary gland NbMM... 34 3.9
AA636986, AA636986 vn05f04.r1 Knowles Solter mouse blastocyst... 34 3.9

AI043768, AI043768 UI-R-C0-jm-d-11-0-UI.s1 UI-R-C0 Rattus nor... 174 1e-42
AA531635, AA531635 TgESTzz29b08.r1 TgME49 invivo Bradyzoite c... 38 0.22
AA944260, AA944260 EST199759 Normalized rat embryo, Bento Soa... 38 0.22
AI008930, AI008930 EST203381 Normalized rat embryo, Bento Soa... 36 0.87
D15788, RICC1258A Rice cDNA, partial sequence (C1258A). 36 0.87
AA963741, AA963741 UI-R-C0-gt-b-09-0-UI.s1 UI-R-C0 Rattus nor... 36 0.87
AA951235, AA951235 LD31601.3prime LD Drosophila melanogaster ... 34 3.5
C20118, C20118 Rice cDNA, partial sequence (E11542_2A) 34 3.5
AA820317, AA820317 LD23876.5prime LD Drosophila melanogaster ... 34 3.5
AA950448, AA950448 LD30237.3prime LD Drosophila melanogaster ... 34 3.5

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U83883, RNU83883 Rattus norvegicus p105 coactivator mRNA, com... 42 0.11
V00722, MMBGL1 Mouse gene for beta-1-globin. 40 0.45
X14061, MMBGCXD M.musculus beta-globin complex DNA for y, bh... 40 0.45
U20824, EHVU20824 Equine herpesvirus 2, complete genome 38 1.8
U04106, PFU04106 Pleurotus fossulatus D1822, mating group VI,... 38 1.8
U04101, POU04101 Pleurotus ostreatus D1742, Japan, mating gro... 38 1.8
AC005174, AC005174 Homo sapiens clone UWGC:g1564a012 from 7p1... 38 1.8
M18680, HUMRGAPS Homo sapiens 5S rRNA pseudogene. 38 1.8
AL022121, MTV025 Mycobacterium tuberculosis H37Rv complete g... 38 1.8
AF038379, AF038379 Leishmania amazonensis ribosomal protein S... 38 1.8
Z11528, THIGPMR T.harzianum mRNA for imidazoleglycerolphosphate 38 1.8
U32622, CTU32622 Comamonas testosteroni TsaR (tsaR), toluenes... 38 1.8
U04102, POU04102 Pleurotus ostreatus D1743, Japan, mating gro... 38 1.8
U04105, PFU04105 Pleurotus fossulatus D1821, mating group VI,... 38 1.8
U04109, PEU04109 Pleurotus eryngii D1832, mating group VI rib... 38 1.8
U65606, BSU65606 Basidiomycete from a bamboo (Phyllostachys p... 38 1.8

HUMAN ESTs

R49969, R49969 yj56c07.s1 Homo sapiens cDNA clone 152748 3' s... 523 e-147
AA834501, AA834501 of21c02.s1 NCI_CGAP_Kid6 Homo sapiens cDNA... 381 e-104
W96422, W96422 ze43a05.s1 Soares retina N2b4HR Homo sapiens c... 315 2e-84
R47821, R47821 yj56c07.r1 Homo sapiens cDNA clone 152748 5'. 214 7e-54
AA761660, AA761660 nz24b09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 212 3e-53
AA887861, AA887861 nq99b07.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 74 2e-11
AA644044, AA644044 nm20b12.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 72 6e-11

AA115963, AA115963 zm78d11.s1 Stratagene neuroepithelium (#93... 40 0.22
AA779271, AA779271 zj43f02.s1 Soares fetal liver spleen 1NFLS... 40 0.22
T65600, T65600 yc76a04.r1 Homo sapiens cDNA clone 21496 5'. 38 0.86
AA515882, AA515882 nf67f10.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 38 0.86
AA664812, AA664812 nu69b05.s1 NCI_CGAP_Alv1 Homo sapiens cDNA... 36 3.4
T83365, T83365 ye03f05.s1 Homo sapiens cDNA clone 116673 3'. 36 3.4
AA009773, AA009773 zi04d04.s1 Soares fetal liver spleen 1NFLS... 36 3.4
AA916894, AA916894 og34g10.s1 NCI_CGAP_Br7 Homo sapiens cDNA ... 36 3.4
N27865, N27865 yy02g03.s1 Homo sapiens cDNA clone 270100 3'. 36 3.4
AA953544, AA953544 om79g06.s1 NCI_CGAP_Kid3 Homo sapiens cDNA... 36 3.4
AA505576, AA505576 nh93f03.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 36 3.4
H30276, H30276 yp42f05.s1 Homo sapiens cDNA clone 190113 3'. 36 3.4
AA699914, AA699914 zi61f08.s1 Soares fetal liver spleen 1NFLS... 36 3.4
AA595583, AA595583 nk92c04.s1 NCI_CGAP_Co11 Homo sapiens cDNA... 36 3.4
AA351139, AA351139 EST58769 Infant brain Homo sapiens cDNA 5'... 36 3.4
AA810167, AA810167 ob88a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 36 3.4
H50257, H50257 yo28a07.r1 Homo sapiens cDNA clone 179220 5'. 36 3.4
W19939, W19939 zb37e09.r1 Soares parathyroid tumor NbHPA Homo... 36 3.4
R19840, R19840 yg30e11.r1 Homo sapiens cDNA clone 33837 5'. 36 3.4
AA514234, AA514234 nf56e10.s1 NCI_CGAP_Co3 Homo sapiens cDNA ... 36 3.4

AA183407, AA183407 ms
AA821640, AA821640 vw
AA289310, AA289310

AA900756, AA900756 UI-R-E0-di-d-04-0-UI.s1 UI-R-E0 Rattus nor... 46 0.001
T18416, T18416 6c02e07t7 etiolated seedling Zea mays cDNA clo... 40 0.069
AA817427, AA817427 LD22827.5prime LD Drosophila melanogaster ... 36 1.1
AA274351, AA274351 TgESTzz25c09.s1 TgME49 invivo Bradyzoite c... 36 1.1
AA391823, AA391823 LD10747.5prime LD Drosophila melanogaster ... 36 1.1
AA274275, AA274275 TgESTzz24b02.s1 TgME49 invivo Bradyzoite c... 34 4.3
R86490, R86490 RABEST068T Oryctolagus cuniculus cDNA clone pR... 34 4.3
AA965817, AA965817 o5g08a1.r1 Aspergillus nidulans 24hr asexu... 34 4.3

SEQ ID NO:560

X81198, L35746, L49403, U21317, Z35640, AL010273, U09850, AF071771, Z96434,

Z50028, X72735, U13072, Z34294, AB002109, X68401, M92840, D88399, Z36238, AF000262, Z46828,

HUMAN ESTs

AA215808, AA215808 zr98b10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 1082 0.0
N75131, N75131 yz29g07.r1 Soares multiple sclerosis 2NbHMSP H... 989 0.0
AA709149, AA709149 zf98g05.s1 Soares fetal heart NbHH19W Homo... 985 0.0
AA428341, AA428341 zw18f09.s1 Soares ovary tumor NbHOT Homo s... 967 0.0
AA043426, AA043426 zk54h09.r1 Soares pregnant uterus NbHPU Ho... 870 0.0
AA878521, AA878521 oj19c01.s1 NCI_CGAP_Kid5 Homo sapiens cDNA... 844 0.0
AA599696, AA599696 ag10h01.s1 Gessler Wilms tumor Homo sapien... 842 0.0
W52304, W52304 zc47c08.r1 Soares senescent fibroblasts NbHSF ... 841 0.0
AA043427, AA043427 zk54h09.s1 Soares pregnant uterus NbHPU Ho... 769 0.0
N64314, N64314 yz46a12.s1 Homo sapiens cDNA clone 286078 3'. 763 0.0
N52360, N52360 yz29g07.s1 Soares multiple sclerosis 2NbHMSP H... 753 0.0
AA290863, AA290863 zt19a08.s1 Soares ovary tumor NbHOT Homo s... 747 0.0
AA768023, AA768023 oa60e03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 728 0.0
AA872018, AA872018 oi05f08.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 718 0.0
AA164765, AA164765 zp01g09.s1 Stratagene ovarian cancer (#937... 716 0.0
AA814881, AA814881 oa75e02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 708 0.0
R86915, R86915 yq30f07.r1 Homo sapiens cDNA clone 197317 5'. 692 0.0
W56703, W56703 zd14e01.r1 Soares fetal heart NbHH19W Homo sap... 642 0.0
R84872, R84872 yq27e01.r1 Soares fetal liver spleen 1NFLS Hom... 636 0.0
D79691, HUM307D10B Human aorta cDNA 5'-end GEN-307D10. 630 e-179
AA025638, AA025638 ze90d11.s1 Soares fetal heart NbHH19W Homo... 626 e-178
AA298883, AA298883 EST114512 Pancreas tumor I Homo sapiens cD... 624 e-177
R86903, R86903 yq30d07.r1 Homo sapiens cDNA clone 197293 5'. 622 e-176
AA033584, AA033584 zk21b12.s1 Soares pregnant uterus NbHPU Ho... 618 e-175
AA633335, AA633335 nq58h09.s1 NCI_CGAP_Co9 Homo sapiens cDNA ... 611 e-173
AA298894, AA298894 EST114513 Pancreas tumor I Homo sapiens cD... 599 e-169
R85806, R85806 yq27e01.s1 Soares fetal liver spleen 1NFLS Hom... 595 e-168
AA872617, AA872617 oi05g07.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 591 e-167
H71458, H71458 yu71a06.s1 Homo sapiens cDNA clone 239218 3'. 587 e-166
AA291045, AA291045 zt19a08.r1 Soares ovary tumor NbHOT Homo s... 563 e-159
H71587, H71587 yu71a06.r1 Homo sapiens cDNA clone 239218 5'. 543 e-153
AA035172, AA035172 zk28g05.s1 Soares pregnant uterus NbHPU Ho... 523 e-147
AA164764, AA164764 zp01g09.r1 Stratagene ovarian cancer (#937... 517 e-145
AA297001, AA297001 EST112550 Adipose tissue, white II Homo sa... 502 e-140
AA296816, AA296816 EST112381 Aorta endothelial cells Homo sap... 500 e-139
AA769090, AA769090 oa74e12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 494 e-138
H54447, H54447 yq91f04.s1 Homo sapiens cDNA clone 203167 3'. 438 e-121
H54537, H54537 yq91f04.r1 Homo sapiens cDNA clone 203167 5'. 436 e-120
AI049757, AI049757 an26g03.x1 Gessler Wilms tumor Homo sapien... 430 e-119

AA033583, AA033583 zk21b12.r1 Soares pregnant uterus NbHPU Ho... 422 e-116
D61748, HUM205G02B Human aorta cDNA 5'-end GEN-205G02. 412 e-113
AA148635, AA148635 zl26d10.r1 Soares pregnant uterus NbHPU Ho... 377 e-102
AA148636, AA148636 zl26d10.s1 Soares pregnant uterus NbHPU Ho... 373 e-101
AA025637, AA025637 ze90d11.r1 Soares fetal heart NbHH19W Homo... 371 e-101
AA932620, AA932620 oo61h04.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 365 4e-99
AA385594, AA385594 EST99296 Thyroid Homo sapiens cDNA 5' end 339 2e-91
AA361957, AA361957 EST71295 T-cell lymphoma Homo sapiens cDNA... 289 2e-76
AA383998, AA383998 EST97483 Thyroid Homo sapiens cDNA 5' end ... 274 1e-71
H22175, H22175 yl38a03.r1 Homo sapiens cDNA clone 160492 5'. 256 3e-66
R50060, R50060 yj59c10.r1 Homo sapiens cDNA clone 153042 5'. 256 3e-66
AA229414, AA229414 nc47f12.r1 NCI_CGAP_Pr3 Homo sapiens cDNA ... 246 3e-63
D20466, HUMGS01440 Human HL60 3'directed MboI cDNA, HUMGS014... 208 6e-52
AA249061, AA249061 114438.seq.F Human fetal heart, Lambda ZAP... 168 5e-40
R86758, R86758 yq30f07.s1 Homo sapiens cDNA clone 197317 3'. 147 2e-33
R58025, R58025 F8018 Fetal heart Homo sapiens cDNA clone F801... 101 1e-19
AA371076, AA371076 EST82846 Prostate gland I Homo sapiens cDN... 42 0.081
AA977111, AA977111 oq24c03.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 40 0.32
AA608923, AA608923 af03b04.s1 Soares testis NHT Homo sapiens ... 38 1.3

gb|AA386999|AA386999 vc81b02.r1 Ko mouse embryo 11 5dpc Mus mus... 668 0.0
gb|AA589082|AA589082 vk24a08.r1 Knowles Solter mouse blastocyst... 658 0.0
gb|AA510881|AA510881 vh59e11.r1 Soares mouse mammary gland NbMM... 617 e-175
gb|AA763574|AA763574 vp07e08.r1 Soares mouse mammary gland NbMM... 615 e-174
gb|AA387423|AA387423 vc84b03.r1 Ko mouse embryo 11 5dpc Mus mus... 549 e-155
gb|AA915333|AA915333 vz28f05.r1 Soares 2NbMT Mus musculus cDNA ... 543 e-153
gb|AA816208|AA816208 vp43c10.r1 Barstead mouse irradiated colon... 444 e-123
gb|AA190043|AA190043 mt91h08.r1 Soares mouse lymph node NbMLN M... 424 e-117
gb|AA207393|AA207393 mv89c09.r1 GuayWoodford Beier mouse kidney... 394 e-108
emb|Z31258|MMTEST693 M.musculus expressed sequence tag MTEST693 309 8e-83
gb|AA930143|AA930143 vz52d11.s1 Soares 2NbMT Mus musculus cDNA ... 293 5e-78
gb|AA170612|AA170612 ms92c09.r1 Soares mouse 3NbMS Mus musculus... 287 3e-76
gb|AA762238|AA762238 vw58h02.r1 Soares mouse mammary gland NMLM... 266 1e-69
gb|AA689028|AA689028 vs02c12.r1 Barstead mouse irradiated colon... 264 4e-69
gb|AA959938|AA959938 vw58h02.s1 Soares mouse mammary gland NMLM... 240 6e-62
dbj|D18511|MUSGS01569 Mouse 3'-directed cDNA, MUSGS01569, clon... 172 1e-41
gb|AA474393|AA474393 vd57g07.r1 Knowles Solter mouse blastocyst... 100 1e-19
gb|W97165|W97165 mf90g05.r1 Soares mouse embryo NbME13.5 14.5 M... 74 8e-12
gb|AA512077|AA512077 vj43f05.r1 Stratagene mouse skin (#937313)... 62 3e-08
gb|AA794521|AA794521 vu68e07.r1 Stratagene mouse skin (#937313)... 54 8e-06
gb|AA155454|AA155454 mn38h12.r1 Beddington mouse embryonic regi... 48 5e-04
gb|W91000|W91000 mf83f06.r1 Soares mouse embryo NbME13.5 14.5 M... 40 0.12

gb|AA219917|AA219917 mv62f05.r1 Soares mouse 3NME12 5 Mus muscu... 38 0.45
gb|AA529349|AA529349 vi35f08.r1 Beddington mouse embryonic regi... 36 1.8
gb|AA754855|AA754855 vu51e08.r1 Soares mouse mammary gland NbMM... 36 1.8

gb|AA850379|AA850379 EST193146 Normalized rat ovary, Bento Soar... 569 e-161
gb|W63375|W63375 TgESTzy68g02.r1 TgME49 Tachyzoite cDNA Toxopla... 394 e-108
gb|AA946379|AA946379 EST201878 Normalized rat lung, Bento Soare... 353 5e-96
gb|AA964427|AA964427 UI-R-E1-gp-a-08-0-UI.s1 UI-R-E1 Rattus nor... 335 1e-90
gb|AA849599|AA849599 EST192366 Normalized rat muscle, Bento Soa... 307 3e-82
gb|AA849595|AA849595 EST192362 Normalized rat muscle, Bento Soa... 307 3e-82
gb|AA850378|AA850378 EST193145 Normalized rat ovary, Bento Soar... 278 3e-73
gb|AA957389|AA957389 UI-R-E1-fu-b-04-0-UI.s1 UI-R-E1 Rattus nor... 157 6e-37
gb|AI012981|AI012981 EST207432 Normalized rat spleen, Bento Soa... 147 6e-34
dbj|C48357|C48357 C.elegans cDNA clone yk469b2 : 5' end, single... 40 0.10
gb|AA440444|AA440444 LD15290.5prime LD Drosophila melanogaster ... 36 1.6
dbj|C22690|C22690 Rice cDNA, partial sequence (S5274_4A) 36 1.6
gb|AA697626|AA697626 HL02895.5prime HL Drosophila melanogaster ... 36 1.6
gb|AA550136|AA550136 1244m3 gmbPfHB3.1, G. Roman Reddy Plasmodi... 36 1.6
gb|T43579|T43579 6842 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 36 1.6
gb|AI030501|AI030501 UI-R-C0-jc-g-02-0-UI.s1 UI-R-C0 Rattus nor... 36 1.6
gb|AA056876|AA056876 SWMFCA987SK Brugia malayi microfilaria cDN... 36 1.6
gb|AA440689|AA440689 LD15550.5prime LD Drosophila melanogaster ... 36 1.6

SEQ ID NO:561

emb|Z47552|HSFMO3 H.sapiens mRNA for flavin-containing monooxyg... 44 0.10
gb|U39966|HSFMO3G7 Homo sapiens flavin containing monooxygenase... 44 0.10
emb|AL021026|HS127D3 Homo sapiens DNA sequence from PAC 127D3 o... 44 0.10
gb|U35007|CPU35007 Carcharhinus plumbeus Ig lambda light chain ... 44 0.10
gb|U35008|CPU35008 Carcharhinus plumbeus Ig lambda light chain ... 44 0.10
dbj|D85068|RICT3A Rice transposable element T3 gene and ret... 42 0.40
dbj|D63711|RICT3 Rice transposon T3 DNA, complete sequence 42 0.40
gb|U01657|U01657 Carcharhinus plumbeus Ig lambda-chain gene, co... 42 0.40
emb|Z92540|HS179I15A Human DNA sequence from PAC 179I15, BRCA2 ... 40 1.6
dbj|AB001569|AB001569 Carrot DNA for transposon Tdc1 40 1.6
gb|AE000613|HPAE000613 Helicobacter pylori section 91 of 134 of... 40 1.6
emb|X07985|DMCUT Drosophila cut locus mRNA for homeodomain-cont... 40 1.6
gb|AC005217|AC005217 Homo sapiens chromosome 5, P1 clone 1047D6... 40 1.6

HUMAN ESTs

gb|AA401219|AA401219 zv63a03.r1 Soares total fetus Nb2HF8 9w Ho... 993 0.0
gb|H69371|H69371 yu19h09.r1 Homo sapiens cDNA clone 234305 5' s... 44 0.049
gb|N62576|N62576 za13d10.s1 Homo sapiens cDNA clone 292435 3' s... 42 0.19
gb|W77763|W77763 zd69c06.r1 Soares fetal heart NbHH19W Homo sap... 40 0.77
gb|R14832|R14832 yf93g05.r1 Homo sapiens cDNA clone 30203 5'. 40 0.77
gb|T90524|T90524 yd40a04.s1 Homo sapiens cDNA clone 110670 3' s... 38 3.0
gb|R91887|R91887 yq04c09.r1 Homo sapiens cDNA clone 195952 5'. 38 3.0
gb|AA586935|AA586935 nn68h03.s1 NCI_CGAP_Lar1 Homo sapiens cDNA... 38 3.0
gb|T46987|T46987 yb12a07.s1 Homo sapiens cDNA clone 70932 3' co... 38 3.0
gb|AA853975|AA853975 aj51f09.s1 Soares testis NHT Homo sapiens ... 38 3.0
gb|T97059|T97059 ye50e01.r1 Homo sapiens cDNA clone 121176 5'. 38 3.0
gb|AA883119|AA883119 am15h02.s1 Soares NFL T GBC S1 Homo sapien... 38 3.0
gb|AA860074|AA860074 ak45b06.s1 Soares testis NHT Homo sapiens ... 38 3.0
gb|AA889618|AA889618 ak28f06.s1 Soares_testis_NHT Homo sapiens ... 38 3.0

gb|AA230450|AA230450 mv73c06.r1 Soares mouse 3NME12 5 Mus muscu... 38 1.1
gb|AA058041|AA058041 mj58e08.r1 Soares mouse embryo NbME13.5 14... 38 1.1
gb|AA152953|AA152953 mq54a03.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.1
gb|W34414|W34414 ma98b07.r1 Soares mouse p3NMF19.5 Mus musculus... 38 1.1
gb|AA465969|AA465969 ve90c06.s1 Knowles Solter mouse 2 cell Mus... 38 1.1
gb|AA261173|AA261173 mz62b11.r1 Soares mouse lymph node NbMLN M... 38 1.1
gb|AA238109|AA238109 mw97b05.r1 Soares mouse NML Mus musculus c... 38 1.1
dbj|C86549|C86549 Mus musculus fertilized egg cDNA 3'-end seque... 38 1.1
gb|AI048677|AI048677 ub29g09.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.1
dbj|D77921|MUSC1A08 Mouse embryonal carcinoma F9 cell cDNA, C1A08 38 1.1
gb|AA396183|AA396183 vb45e04.r1 Soares mouse lymph node NbMLN M... 38 1.1
gb|AA465898|AA465898 vc62f12.s1 Knowles Solter mouse 2 cell Mus... 36 4.3
gb|AA041869|AA041869 mj05b12.r1 Soares mouse embryo NbME13.5 14... 36 4.3
gb|AA637824|AA637824 vr21f11.r1 Barstead mouse myotubes MPLRB5 ... 36 4.3
gb|W82563|W82563 mf05g06.r1 Soares mouse p3NMF19.5 Mus musculus... 36 4.3
gb|AA389972|AA389972 vb30e03.r1 Soares mouse lymph node NbMLN M... 36 4.3
gb|AA396253|AA396253 vb45f08.r1 Soares mouse lymph node NbMLN M... 36 4.3
gb|AA920907|AA920907 vy84f04.r1 Stratagene mouse macrophage (#9... 36 4.3
gb|AA517166|AA517166 vh98h05.r1 Barstead mouse myotubes MPLRB5 ... 36 4.3
gb|AA433599|AA433599 vf47a05.r1 Soares mouse NbMH Mus musculus ... 36 4.3
gb|AA867252|AA867252 vx25c01.r1 Soares 2NbMT Mus musculus cDNA ... 36 4.3
dbj|C85619|C85619 Mus musculus fertilized egg cDNA 3'-end seque... 36 4.3
gb|AA260277|AA260277 va93g05.r1 Soares mouse 3NME12 5 Mus muscu... 36 4.3
gb|AA172548|AA172548 mt04g11.r1 Soares mouse 3NbMS Mus musculus... 36 4.3
gb|AA266879|AA266879 mz96a02.r1 Soares mouse lymph node NbMLN M... 36 4.3
gb|AA473019|AA473019 vd43e06.r1 Barstead MPLRB1 Mus musculus cD... 36 4.3

gb|R47549|R47549 SW3ICA119SK Brugia malayi infective larva cDNA... 40 0.24
gb|H32651|H32651 EST107947 Rat PC-12 cells, untreated Rattus sp... 38 0.96
gb|AA955987|AA955987 UI-R-E1-fb-f-06-0-UI.s1 UI-R-E1 Rattus nor... 38 0.96
gb|AA819638|AA819638 UI-R-A0-an-f-03-0-UI.s1 UI-R-A0 Rattus nor... 38 0.96
gb|AI010914|AI010914 EST205365 Normalized rat muscle, Bento Soa... 38 0.96
gb|AA893199|AA893199 EST197002 Normalized rat kidney, Bento Soa... 38 0.96
gb|AA945176|AA945176 EST200675 Normalized rat liver, Bento Soar... 38 0.96
gb|R95272|R95272 SWOvL3CA167SK Onchocerca volvulus infective la... 36 3.8
gb|AA917208|AA917208 ka05f02.s1 Onchocerca volvulus infective l... 36 3.8
dbj|C62023|C62023 C.elegans cDNA clone yk249d5 : 5' end, single... 36 3.8
gb|AI013322|AI013322 EST207997 Normalized rat spleen, Bento Soa... 36 3.8
gb|AI043280|AI043280 TENU0920 T. cruzi epimastigote normalized ... 36 3.8
gb|AI009422|AI009422 EST203873 Normalized rat heart, Bento Soar... 36 3.8
gb|AI012655|AI012655 EST207106 Normalized rat placenta, Bento S... 36 3.8
dbj|C62878|C62878 C.elegans cDNA clone yk296d4 : 5' end, single... 36 3.8
gb|AA915818|AA915818 SWOvL3CA1269SK Onchocerca volvulus infecti... 36 3.8
gb|W00009|W00009 TgESTzy75b07.r1 TgRH Tachyzoite cDNA Toxoplasm... 36 3.8
gb|AA943503|AA943503 EST199002 Normalized rat brain, Bento Soar... 36 3.8
gb|AA956933|AA956933 UI-R-E1-fl-b-08-0-UI.s1 UI-R-E1 Rattus nor... 36 3.8
gb|H54977|H54977 HHU16a Sorghum bicolor cv. TX430 Sorghum bicol... 36 3.8

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gb|AC000112|HSAC000112 Human PAC clone DJ149P21, complete seque... 44 0.082
gb|U50197|CELF25E2 Caenorhabditis elegans cosmid F25E2. 44 0.082
dbj|AB007727|AB007727 Arabidopsis thaliana genomic DNA, chromos... 44 0.082
gb|U02562|BSU02562 Bacillus subtilis N-acetylglucosaminidase (l... 42 0.32
dbj|D45048|BACORFX Bacillus subtilis gene for beta-N-acetylgluc... 42 0.32
emb|Z70683|CEF13B12 Caenorhabditis elegans cosmid F13B12, compl... 40 1.3
emb|AL023828|CEY17G7B Caenorhabditis elegans cosmid Y17G7B, com... 40 1.3
gb|U39740|CELZC64 Caenorhabditis elegans cosmid ZC64. 40 1.3
gb|AF006490|AF006490 Gossypium hirsutum adenine nucleotide tran... 40 1.3
emb|AL010170|PFSC03098 Plasmodium falciparum DNA *** SEQUENCING... 40 1.3
gb|U53701|GHU53701 Gossypium hirsutum alcohol dehydrogenase 2d 40 1.3

HUMAN ESTs

gb|AA670455|AA670455 ae62h05.s1 Stratagene lung carcinoma 93721... 852 0.0
gb|AA251062|AA251062 zs07c10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 795 0.0

gb|AA669916|AA669916 ag42h08.s1 Jia bone marrow stroma Homo sap... 638 0.0
gb|AA300058|AA300058 EST12665 Uterus tumor I Homo sapiens cDNA ... 587 e-165
gb|AA664277|AA664277 ac08c05.s1 Stratagene HeLa cell s3 937216 ... 549 e-154
gb|AA373224|AA373224 EST85230 HSC172 cells I Homo sapiens cDNA ... 529 e-148
gb|AA225705|AA225705 nc10b05.r1 NCI_CGAP_Pr1 Homo sapiens cDNA ... 515 e-144
gb|W27883|W27883 39b10 Human retina cDNA randomly primed sublib... 484 e-134
gb|R24643|R24643 yh36g05.r1 Homo sapiens cDNA clone 131864 5'. 438 e-121
gb|N93137|N93137 zb28h06.s1 Homo sapiens cDNA clone 304955 3'. 432 e-119
gb|AA250933|AA250933 zs07d01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 426 e-117
gb|AA216370|AA216370 nc10b05.s1 NCI_CGAP_Pr1 Homo sapiens cDNA ... 398 e-109
gb|H26939|H26939 yl64g01.r1 Homo sapiens cDNA clone 163056 5'. 394 e-108
gb|H30169|H30169 yo58g09.r1 Homo sapiens cDNA clone 182176 5'. 394 e-108
gb|W38854|W38854 zb28h06.r1 Soares parathyroid tumor NbHPA Homo... 359 5e-97
gb|AA602297|AA602297 np25a11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 281 1e-73
gb|AA167151|AA167151 zp06e09.r1 Stratagene ovarian cancer (#937... 256 6e-66
gb|AA172387|AA172387 zo99d03.s1 Stratagene ovarian cancer (#937... 234 2e-59
gb|AA173748|AA173748 zo99d03.r1 Stratagene ovarian cancer (#937... 224 2e-56
gb|T83979|T83979 yd66a11.s1 Homo sapiens cDNA clone 113180 3'. 220 3e-55
dbj|D61540|HUM415A08B Human fetal brain cDNA 5'-end GEN-415A08. 194 2e-47
gb|N45148|N45148 yv25a05.r1 Homo sapiens cDNA clone 243728 5'. 165 2e-38
gb|AA642960|AA642960 60f07.s1 NCI_CGAP_Lym3 Homo sapiens cDNA... 147 4e-33
gb|R90980|R90980 yp93a03.r1 Homo sapiens cDNA clone 194956 5' s... 40 0.62
gb|AA521500|AA521500 aa73h08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA... 40 0.62
gb|H82921|H82921 yq46h10.s1 Homo sapiens cDNA clone 198883 3' s... 40 0.62
gb|AA294871|AA294871 EST100023 Pancreas tumor I Homo sapiens cD... 38 2.4
dbj|D63191|HUM503F11B Human placenta cDNA 5'-end GEN-503F11. 38 2.4
gb|AA211096|AA211096 zq89g01.s1 Stratagene hNT neuron (#937233)... 38 2.4

gb|AA840137|AA840137 ud01e08.r1 Soares mouse uterus NMPu Mus mu... 383 e-104
gb|AA145994|AA145994 mr13h04.r1 Soares mouse 3NbMS Mus musculus... 345 3e-93
gb|AA146365|AA146365 mr05d05.r1 Soares mouse 3NbMS Mus musculus... 236 2e-60
gb|AA203902|AA203902 mu60f02.r1 Soares mouse lymph node NbMLN M... 236 2e-60
gb|AA204516|AA204516 mu66c10.r1 Soares mouse lymph node NbMLN M... 182 2e-44
gb|AA137343|AA137343 mq80g08.r1 Stratagene mouse melanoma (#937... 52 6e-05
gb|AA174717|AA174717 ms67a01.r1 Soares mouse 3NbMS Mus musculus... 48 0.001
gb|W34073|W34073 ma85d10.r1 Soares mouse p3NMF19.5 Mus musculus... 48 0.001
gb|AA289493|AA289493 vb36b01.r1 Soares mouse lymph node NbMLN M... 48 0.001
gb|AA177700|AA177700 mt33e12.r1 Soares mouse 3NbMS Mus musculus... 48 0.001
gb|AA146021|AA146021 mr13e03.r1 Soares mouse 3NbMS Mus musculus... 48 0.001
gb|AA155352|AA155352 mn43d09.r1 Beddington mouse embryonic regi... 46 0.004
gb|AA880874|AA880874 vx33b02.r1 Stratagene mouse lung 937302 Mu... 42 0.056

gb|AA590520|AA590520 vi54b08.r1 Beddington mouse embryonic regi... 38 0.88
gb|AA596629|AA596629 vm56e06.r1 Stratagene mouse Tcell 937311 M... 38 0.88
dbj|D76657|MUS75H09 Mouse embryonal carcinoma F9 cell cDNA, 75H09 38 0.88
gb|AA050336|AA050336 mj12f05.r1 Soares mouse embryo NbME13.5 14... 38 0.88
gb|AA120196|AA120196 mn35a12.r1 Beddington mouse embryonic regi... 38 0.88
gb|W85267|W85267 mf42c06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.5
gb|AA239372|AA239372 my38f03.r1 Barstead mouse pooled organs MP... 36 3.5
gb|AA497891|AA497891 vi73c07.r1 Stratagene mouse testis (#93730... 36 3.5
gb|AA673053|AA673053 vn45e05.r1 Barstead mouse myotubes MPLRB5 ... 36 3.5
emb|Z36324|MM224 M.musculus mRNA (clone 224) for expressed sequ... 36 3.5
gb|AI021128|AI021128 ub01f06.r1 Soares mouse mammary gland NbMM... 36 3.5
gb|AA403424|AA403424 mz56f07.r1 Barstead mouse pooled organs MP... 36 3.5
gb|W66683|W66683 me23g11.r1 Soares mouse embryo NbME13.5 14.5 M... 36 3.5
gb|AA689022|AA689022 vs02c03.r1 Barstead mouse irradiated colon... 36 3.5
gb|AA574590|AA574590 vn63h11.r1 Barstead mouse proximal colon M... 36 3.5

dbj|C90696|C90696 Dictyostelium discoideum slug cDNA, clone SSJ634 38 0.78
gb|AA269052|AA269052 MA1MA052.AA3 S. mansoni adult Lambda Zap S... 38 0.78
gb|AA998786|AA998786 UI-R-C0-im-e-11-0-UI.s1 UI-R-C0 Rattus nor... 38 0.78
gb|H33464|H33464 EST109494 Rat PC-12 cells, NGF-treated (9 days... 38 0.78
gb|AA390721|AA390721 LD09459.5prime LD Drosophila melanogaster ... 36 3.1
dbj|C83908|C83908 Dictyostelium discoideum slug cDNA, clone SSA567 36 3.1
gb|AA202425|AA202425 LD02606.5prime LD Drosophila melanogaster ... 36 3.1
gb|AI030951|AI030951 UI-R-C0-jf-d-04-0-UI.s1 UI-R-C0 Rattus nor... 36 3.1
gb|N60251|N60251 TgESTzy11d04.r1 TgRH Tachyzoite cDNA (Toxoplasm... 36 3.1
gb|AA246875|AA246875 LD05855.5prime LD Drosophila melanogaster ... 36 3.1
gb|AA803682|AA803682 GM13955.5prime GM Drosophila melanogaster ... 36 3.1
gb|AA997528|AA997528 UI-R-C0-hw-h-11-0-UI.s1 UI-R-C0 Rattus nor... 36 3.1
gb|AA695197|AA695197 GM02389.5prime GM Drosophila melanogaster ... 36 3.1
gb|AA567339|AA567339 HL01077.5prime HL Drosophila melanogaster ... 36 3.1
gb|AA950648|AA950648 LD30547.5prime LD Drosophila melanogaster ... 36 3.1

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substantially identical to D86956

SEQ ID NO:564

gb|AC004505|AC004505 Homo sapiens chromosome 20, P1 clone 86C1 ... 176 1e-41
gb|S78798|S78798 1-phosphatidylinositol-4-phosphate 5-kinase is... 115 4e-23
gb|U48696|HSU48696 Human mariner-like element-containing mRNA, ... 115 4e-23
gb|U66300|LEU66300 Lycopersicon esculentum heat shock protein (... 115 4e-23
gb|AF045432|AF045432 Danio rerio stem cell leukemia protein (ta... 111 6e-22
emb|Z97178|BVRNAEF2 Beta vulgaris cDNA for elongation factor 2 107 9e-21
gb|U39066|MMU39066 Murine MAP kinase kinase 6c mRNA, complete cds. 101 6e-19
gb|U37573|XXU37573 Shuttle expression vector pBKCMV. 96 4e-17
gb|AF033097|AF033097 Avena sativa nonphototropic hypocotyl 1 (N... 90 2e-15
gb|AF027174|AF027174 Arabidopsis thaliana cellulose synthase ca... 86 3e-14
gb|U65376|CFU65376 Canis familiaris rod photoreceptor transduci... 84 1e-13
gb|AF033565|AF033565 Mus musculus cdc2/CDC28-like protein kinas... 82 5e-13
emb|Z49980|HS2AMCP H.sapiens mRNA for ets-like protein (clone 7... 82 5e-13
emb|AJ001103|LLARCAB Lactococcus lactis arcA and arcB genes 80 2e-12
gb|U52868|CFU52868 Canis familiaris retinal cyclic-GMP phosphod... 80 2e-12
gb|G29058|G29058 chicken STS ADL368 76 3e-11
gb|G29060|G29060 chicken STS ADL352 76 3e-11
gb|U34048|HDU34048 Haemophilus ducreyi hemoglobin-binding prote... 76 3e-11
gb|U44386|SLU44386 Solanum lycopersicum heat shock protein (TFH... 68 8e-09
gb|S83098|S83098 ribosomal protein S3 [Ambystoma mexicanum=Mexi... 66 3e-08
gb|U48697|HSU48697 Human mariner-like element-containing mRNA, ... 60 2e-06
gb|AF033096|AF033096 Avena sativa nonphototropic hypocotyl 1 (N... 60 2e-06
emb|X99051|LLATTMSAT L.lagopus ATT microsatellite, locus LLST1 58 8e-06
gb|U41811|HAU41811 Homarus americanus beta-I tubulin mRNA, comp... 46 0.029
emb|X99055|LLCAMSAT1 L.lagopus CA microsatellite, locus LLSD5 44 0.12
emb|X65215|BTMISATN B.taurus microsatellite DNA (624bp) 44 0.12
gb|AE001023|AE001023 Archaeoglobus fulgidus section 84 of 172 o... 42 0.46
emb|X80164|HSPDCM4 H.salinarium phage dcm4 Virus DNA 42 0.46
emb|X87859|MTCMAJ12S C.major mitochondrial gene for 12S ribosom... 42 0.46
emb|X87861|MTCPAL12S C.pallidus mitochondrial gene for 12S ribo... 42 0.46
gb|L13767|STMSEC101A Streptomyus lividans sec101 gene, 5' end p... 42 0.46
emb|Y08962|OSTRAMBPR O.sativa mRNA for transmembrane protein >g... 40 1.8
gb|S65686|S65686 {multiple cloning sites, vector} [bacteriophag... 40 1.8
gb|J02871|HUMCP45IV Human lung cytochrome P450 (IV subfamily) B... 40 1.8
dbj|D10450|HUMRTVE Human genomic DNA, retrovirus-like element 40 1.8
gb|S65683|S65683 {multiple cloning sites, vector} [bacteriophag... 40 1.8
gb|L14950|PIGALDRED Sus scrofa aldose reductase mRNA, complete ... 40 1.8
gb|S65693|S65693 {multiple cloning sites, vector} [bacteriophag... 40 1.8
gb|S65694|S65694 {multiple cloning sites, vector} [bacteriophag... 40 1.8
emb|AJ223292|SPAJ3292 Streptococcus pyogenes SOD gene, complete... 40 1.8
gb|U25846|HAU25846 Homarus americanus clone LOB5 farnesoic acid... 40 1.8
emb|X16699|HSP450P2 Human mRNA for cytochrome P-450HP 40 1.8
gb|U37100|HSU37100 Homo sapiens aldose reductase-like peptide m... 40 1.8

HUMAN ESTs

gb|AA305996|AA305996 EST177003 Jurkat T-cells VI Homo sapiens c... 942 0.0
gb|AA975279|AA975279 oq36e08.s1 NCI_CGAP_GC4 Homo sapiens cDNA ... 900 0.0
gb|AA426359|AA426359 zw11b02.r1 Soares NhHMPu S1 Homo sapiens c... 868 0.0
gb|AA424296|AA424296 zv90b08.r1 Soares NhHMPu S1 Homo sapiens c... 749 0.0
gb|AA632259|AA632259 np67d04.s1 NCI_CGAP_Br2 Homo sapiens cDNA ... 730 0.0
gb|H80377|H80377 yu59e01.r1 Homo sapiens cDNA clone 230424 5'. 658 0.0
gb|AA515175|AA515175 ng68f10.s1 NCI_CGAP_Lip2 Homo sapiens cDNA... 615 e-174
gb|AA351770|AA351770 EST59616 Infant brain Homo sapiens cDNA 5'... 611 e-172
gb|AA426522|AA426522 zw11b02.s1 Soares NhHMPu S1 Homo sapiens c... 587 e-165
gb|AA676220|AA676220 zi22a12.s1 Soares fetal liver spleen 1NFLS... 585 e-165
gb|R35132|R35132 yg60e09.r1 Homo sapiens cDNA clone 36874 5'. 579 e-163
gb|H80280|H80280 yu59e01.s1 Homo sapiens cDNA clone 230424 3'. 579 e-163
gb|H81145|H81145 yu60e01.r1 Homo sapiens cDNA clone 230520 5'. 561 e-157
gb|AA311105|AA311105 EST18187 Heart I Homo sapiens cDNA 5' end 533 e-149
gb|AA380530|AA380530 EST93691 Supt cells Homo sapiens cDNA 5' end 527 e-147
gb|H81050|H81050 yu60e01.s1 Homo sapiens cDNA clone 230520 3'. 500 e-139
gb|AA460005|AA460005 zx49g07.s1 Soares testis NHT Homo sapiens ... 482 e-134
gb|AA076450|AA076450 zm91d12.r1 Stratagene ovarian cancer (#937... 466 e-129
gb|N43873|N43873 yy43e09.r1 Homo sapiens cDNA clone 274024 5'. 452 e-125
gb|AA076451|AA076451 zm91d12.s1 Stratagene ovarian cancer (#937... 418 e-115
gb|AA907095|AA907095 ol03b12.s1 NCI_CGAP_Lu5 Homo sapiens cDNA ... 414 e-113
gb|W01027|W01027 za56g07.r1 Soares fetal liver spleen 1NFLS Hom... 262 1e-67
gb|AA127183|AA127183 zn29d11.r1 Stratagene neuroepithelium NT2R... 222 1e-55
gb|H65491|H65491 yr56a08.s1 Homo sapiens cDNA clone 209270 3'. 222 1e-55
gb|N48543|N48543 yy49d08.r1 Homo sapiens cDNA clone 276879 5'. 210 4e-52
gb|R32579|R32579 yh54h06.r1 Homo sapiens cDNA clone 133595 5'. 194 2e-47
gb|AA247827|AA247827 j0778.seq.F Human fetal heart, Lambda ZAP ... 117 5e-24
N84048, (many others similar, but smaller)

gb|AA589598|AA589598 vl49d08.s1 Stratagene mouse skin (#937313)... 398 e-109
gb|AA647465|AA647465 vq82f02.s1 Knowles Solter mouse 2 cell Mus... 385 e-105
gb|AA510284|AA510284 vh58f02.r1 Soares mouse mammary gland NbMM... 345 4e-93
gb|AA028696|AA028696 mi12e12.r1 Soares mouse p3NMF19.5 Mus musc... 307 9e-82
gb|N28081|N28081 MDB1409R Mouse brain, Stratagene Mus musculus ... 244 1e-62
gb|AA177452|AA177452 mt24c12.r1 Soares mouse 3NbMS Mus musculus... 226 3e-57
gb|N28080|N28080 MDB1409 Mouse brain, Stratagene Mus musculus c... 226 3e-57
dbj|C88310|C88310 Mus musculus fertilized egg cDNA 3'-end seque... 226 3e-57
gb|AA763786|AA763786 vo99g12.r1 Soares mouse mammary gland NbMM... 94 2e-17
gb|AA667535|AA667535 vv18b12.r1 Stratagene mouse heart (#937316... 40 0.31
gb|AA208274|AA208274 mv96a01.r1 GuayWoodford Beier mouse kidney... 38 1.2

gb|AA444814|AA444814 vg50e04.r1 Soares mouse mammary gland NbMM... 38 1.2
gb|AA763341|AA763341 vw53b12.r1 Soares mouse mammary gland NMLM... 38 1.2
gb|AA110827|AA110827 mp57a12.r1 Soares 2NbMT Mus musculus cDNA ... 38 1.2
gb|AA691932|AA691932 vt06b04.r1 Barstead mouse myotubes MPLRB5 ... 38 1.2
gb|W77233|W77233 me61f11.r1 Soares mouse embryo NbME13.5 14.5 M... 38 1.2
gb|AA072872|AA072872 mm80g08.r1 Stratagene mouse embryonic carc... 38 1.2
gb|AA980630|AA980630 ua43f05.r1 Soares mouse mammary gland NbMM... 36 4.9
gb|AA065522|AA065522 ml54d09.r1 Stratagene mouse testis (#93730... 36 4.9
gb|AA982398|AA982398 uh07b08.r1 Soares mouse hypothalamus NMHy ... 36 4.9
gb|W62610|W62610 md58c06.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.9
~~gb|AA286651|AA286651 vb79b02.r1 Soares mouse 3NME12 5 Mus muscu... 36 4.9~~
gb|AA399772|AA399772 vd70g05.r1 Beddington mouse embryonic regi... 36 4.9
gb|AA510475|AA510475 vg32h08.r1 Soares mouse mammary gland NbMM... 36 4.9
gb|AA109064|AA109064 ml63g02.r1 Stratagene mouse testis (#93730... 36 4.9
gb|AA033485|AA033485 mi42c08.r1 Soares mouse embryo NbME13.5 14... 36 4.9
gb|W57221|W57221 md59g10.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.9
gb|AA467106|AA467106 vd98b04.r1 Soares mouse NbMH Mus musculus ... 36 4.9
~~gb|W97470|W97470 mf95a11.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.9~~
gb|AA606917|AA606917 vm91c05.r1 Knowles Solter mouse blastocyst... 36 4.9
dbj|C78330|C78330 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 36 4.9
gb|AA013753|AA013753 mh26h12.r1 Soares mouse placenta 4NbMP13.5... 36 4.9
gb|AA145240|AA145240 mr12a03.r1 Soares mouse 3NbMS Mus musculus... 36 4.9
gb|AA245533|AA245533 mx03c11.r1 Soares mouse NML Mus musculus c... 36 4.9
gb|AA770893|AA770893 vt13a08.r1 Barstead mouse myotubes MPLRB5 ... 36 4.9
dbj|C79987|C79987 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 36 4.9
gb|AA014027|AA014027 mh24a12.r1 Soares mouse placenta 4NbMP13.5... 36 4.9
dbj|C89051|C89051 Mus musculus early blastocyst cDNA, clone 01B... 36 4.9
gb|AA058308|AA058308 mj59e09.r1 Soares mouse embryo NbME13.5 14... 36 4.9
gb|AA673826|AA673826 vu08h10.r1 Barstead mouse myotubes MPLRB5 ... 36 4.9
gb|AA637080|AA637080 vn07h04.r1 Knowles Solter mouse blastocyst... 36 4.9
gb|W44292|W44292 mc80c07.r1 Soares mouse embryo NbME13.5 14.5 M... 36 4.9

gb|AA955972|AA955972 UI-R-E1-ff-d-10-0-UI.s1 UI-R-E1 Rattus nor... 159 4e-37
gb|AA957275|AA957275 UI-R-E1-fq-f-08-0-UI.s1 UI-R-E1 Rattus nor... 157 2e-36
emb|Z84031|SSZ84031 S.scrofa mRNA; expressed sequence tag (5'; ... 111 9e-23
gb|AF041408|AF041408 Fragaria x ananassa clone FA110b 96 5e-18
gb|AA933116|AA933116 SWBmL3SA048T3 Brugia malayi L3 subtracted ... 58 1e-06
gb|AA933363|AA933363 SWBmL3SA615T3 Brugia malayi L3 subtracted ... 52 7e-05
gb|AA660164|AA660164 00001 MtRHE Medicago truncatula cDNA 5' si... 50 3e-04
gb|N37420|N37420 18647 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 44 0.018
gb|H35981|H35981 14503 Lambda-PRL2 Arabidopsis thaliana cDNA cl... 44 0.018
gb|AA882627|AA882627 TENS0198 T. cruzi epimastigote normalized ... 44 0.018
gb|AI026481|AI026481 TENU0693 T. cruzi epimastigote normalized ... 42 0.070
gb|AA946369|AA946369 EST201868 Normalized rat lung, Bento Soare... 42 0.070

gb|AI010371|AI010371 EST204822 Normalized rat lung, Bento Soare... 42 0.070
gb|AI010257|AI010257 EST204708 Normalized rat lung, Bento Soare... 42 0.070
dbj|D39318|RICR3325A Rice cDNA, partial sequence (R3325_1A). 40 0.28
gb|U40140|OSU40140 Oryza sativa clone pFDRRC22 mRNA sequence. 40 0.28
gb|AI009132|AI009132 EST203583 Normalized rat embryo, Bento Soa... 40 0.28
dbj|D47291|RICS12574A Rice cDNA, partial sequence (S12574_1A). 40 0.28
dbj|D47316|RICS12613A Rice cDNA, partial sequence (S12613_1A). 40 0.28
gb|T42265|T42265 5528 Lambda-PRL2 Arabidopsis thaliana cDNA clo... 40 0.28
dbj|D47631|RICS13239A Rice cDNA, partial sequence (S13239_1A). 40 0.28
gb|AI013513|AI013513 EST208188 Normalized rat spleen, Bento Soa... 40 0.28
gb|AA751980|AA751980 96AS0896 Rice Immature Seed Lambda ZAPII c... 40 0.28
gb|AA660165|AA660165 00002 MtRHE Medicago truncatula cDNA 5' si... 40 0.28
emb|Z34868|ATTS3597 A. thaliana transcribed sequence; clone FAF... 40 0.28
dbj|D39131|RICR2302A Rice cDNA, partial sequence (R2302_1A). 40 0.28
gb|AA963968|AA963968 UI-R-C0-gs-b-05-0-UI.s1 UI-R-C0 Rattus nor... 40 0.28
gb|AA866346|AA866346 UI-R-A0-bm-a-05-0-UI.s1 UI-R-A0 Rattus nor... 40 0.28
gb|AI044437|AI044437 UI-R-C1-js-e-06-0-UI.s1 UI-R-C1 Rattus nor... 40 0.28
dbj|D41811|RICS4634A Rice cDNA, partial sequence (S4634_1A). 40 0.28
dbj|C19261|C19261 Rice cDNA, partial sequence (E10176_1A) 40 0.28
dbj|D48409|RICS14588A Rice cDNA, partial sequence (S14588_1A). 40 0.28
dbj|C26556|C26556 Rice cDNA, partial sequence (C12586_1A) 40 0.28
dbj|D47831|RICS13548A Rice cDNA, partial sequence (S13548_1A). 40 0.28
dbj|C72152|C72152 Rice cDNA, partial sequence (E1094_3A) 40 0.28
dbj|D46553|RICS11305A Rice cDNA, partial sequence (S11305_2A). 40 0.28
gb|AI028926|AI0289 (and many others of similar score)

SEQ ID NO:565

emb|X68308|OOLPLIP O.ovis mRNA for lipoprotein lipase 40 1.2
gb|AE000660|HUAE000660 Homo sapiens T-cell receptor alpha delta... 40 1.2
emb|AL022333|HS474I12 Human DNA sequence *** SEQUENCING IN PROG... 38 4.6
emb|Z12618|CFTRG C.fasciculata gene encoding trypanothione redu... 38 4.6
gb|M81651|HUMSEMIIB Human semenogelin II (SEMGII) gene, complet... 38 4.6
gb|M96980|HUMMYT1A Homo sapiens myelin transcription factor 1 (... 38 4.6
gb|U89688|ACU89688 Acanthamoeba castellanii myosin-I binding pr... 38 4.6
gb|AC002497|AC002497 Human Cosmid g1940a142 from 7q31.3, comple... 38 4.6
gb|M81652|HUMSMNGLN Homo sapiens semenogelin II mRNA, complete ... 38 4.6
gb|M25665|HUMNCF1A Human neutrophil cytosol factor 1 (NCF-47k) ... 38 4.6
gb|M73325|TRFTRPREDC Crithidia fasciculata trypanothione reduct... 38 4.6
gb|M73324|TRFTRPREDB Crithidia fasciculata trypanothione reduct... 38 4.6
emb|X92589|MMSEMIIGN M.mulatta semenogelin II gene 38 4.6
emb|Z47556|HSSG1SG2 H.sapiens genes for semenogelin I and semen... 38 4.6
gb|AC004753|AC004753 Homo sapiens chromosome 16, cosmid clone R... 38 4.6
gb|M55067|HUMNADPHO Human 47-kD autosomal chronic granulomatous... 38 4.6

gb|M73323|TRFTRPREDA Crithidia fasciculata trypanothione reduct... 38 4.6

HUMAN ESTs

gb|R11942|R11942 yf54c05.r1 Homo sapiens cDNA clone 25950 5'. 656 0.0
gb|AA366384|AA366384 EST77326 Pancreas tumor III Homo sapiens c... 470 e-130
gb|T12566|T12566 CHR90086 Homo sapiens genomic clone P94_24 5' ... 133 5e-29
gb|R37032|R37032 yf54c05.s1 Homo sapiens cDNA clone 25950 3'. 44 0.036
gb|AA661650|AA661650 nv02h12.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
~~gb|AA261982|AA261982 zs20d03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2~~
gb|AA588219|AA588219 no24c11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA250891|AA250891 zs06c06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
gb|AA244177|AA244177 nc05a02.r1 NCI_CGAP_Pr1 Homo sapiens cDNA ... 38 2.2
gb|AA715147|AA715147 nv10d05.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA659887|AA659887 nv03a10.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA627890|AA627890 nq70a08.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
~~gb|AA603596|AA603596 np27b11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2~~
gb|AA613738|AA613738 np25h09.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA715248|AA715248 nv10h06.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AI038487|AI038487 ow25d12.x1 Soares_parathyroid_tumor_NbHPA ... 38 2.2
gb|AA252786|AA252786 zs26f10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
gb|AA287819|AA287819 zs50h04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
gb|AA564176|AA564176 nj04c08.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 38 2.2
gb|AA643870|AA643870 np26h07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA280371|AA280371 zt05f07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
gb|R00687|R00687 ye78h08.r1 Homo sapiens cDNA clone 123903 5' s... 38 2.2
gb|AA587820|AA587820 nj06h05.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 38 2.2
gb|AA588443|AA588443 no22c11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA568385|AA568385 nl88f06.s1 NCI_CGAP_Co10 Homo sapiens cDNA... 38 2.2
gb|AA281831|AA281831 zt06c08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
gb|AA700438|AA700438 zj74b08.s1 Soares fetal liver spleen 1NFLS... 38 2.2
gb|AA689530|AA689530 ns66e07.r1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA688300|AA688300 nv14a09.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA687962|AA687962 nv13h04.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA526586|AA526586 ni96f11.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 38 2.2
gb|AA642589|AA642589 nq73f04.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA541594|AA541594 ni89g07.s1 NCI_CGAP_Pr21 Homo sapiens cDNA... 38 2.2
gb|AA278713|AA278713 zs76h02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2
gb|T58661|T58661 ya94a07.r1 Homo sapiens cDNA clone 69300 5' si... 38 2.2
gb|AA689473|AA689473 ns66e07.s1 NCI_CGAP_Pr22 Homo sapiens cDNA... 38 2.2
gb|AA459023|AA459023 aa26a09.r1 NCI_CGAP_GCB1 Homo sapiens cDNA... 38 2.2

dbj|C76752|C76752 Mus musculus 3.5-dpc blastocyst cDNA 3'-end s... 60 2e-07
gb|AA123048|AA123048 mn32g01.r1 Beddington mouse embryonic regi... 36 3.2
gb|AA616529|AA616529 vo10e01.r1 Barstead mouse myotubes MPLRB5 ... 36 3.2
gb|AA254370|AA254370 va13h09.r1 Soares mouse lymph node NbMLN M... 36 3.2
gb|AA537288|AA537288 vk46c04.r1 Soares mouse mammary gland NbMM... 36 3.2
gb|AA462365|AA462365 vg74c05.r1 Soares mouse NbMH Mus musculus ... 36 3.2
gb|AA589462|AA589462 vl47g07.s1 Stratagene mouse skin (#937313)... 36 3.2
gb|AA968017|AA968017 uh06h10.r1 Soares mouse hypothalamus NMHy ... 36 3.2

dbj|C93868|C93868 Dictyostelium discoideum slug cDNA, clone SSL809 36 2.8
gb|AA531984|AA531984 TgESTzz46b06.r1 TgME49 invivo Bradyzoite c... 36 2.8
gb|N60418|N60418 TgESTzy07a10.r1 TgRH Tachyzoite cDNA Toxoplasm... 36 2.8
gb|H32045|H32045 EST106774 Rat PC-12 cells, untreated Rattus sp... 36 2.8
gb|AA956789|AA956789 UI-R-E1-fr-h-01-0-UI.s1 UI-R-E1 Rattus nor... 36 2.8
gb|H33275|H33275 EST109117 Rat PC-12 cells, NGF-treated (9 days... 36 2.8
gb|AA531938|AA531938 TgESTzz45b08.r1 TgME49 invivo Bradyzoite c... 36 2.8
dbj|D41507|RICS4044A Rice cDNA, partial sequence (S4044_1A). 36 2.8
gb|AA799411|AA799411 EST188908 Normalized rat heart, Bento Soar... 36 2.8
gb|AA519671|AA519671 TgESTzz27c10.r1 TgME49 invivo Bradyzoite c... 36 2.8
dbj|D40678|RICS2786A Rice cDNA, partial sequence (S2786_1A). 36 2.8
gb|AA012430|AA012430 TgESTzz22b12.r1 TgME49cDNA Toxoplasma gond... 36 2.8
dbj|D40551|RICS2612A Rice cDNA, partial sequence (S2612_1A). 36 2.8
gb|AI008452|AI008452 EST202903 Normalized rat embryo, Bento Soa... 36 2.8
dbj|D41253|RICS3620A Rice cDNA, partial sequence (S3620_1A). 36 2.8
gb|AA923843|AA923843 UI-R-A1-dr-f-04-0-UI.s1 UI-R-A1 Rattus nor... 36 2.8
gb|AA799410|AA799410 EST188907 Normalized rat heart, Bento Soar... 36 2.8

We claim:

1. A method of diagnosing a disorder characterized by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule, comprising:

contacting a biological sample isolated from a subject with an agent that specifically binds to the nucleic acid molecule, an expression product thereof, or a fragment of an expression product thereof complexed with an HLA molecule, wherein the nucleic acid molecule is a NA Group 1 nucleic acid molecule, and

determining the interaction between the agent and the nucleic acid molecule or the expression product as a determination of the disorder.

2. The method of claim 1, wherein the agent is selected from the group consisting of

(a) a nucleotide acid molecule comprising NA group 1 nucleic acid molecules or a fragment thereof,

(b) a nucleic acid molecule comprising NA group 3 nucleic acid molecules or a fragment thereof,

(c) a nucleic acid molecule comprising NA group 17 nucleic acid molecules or a fragment thereof,

(d) an antibody that binds to an expression product of NA group 1 nucleic acids,

(e) an antibody that binds to an expression product of NA group 3 nucleic acids,

(f)

an antibody that binds to an expression product of NA group 17 nucleic acids,

(g)

and agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 1 nucleic acid,

(h)

an agent that binds to a complex of an HLA molecule and a fragment of an ~~expression product of a NA group 3 nucleic acid, and~~

(I)

an agent that binds to a complex of an HLA molecule and a fragment of an expression product of a NA group 17 nucleic acid.

3. The method of claim 1, wherein the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which is specific for a different human cancer associated antigen precursor, and wherein said plurality of agents is at least 2, at least 3, at least 4, at least 4, at least 6, at least 7, or at least 8, at least 9 or at least 10 such agents.

4. The method of claims 1-3, wherein the agent is specific for a human cancer associated antigen precursor that is a breast, a gastric, a lung, a prostate, a renal or a colon cancer associated antigen precursor.

5. A method for determining regression, progression or onset of a condition characterized by expression of abnormal levels of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule, comprising

monitoring a sample, from a patient who has or is suspected of having the condition, for a parameter selected from the group consisting of

(I)

the protein,

(ii)

a peptide derived from the protein,

(iii)

an antibody which selectively binds the protein or peptide, and

(iv)

cytolytic T cells specific for a complex of the peptide derived from the protein and an MHC molecule,

as a determination of regression, progression or onset of said condition.

6. The method of claim 5, wherein the sample is a body fluid, a body effusion or a tissue.

7. The method of claim 5, wherein the step of monitoring comprises contacting the sample with a detectable agent selected from the group consisting of

(a)

an antibody which selectively binds the protein of (I), or the peptide of (ii),

(b)

a protein or peptide which binds the antibody of (iii), and

(c)

a cell which presents the complex of the peptide and MHC molecule of (iv).

8. The method of claim 7, wherein the antibody, the protein, the peptide or the cell is labeled with a radioactive label or an enzyme.

9. The method of claim 5, comprising assaying the sample for the peptide.

10. The method of claim 5, wherein the nucleic acid molecule is a NA Group 3 molecule.

11. The method of claim 5, wherein the nucleic acid molecule is a NA Group 11 molecule.

12. The method of claim 5, wherein the nucleic acid molecule is a NA Group 12 molecule.

13. The method of claim 5, wherein the nucleic acid molecule is a NA Group 13 molecule.

14. The method of claim 5, wherein the nucleic acid molecule is a NA Group 14 molecule.

15. The method of claim 5, wherein the nucleic acid molecule is a NA Group 15 molecule.

16. The method of claim 5, wherein the nucleic acid molecule is a NA Group 16 molecule.

17. The method of claim 5, wherein the protein is a plurality of proteins, the parameter is a plurality of parameters, each of the plurality of parameters being specific for a different of the plurality of proteins.

18. A pharmaceutical preparation for a human subject comprising

an agent which when administered to the subject enriches selectively the presence of complexes of an HLA molecule and a human cancer associated antigen, and

a pharmaceutically acceptable carrier, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule comprises a NA Group 1 molecule.

19. The pharmaceutical preparation of claim 18, wherein the agent comprises a plurality of agents, each of which enriches selectively in the subject complexes of an HLA molecule and a different human cancer associated antigen.

20. The pharmaceutical preparation of claim 19, wherein the plurality is at least two, at least three, at least four or at least 5 different such agents.

21. The pharmaceutical preparation of claim 18, wherein the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

22. The pharmaceutical preparation of claim 18, wherein the agent is selected from the group consisting of

(1) an isolated polypeptide comprising the human cancer associated antigen, or a functional variant thereof,

(2) an isolated nucleic acid operably linked to a promoter for expressing the isolated polypeptide, or functional variant thereof,

(3) a host cell expressing the isolated polypeptide, or functional variant thereof, and

(4) isolated complexes of the polypeptide, or functional variant thereof, and an HLA molecule.

23. The pharmaceutical preparation of claims 18-22, further comprising an adjuvant.

24. The pharmaceutical preparation of claim 18, wherein the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell is nonproliferative.

25. The pharmaceutical preparation of claim 18, wherein the agent is a cell expressing an isolated polypeptide comprising the human cancer associated antigen or a functional variant thereof, and wherein the cell expresses an HLA molecule that binds the polypeptide.

26. The pharmaceutical preparation of claim 18, wherein the agent is at least two, at least three, at least four or at least five different polypeptides, each coding for a different human cancer associated antigen or functional variant thereof.

27. The pharmaceutical preparation of claim 18, wherein the agent is a PP Group 2 polypeptide.

28. The pharmaceutical preparation of claim 18, wherein the agent is a PP Group 3 polypeptide or a PP Group 4 polypeptide.

29. The pharmaceutical preparation of claim 25, wherein the cell expresses one or both of the polypeptide and HLA molecule recombinantly.

30. The pharmaceutical preparation of claim 25, wherein the cell is nonproliferative.

31. A composition comprising an isolated agent that binds selectively a PP Group 1 polypeptide.

32. The composition of matter of claim 31, wherein the agent binds selectively a PP Group 3 polypeptide.

33. The composition of matter of claim 31, wherein the agent binds selectively a PP Group 11 polypeptide.

34. The composition of matter of claim 31, wherein the agent binds selectively a PP Group 12 polypeptide.

35. The composition of matter of claim 31, wherein the agent binds selectively a PP Group 13 polypeptide.

36. The composition of matter of claim 31, wherein the agent binds selectively a PP Group 14 polypeptide.

37. The composition of matter of claim 31, wherein the agent binds selectively a PP Group 15 polypeptide.

38. The composition of matter of claim 31, wherein the agent binds selectively a PP Group 16 polypeptide.

39. The composition of claims 31-38, wherein the agent is a plurality of different agents that bind selectively at least two, at least three, at least four, or at least five different such polypeptides.

40. The composition of claims 31-38, wherein the agent is an antibody.

41. The composition of claim 39, wherein the agent is an antibody.

42. A composition of matter comprising
a conjugate of the agent of claims 31-41 and a therapeutic or diagnostic agent.

43. The composition of matter of claim 42, wherein the conjugate is of the agent and a therapeutic or diagnostic that is a toxin.

44. A pharmaceutical composition comprising an isolated nucleic acid molecule selected from the group consisting of:
(1)
NA Group 1 molecules, and

(2)
NA Group 2 molecules, and a pharmaceutically acceptable carrier.

45. The pharmaceutical composition of claim 44, wherein the isolated nucleic acid molecule comprises a NA Group 3 or NA Group 4 molecule.

46. The pharmaceutical composition of claim 44, wherein the isolated nucleic acid molecule comprises at least two isolated nucleic acid molecules coding for two different polypeptides, each polypeptide comprising a different human cancer associated antigen.

47. The pharmaceutical composition of claims 44-46 further comprising an expression vector with a promoter operably linked to the isolated nucleic acid molecule.

48. The pharmaceutical composition of claims 44-46 further comprising a host cell recombinantly expressing the isolated nucleic acid molecule.

49. A pharmaceutical composition comprising an isolated polypeptide comprising a PP Group 1 or a PP Group 2 polypeptide, and a pharmaceutically acceptable carrier.

50. The pharmaceutical composition of claim 49, wherein the isolated polypeptide comprises a PP Group 3 or a PP Group 4 polypeptide.

51. The pharmaceutical composition of claim 49, wherein the isolated polypeptide comprises at least two different polypeptides, each comprising a different human cancer associated antigen.

52. The pharmaceutical composition of claim 49, wherein the isolated polypeptides are PP Group 11 polypeptides or HLA binding fragments thereof.

53. The pharmaceutical composition of claim 49, wherein the isolated polypeptides are PP Group 12 polypeptides or HLA binding fragments thereof.

54. The pharmaceutical composition of claim 49, wherein the isolated polypeptides are PP Group 13 polypeptides or HLA binding fragments thereof.

55. The pharmaceutical composition of claim 49, wherein the isolated polypeptides are PP Group 14 polypeptides or HLA binding fragments thereof.

56. The pharmaceutical composition of claim 49, wherein the isolated polypeptides are PP Group 15 polypeptides or HLA binding fragments thereof.

57. The pharmaceutical composition of claim 49, wherein the isolated polypeptides are PP Group 16 polypeptides or HLA binding fragments thereof.

58. The pharmaceutical composition of claims 49-57, further comprising an adjuvant.

59. An isolated nucleic acid molecule comprising a NA Group 3 molecule.

60. An isolated nucleic acid molecule comprising a NA Group 4 molecule.

61. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 11 molecule or a fragment thereof.

62. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 12 molecule or a fragment thereof.

63. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 13 molecule or a fragment thereof.

64. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 14 molecule or a fragment thereof.

65. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 15 molecule or a fragment thereof.

66. The isolated nucleic acid molecule of claims 59-60, wherein the molecule is a Group 16 molecule or a fragment thereof.

67. An isolated nucleic acid molecule selected from the group consisting of

(a)

a fragment of a nucleic acid selected from the group of nucleic acid consisting of SEQ ID NOs presenting nucleic acid sequences among SEQ ID NOs. 1-816, of sufficient length to represent a sequence unique within the human genome, and identifying a nucleic acid encoding a human cancer associated antigen precursor,

(b)

complements of (a),

provided that the fragment includes a sequence of contiguous nucleotides which is not identical to any sequence selected from the sequence group consisting of

(1) sequences having the GenBank accession numbers of Table 1 **(correct?)**,

(2) complements of (1), and

(3) fragments of (1) and (2).

68. The isolated nucleic acid molecule of claim 67, wherein the sequence of contiguous nucleotides is selected from the group consisting of:

(1)

at least two contiguous nucleotides nonidentical to the sequence group,

(2)

at least three contiguous nucleotides nonidentical to the sequence group,

(3)

at least four contiguous nucleotides nonidentical to the sequence group,

(4)

at least five contiguous nucleotides nonidentical to the sequence group,

(5)

at least six contiguous nucleotides nonidentical to the sequence group,

(6)

at least seven contiguous nucleotides nonidentical to the sequence group.

69. The isolated nucleic acid molecule of claim 67, wherein the fragment has a size selected from the group consisting of at least: 8 nucleotides, 10 nucleotides, 12 nucleotides, 14 nucleotides, 16 nucleotides, 18 nucleotides, 20, nucleotides, 22 nucleotides, 24 nucleotides, 26 nucleotides, 28 nucleotides, 30 nucleotides, 50 nucleotides, 75 nucleotides, 100 nucleotides, and 200 nucleotides.

70. The isolated nucleic acid molecule of claim 67, wherein the molecule encodes a polypeptide which, or a fragment of which, binds a human HLA receptor or a human antibody.

71. An expression vector comprising an isolated nucleic acid molecule of claims 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69 or 70 operably linked to a promoter.

72. An expression vector comprising a nucleic acid operably linked to a promoter, wherein the nucleic acid is a NA Group 2 molecule.

73. An expression vector comprising a NA Group 1 or Group 2 molecule and a nucleic acid encoding an HLA molecule.

74. A host cell transformed or transfected with an expression vector of claims 71, 72, or 73.

75. A host cell transformed or transfected with an expression vector of claim 71 or claim 72 and further comprising a nucleic acid encoding HLA.

76. An isolated polypeptide encoded by the isolated nucleic acid molecule of claims 59, 60, 61, 62, 63, 64, 65, or 66.

77. A fragment of the polypeptide of claim 76 which is immunogenic.

78. The fragment of claim 77, wherein the fragment, or a portion of the fragment, binds HLA or a human antibody.

79. An isolated fragment of a human cancer associated antigen precursor which, or portion of which, binds HLA or a human antibody, wherein the precursor is encoded by a nucleic acid molecule that is a NA Group 1 molecule.

80. The fragment of claim 79, wherein the fragment is part of a complex with HLA.

81. The fragment of claim 79, wherein the fragment is between 8 and 12 amino acids in length.

82. An isolated polypeptide comprising a fragment of the polypeptide of claim 76 of sufficient length to represent a sequence unique within the human genome and identifying a polypeptide that is a human cancer associated antigen precursor.

83. A kit for detecting the presence of the expression of a human cancer associated antigen precursor comprising

a pair of isolated nucleic acid molecules each of which consists essentially of a molecule selected from the group consisting of

(a) a 12-32 nucleotide contiguous segment of the nucleotide sequence of any of the NA Group 1 molecules and

(b) complements of ("a"), wherein the contiguous segments are nonoverlapping.

84. The kit of claim 83, wherein the pair of isolated nucleic acid molecules is constructed and arranged to selectively amplify an isolated nucleic acid molecule that is a NA Group 3 molecule.

85. A method for treating a subject with a disorder characterized by expression of a human cancer associated antigen precursor, comprising

administering to the subject an amount of an agent, which enriches selectively in the subject the presence of complexes of an HLA molecule and a human cancer associated antigen, effective to ameliorate the disorder, wherein the human cancer associated antigen is a fragment of a human cancer associated antigen precursor encoded by a nucleic acid molecule selected from the group consisting of

(a)

a nucleic acid molecule comprising NA group 1 nucleic acid molecules,

(b)

a nucleic acid molecule comprising NA group 3 nucleic acid molecules,

(c)

a nucleic acid molecule comprising NA group 17 nucleic acid molecules.

86. The method of claim 85, wherein the disorder is characterized by expression of a plurality of human cancer associated antigen precursors and wherein the agent is a plurality of agents, each of which enriches selectively in the subject the presence of complexes of an HLA molecule and a different human cancer associated antigen.

87. The method of claim 86, wherein the plurality is at least 2, at least 3, at least 4, or at least 5 such agents.

88. The method of claims 85-87, wherein the agent is an isolated polypeptide selected from the group consisting of PP Group 1, PP Group 2, PP Group 3, PP Group 4, PP Group 5, PP Group 6, PP Group 7, PP Group 8, PP Group 9, PP Group 10, PP Group 11, PP Group 12, PP Group 13, PP Group 14, PP Group 15, PP Group 16 and PP Group 17 polypeptides.

89. The method of claims 85-88, wherein the disorder is cancer.

90. A method for treating a subject having a condition characterized by expression of a human cancer associated antigen precursor in cells of the subject, comprising:

(I) removing an immunoreactive cell containing sample from the subject,

(ii) contacting the immunoreactive cell containing sample to the host cell under conditions favoring production of cytolytic T cells against a human cancer associated antigen which is a fragment of the precursor,

(iii) introducing the cytolytic T cells to the subject in an amount effective to lyse cells which express the human cancer associated antigen, wherein the host cell is transformed or transfected with an expression vector comprising an isolated nucleic acid molecule operably linked to a promoter, the isolated nucleic acid molecule being selected from the group of nucleic acid molecules consisting of NA Group 1, NA Group 2, NA Group 3, NA Group 4, NA Group 5, NA Group 6, NA Group 7, NA Group 8, NA Group 9, NA Group 10, NA Group 11, NA Group 12, NA Group 13, NA Group 14, NA Group 15, NA Group 16, and NA Group 17.

91. The method of claim 90, wherein the host cell recombinantly expresses an HLA molecule which binds the human cancer associated antigen.

92. The method of claim 90, wherein the host cell endogenously expresses an HLA molecule which binds the human cancer associated antigen.

93. A method for treating a subject having a condition characterized by expression of a human cancer associated antigen precursor in cells of the subject, comprising:

(I) identifying a nucleic acid molecule expressed by the cells associated with said condition, wherein said nucleic acid molecule is a NA Group 1 molecule

(ii) transfecting a host cell with a nucleic acid selected from the group consisting of:

(a) the nucleic acid molecule identified,

(b) a fragment of the nucleic acid identified which includes a segment coding for a human cancer associated antigen,

(c) deletions, substitutions or additions to (a) or (b), and

(d)

degenerates of (a), (b), or (c);

(iii)

culturing said transfected host cells to express the transfected nucleic acid molecule, and;

(iv)

introducing an amount of said host cells or an extract thereof to the subject effective to increase an immune response against the cells of the subject associated with the condition.

94. The method of claim 93, further comprising:

(a) identifying an MHC molecule which presents a portion of an expression product of the nucleic acid molecule,

wherein the host cell expresses the same MHC molecule as identified in (a) and wherein the host cell presents an MHC binding portion of the expression product of the nucleic acid molecule.

95. The method of claim 93, wherein the immune response comprises a B-cell response or a T cell response.

96. The method of claim 95, wherein the response is a T-cell response which comprises generation of cytolytic T-cells specific for the host cells presenting the portion of the expression product of the nucleic acid molecule or cells of the subject expressing the human cancer associated antigen.

97. The method of claim 93, wherein the nucleic acid molecule is a NA Group 3 molecule.

98. The method of claims 93 or 94, further comprising treating the host cells to render them non-proliferative.

99. A method for treating or diagnosing or monitoring a subject having a condition characterized by expression of an abnormal amount of a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule, comprising

administering to the subject an antibody which specifically binds to the protein or a peptide derived therefrom, the antibody being coupled to a therapeutically useful agent, in an amount effective to treat the condition.

100. The method of claim 99, wherein the antibody is a monoclonal antibody.

101. The method of claim 100, wherein the monoclonal antibody is a chimeric antibody or a humanized antibody.

102. A method for treating a condition characterized by expression in a subject of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

administering to a subject a pharmaceutical composition of any one of claims 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 47, and 58 in an amount effective to prevent, delay the onset of, or inhibit the condition in the subject.

103. The method of claim 102, wherein the condition is cancer.

104. The method of claims 102-103, further comprising first identifying that the subject expresses in a tissue abnormal amounts of the protein.

105. A method for treating a subject having a condition characterized by expression of abnormal amounts of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

(I) identifying cells from the subject which express abnormal amounts of the protein;

(ii) isolating a sample of the cells;

(iii) cultivating the cells, and

(iv) introducing the cells to the subject in an amount effective to provoke an immune response against the cells.

106. The method of claim 105, wherein the cells express a protein selected from the group consisting of a PP Group 11 protein, a PP Group 12 protein, a PP Group 13 protein, PP Group 14 protein, a PP Group 15 protein and a PP Group 16 protein.

107. The method of claim 105, further comprising rendering the cells non-proliferative, prior to introducing them to the subject.

108. A method for treating a pathological cell condition characterized by aberrant expression of a protein encoded by a nucleic acid molecule that is a NA Group 1 nucleic acid molecule, comprising

administering to a subject in need thereof an effective amount of an agent which inhibits the expression or activity of the protein.

109. The method of claim 108, wherein the agent is an inhibiting antibody which selectively binds to the protein and wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

110. The method of claim 108, wherein the agent is an antisense nucleic acid molecule which selectively binds to the nucleic acid molecule which encodes the protein.

111. The method of claim 108, wherein the nucleic acid molecule is a NA Group 3 nucleic acid molecule.

112. A composition of matter useful in stimulating an immune response to a plurality of a protein encoded by nucleic acid molecules that are NA Group 1 molecules, comprising

a plurality of peptides derived from the amino acid sequences of the proteins, wherein the peptides bind to one or more MHC molecules presented on the surface of the cells which express an abnormal amount of the protein.

113. The composition of matter of claim 112, wherein at least a portion of the plurality of peptides bind to MHC molecules and elicit a cytolytic response thereto.

114. The composition of matter of claim 113, further comprising an adjuvant.

115. The composition of matter of claim 114, wherein said adjuvant is a saponin, GM-CSF, or an interleukin.

116. An isolated antibody which selectively binds to a complex of:

(i)

a peptide derived from a protein encoded by a nucleic acid molecule that is a NA Group 1 molecule and

(ii)

and an MHC molecule to which binds the peptide to form the complex, wherein the isolated antibody does not bind to (I) or (ii) alone.

117. The antibody of claim 116, wherein the antibody is a monoclonal antibody, a chimeric antibody or a humanized antibody.

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NY-LU-12   KEESPPPPKVVHPLIGLLGEYGGDSDYEEEEEEQTPPPQPRTAQPQKREEQTKKENEEDKLTDWNKLACLLCRRQFPNKEVL 970
LUCA15     PELVRNGDEEHPLKRGLVAAYSGDSDNEE...................ELVERLESEEEKLADWKKMACLLCRRQFPNKDAL 662
DXS8237E   DLPKLASDDRPSPPRGLVAAYSGESDSEE...................EQERGGPEREEKLTDWQKLACLLCRRQFPSKEAL 233

NY-LU-12   IKHQQLSDLPKQHLEIHRKIKQSEQELAYLERRERE.GKFKGRGNDRREKLQSFDSPERKRIKYSRETDS..DRKLVDKEDID 1050
LUCA15     VRHQQLSDLHKQNMDIYRRSRLSEQELEALELRERE.MKYRDRAAERREKYGIPEPPEPKRKKQFDAGTV..NYEQPTKDGID 742
DXS8237E   IRHQQLSGLHKQHLEIHRRAHLSEHELEALEKNDMEQMKYRDRAAERREKYGIPEPPEPKRRKYGGISTASVDFEQPTKDGLC 316

NY-LU-12   TSSKGGCVQQATGWRKGTGLGYGHPGLASSEEAEGRMRGPSVGASGKTSKRQSNETYRDAVRRVMFARYKELD 1123
LUCA15     HSNIGNKMLQAMGWREGSGLGRKCQGITAPIEAQVRLKGAGLGAKGSAYGLSGADSYKDAVRKAMFARFIEME 815
DXS8237E   SDNIGSRMLQAMGWKEGSGLGRKKQGIVTPIEAQTRVRGSGLGARGSSYGVTSTESYKETLHKTMVTRFNEAQ 389
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Figure 1

AAGGAGGAGCGGGCCGTGGAGGCTTCGCCCCCTACTACTGCTATAACGAGAAGTTGGTATAAAAAGGATTTACTTGTTGGGGCCCTCTTGATAAAAAGA 100

GATGTGGGGGGATTCTCGACCTGCTAACAGAACTGGACCTTTTCGTGGCAGCCAAGAAGAAAGGTTTGCTCCCGGGTCGAACCAGGATTATCCTCCTCCT 200
1 M W G D S R P A N R T G P Y R G S Q F E E R F A P G N H R D Y P P P

CCCCTTAAGAGTCATGCTCAAGAGAGACACTCTGGCAACTTTCCTGGCAGAGATTCACTTCCCTTTGATTTCCAGGGGCATTCGGGGCCTCCTTTTGCAA 300
34 P L K S H A Q E R H S G N F P G R D S L P F D F Q G H S G P P F A

ATGTAGAGGAGCATTCTTTCAGCTATGGAGCTAGAGACGGACCGCATGGGACTATCGACGAGGGGGAGGGACCTGCACATGATTTCAGGGGGGGAGATTT 400
67 N V E E H S F S Y G A R D G P H G D Y R G G K G P G H D F R G G D F

TTCGTCTTCTGATTTCCAGAGCAGAGATTCATCACAGTTGGACTTCAGGGGTAGGGACTCACATTCTGGGATTTTCGGGATAGAGAAGGACCACCTATG 500
101 S S S D F Q S R D S S Q L D F R G R S T H S G D F R E R E G P P M

GACTATAGGGGTGGAGATGGTACTTCTATGGATTATAGAGGTAGGGAAGCACCTCATATGAACTACAGAGACAGGGATCCTCACGCTGTGGACTTCAGAG 600
134 D Y R G G D G T S M D Y R G R E A P H M N Y R D R D A H A V D F R

GTAGGGATGCTCCTCCATCGACTTCAGGGGCCGGGGGACTTATGATTTAGATTTTAGAGGCCGGGATGGATCCCATGCAGATTTTAGGGGAAGGGATTT 700
167 G R D A P P S D F R G R G T Y D L D F R G R D G S H A D F R G R E L

ATCAGATTTGGATTTTAGGGCCAGAGAACAGTCCCGTTCTGATTTTAGGAATAGAGATGTATCTGATTTGGACTTTAGAGACAAAGACGGAACACAAGTA 800
201 S D L D F R A R E Q S R S D F R N R D V S D L D F R D K D G T Q V

GACTTTAGAGGCCGAGGTTCAGGTACTACTGATCTAGACTTTAGGGACAGGGATACGCCACATTCTGATTTCAGAGGTAGACACCGATCTAGGACTGATC 900
234 D F R G R G S G T T D L D F R D R D T P H S D F R G R H R S R T D

AGGATTTTAGGGGCAGAGAGATGGGATCTTGTATGGAATTTAAAGATAGGGAGATGCCCCCTGTGGATCCAAATATTTTGGATTACATTCAGCCCTCTAC 1000
267 Q D F R G R E M G S C M E F K D R E M P P V D P N I L D Y I Q P S T

ACAAGATAGAGAACATTCTGGTATGAATGTGAACAGGAGAGAAGAATCCACACACGACCATACGATAGAAAGGCCTGCTTTTGGCATTCAGAAGGGAGAA 1100
301 Q D R E H S G M N V N R R E E S T H D H T I E R P A F G I Q K G E

TTTGAGCATTCAGAAACAAGAGAAGGAGAAACACAAGGTGTAGCCTTTGAACATGAGTCTCCAGCAGACTTTCAGAACAGCCAAAGTCCAGTTCAAGACC 1200
334 F E H S E T R E G E T Q G V A F E H E S P A D F Q N S Q S P V Q D

AAGATAAGTCACAGCTTTCTGGACGTGAAGAGCAGAGTTCAGATGCTGGTCTGTTTAAAGAAGAAGGCGGTCTGGACTTTCTTGGGCGGCAAGACACCGA 1300
367 Q D K S Q L S G R E E Q S S D A G L F K E E G G L D F L G R Q D T D

TTACAGAAGCATGGAGTACCGTGATGTGGATCATAGGCTGCCAGGAAGCCAGATGTTTGGCTATGGCCAGAGCAAGTCTTTTCCAGAGGGCAAAACTGCC 1400
401 Y R S M E Y R D V D H R L P G S Q M F G Y G Q S K S F P E G K T A

CGAGATGCCCAACGGGACCTTCAGGATCAAGATTATAGGACGGGCCCAAGTGAGGAGAAACCCAGCAGGCTTATTCGATTAAGTGGGGTACCTGAAGATG 1500
434 R D A Q R D L Q D Q D Y R T G P S E E K P S R L I R L S G V P E D

Figure 2

1586

1644

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467  CTACAAAAGAACAGATTCTTAATGCTTTTCGGACTCCTGATGGCATGCCTGTAAAGAACTTGCAGTTGAAGGAGTATAACACAGTTACGACTATGGCTT
     A  T  K  E  E  I  L  N  A  F  R  T  P  D  G  M  P  V  K  N  L  Q  L  K  E  Y  N  T  G  Y  D  Y  G  Y   1600

501  TGTCTGCCGTGGAGTTTTCAGTCTTGGAAGATGCCATCTGATGCTCTCAGGCCAACCAGGAACTCTAATGATCCAGGACAAAGAAGTTACCTTGGAGTAT
     V  C  V  E  F  S  L  L  E  D  A  I  G  C  H  E  A  N  Q  G  T  L  H  I  Q  D  K  E  V  T  L  E  Y   1700

534  GTATCAAGCCTGGATTTTTGGTACTGCAAACGATGTAAGGCAAACATTGGTGGGCACCGATCTTCCTGTTCATTCTGCAAGAACCCAAGAGAAGTGACAG
     V  S  S  L  D  F  W  Y  C  K  R  C  K  A  N  I  G  G  H  R  S  S  C  S  F  C  K  N  P  R  E  V  T   1800

567  AGGCCAAGCAAGAATTAATAACCTACCCTCAGCCTCAGAAAACATCCATACCAGCACCATTGGAAAAACAGCCCAACCAGCCCCTAAGACCAGCTGATAA
     E  A  K  Q  E  L  I  T  Y  P  Q  P  Q  K  T  S  I  P  A  P  L  E  K  Q  P  N  Q  P  L  R  P  A  D  K   1900

601  GGAACCTGAACCCAGGAAGACCGAAGAAGGCCAAGAGTCAGCTTAGGACATCAAAAGAGACAAGCAGAAAGGTATCTGCCTCCTTCTCGAAGGGAAGCG
     E  P  E  P  R  K  R  E  E  G  Q  E  S  R  L  G  H  Q  K  R  E  A  E  R  Y  L  P  P  S  R  K  E  G   2000

634  CCAACTTTCCGAAGAGACCGAGAGAGGGAGTCATCGTCTGGAGAGACACGCCAGCATGGAGAGAGCAAAACTATCATGCTAAAGCGTATCTATCGTTCCA
     P  T  F  R  R  D  R  F  R  E  S  W  S  G  E  T  R  Q  D  G  E  S  K  T  I  M  L  K  R  I  Y  R  S   2100

667  CACCACCTGAGGTGATAGTGGAAGTGCTGGAGCCCTATGTCCGCCTTACTACTGCCAACGTCCGTATCATCAAGAACAGAACAGGCCCTATGGGGCATAC
     T  P  P  E  V  I  V  E  V  L  E  P  Y  V  R  L  T  T  A  N  V  R  I  I  K  N  R  T  G  P  M  G  H  T   2200

701  CTATGGCTTTATTGACCTCGACTCCCATGTGGAAGCTCTTCGTGTGGTGAAGATCTTACAGAACCTTGATCCGCCATTTAGCATTGATGGGAAGATGGTA
     Y  G  F  I  D  L  D  S  H  V  E  A  L  R  V  V  K  I  L  Q  N  L  D  P  P  F  S  I  D  G  K  M  V   2300

734  GCTCTAAACCTGGCCACTGGAAAACGAAGAAATGATTCTGGCGACCATTCTGACCACATGCATTACTATCAGGGTAAAAAATATTTCCGAGATAGGAGGG
     A  V  N  L  A  T  G  K  R  R  N  D  S  G  D  H  S  D  H  M  H  Y  Y  Q  G  K  K  Y  F  R  D  R  R   2400

767  GAGGTGGCAGAAATTCAGACTGGTCTTCAGATACAAATCGACAAGGACAACAGTCATCATCTGACTGCTACATATATGATTCTGCTAGTGGCTACTATTA
     G  G  G  R  N  S  D  W  S  S  D  T  N  R  Q  G  Q  Q  S  S  S  D  C  Y  I  Y  D  S  A  S  G  Y  Y   2500

801  TGACCCCTTGGCAGGAACTTATTATGACCCCAATACCCAGCAAGAAGTCTATGTGCCCCAGGATCCTGGATTACCTGAGGAAGAAGAGATCAAGGAAAAA
     D  P  L  A  G  T  Y  Y  D  P  N  T  Q  Q  E  V  Y  V  P  Q  D  P  G  L  P  E  E  E  E  I  K  E  K   2600

834  AAACCCACCAGTCAAGGAAAGTCAAGTAGCAAGAAGGAAATGTCTAAAAGAGATGGCAAGGAGAAAAAAGACAGAGGAGTGACCAGGTTTCAGGAAAATG
     K  P  T  S  Q  G  K  S  S  S  K  K  E  M  S  K  R  D  G  K  E  K  K  D  R  G  V  T  R  F  Q  E  N   2700

867  CCAGTGAAGGGAAGGCCCCTGCAGAAGACGTCTTTAAGAAGCCTCTGCCTCCTACTGTGAAGAAGGAAGAGAGTCCCCCTCCACCTAAGGTGGTAAACCC
     A  S  E  G  K  A  P  A  E  D  V  F  K  K  P  L  P  P  T  V  K  K  E  E  S  P  P  P  P  K  V  V  N  P   2800

901  ACTGATCGGCCTCTTGGGTGAATATGGAGGAGACAGTGACTATGAGGAGGAAGAAGAGGAGGAACAGACCCCTCCCCCACAGCCCCGCACAGCACAGCCC
     L  I  G  L  L  G  E  Y  G  G  D  S  D  Y  E  E  E  E  E  E  E  Q  T  P  P  P  Q  P  R  T  A  Q  P   2900

934  CAGAAGCGAGAGGAGCAGAAAACCAAGAAGGAGAATGAAGAAGACAAAGTCACTGACTGGAATAAACTGGCTTGTCTGCTTTGCAGAAGGCAGTTTCCCAATA
     Q  K  R  E  E  Q  T  K  K  E  N  E  E  D  K  V  T  D  W  N  K  L  A  C  L  L  C  R  R  Q  F  P  N   3000
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Fig 2 (cont'd)

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      AAGAAGTTCTGATCAAACACCAGCAGCTGTCAGACCTGCACAAGCAAAACCTGGAAATCCACCGGAAGATAAAACAGTCTGAGCAGGAGCTAGCCTATCT    3100
967    K  E  V  L  I  K  H  Q  Q  L  S  D  L  H  K  Q  N  L  E  I  H  R  K  I  K  Q  S  E  Q  E  L  A  Y  L

      GGAAAGGAGAGAACGAGAGGGAAAGTTTAAAGGAAGAGCAAATCATCCAGGGAAAAGCTCCAGTCTTTTGACTCTCCAGAAAGGAAACGGATTAAGTAC    3200
1001   E  R  R  E  R  E  G  K  F  E  G  E  S  R  D  R  R  E  K  L  Q  S  F  D  S  P  E  R  K  R  I  K  Y

      TCTACGGAAACTGACAGTGATCGTAAACTGGTTGATAAAGAAGATATCGACACTAGCAGCAAAGGAGGCTGTGTCCAACAGGCTACTGGCTGGAGGAAAG    3300
1034   S  R  E  T  D  S  D  R  K  L  V  D  K  E  D  I  D  T  S  S  K  G  G  C  V  Q  Q  A  T  G  W  R  K

      GGACAGGCCTGGGATATGGCCATCCTGGATTGGCTTCATCAGAGGAGGCTGAAGGCCGGATCAGGGGCCCCAGTGTTGGAGCCTCAGGAAGAACCAGCAA    3400
1067   G  T  G  L  G  Y  G  H  P  G  L  A  S  S  E  E  A  E  G  R  N  R  G  P  S  V  G  A  S  G  R  T  S  K

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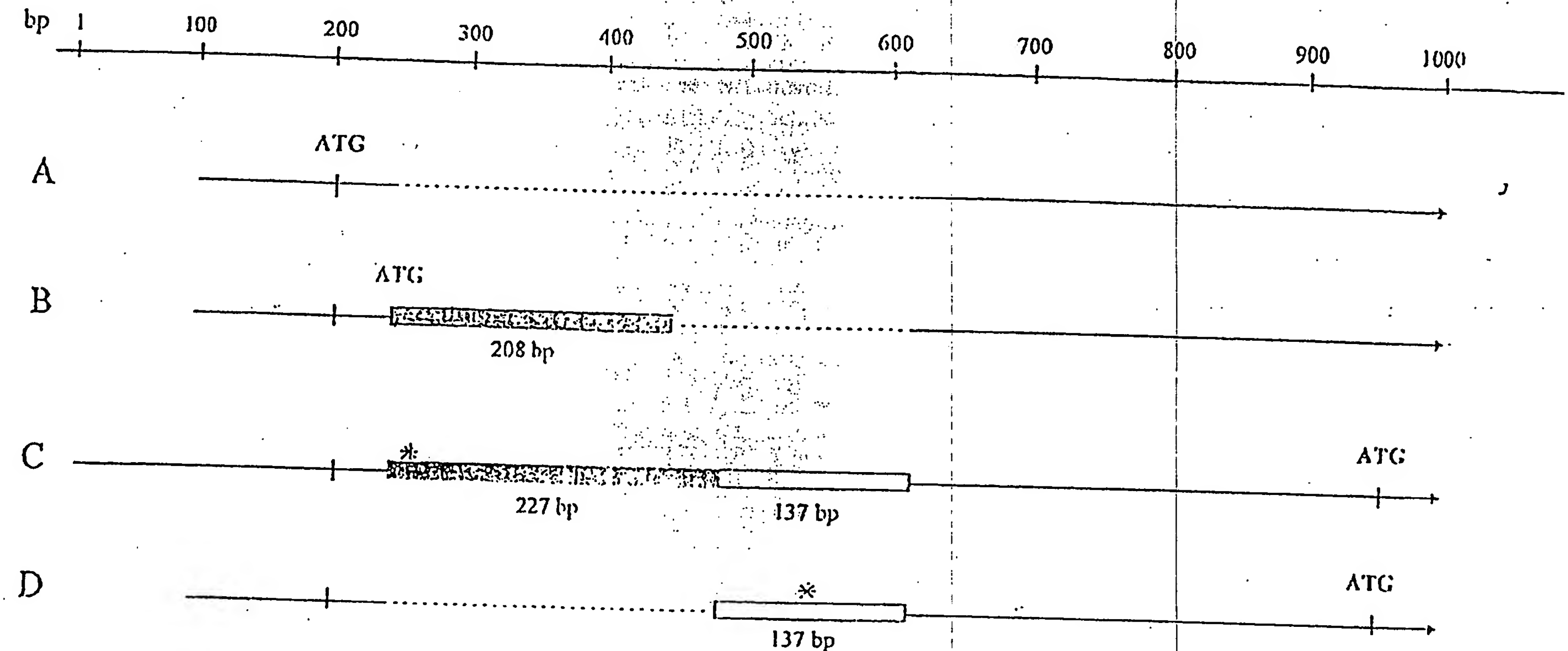
Fig 2(cont'd)



Transcript Variant B

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Fig. 3a

Figure 3b.

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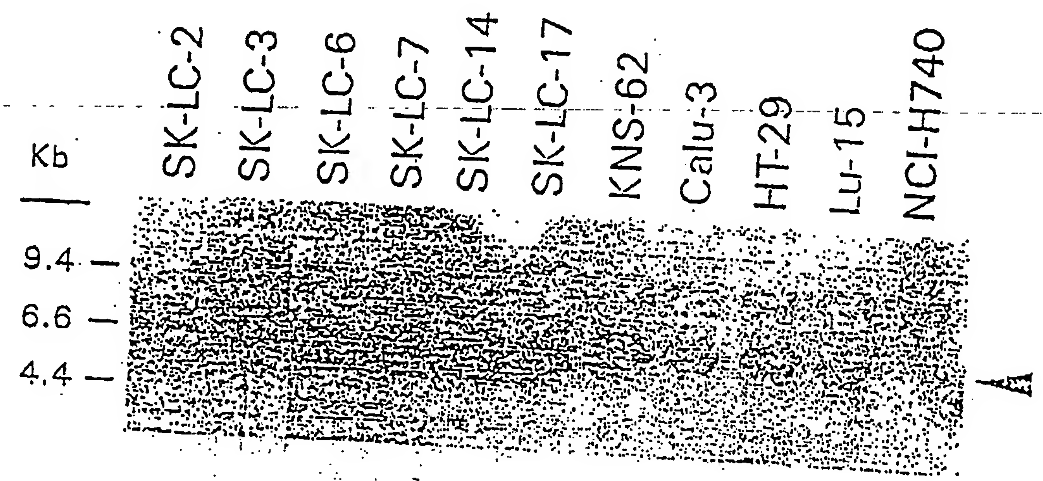
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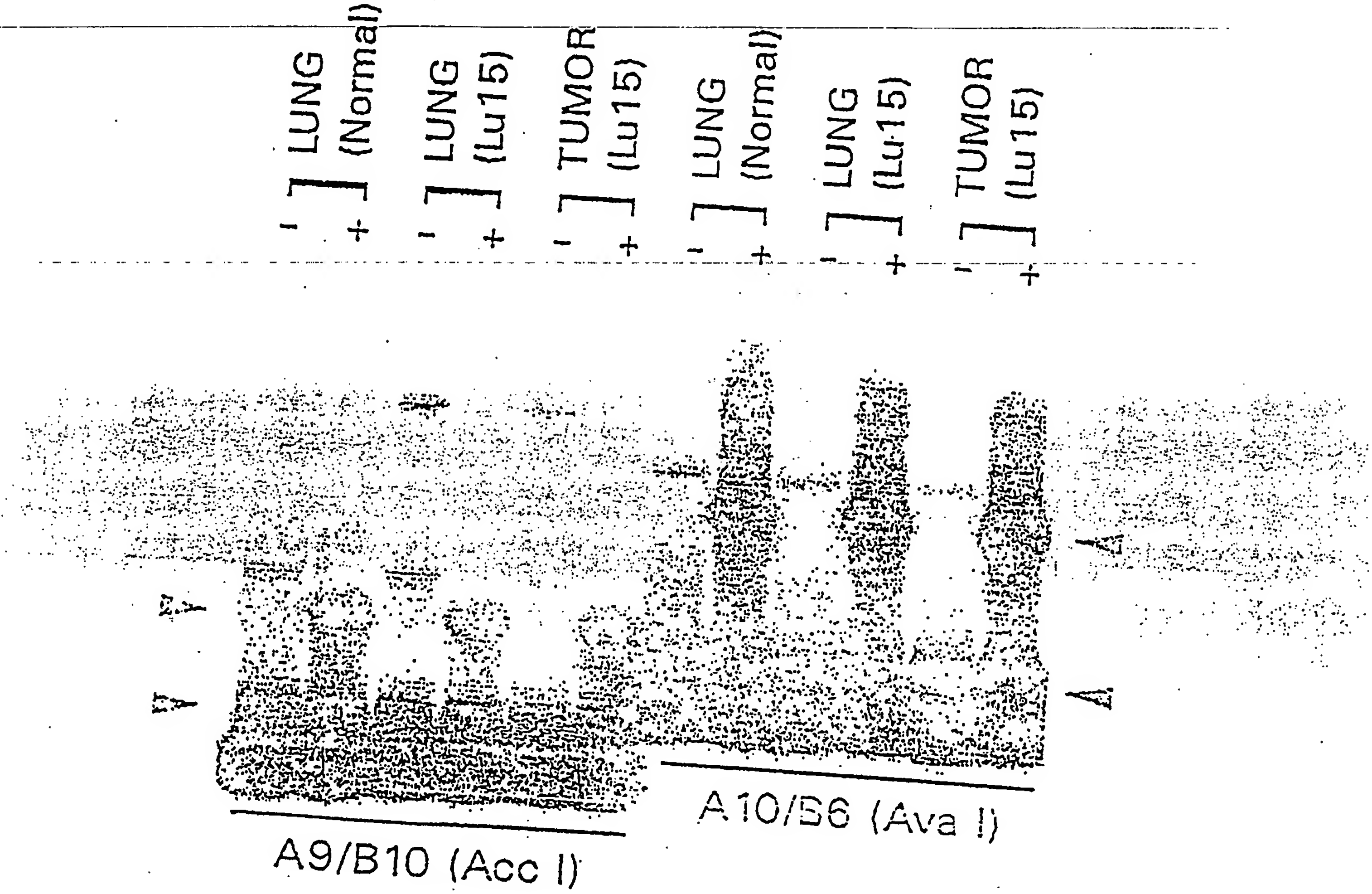
4.4

Figure 4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A9/B10 (Acc I)
A10/B6 (Ava I)

Figure 5

SEQUENCE LISTING

<110> Ludwig Institute for Cancer Research
Old, Lloyd J.
Scanlan, Matthew J.
Stockert, Elisabeth
Gure, Ali
Chen, Yao-Tseng
Gout, Ivan
O'Hare, Michael
Obata, Yuichi
Pfreundschuh, Michael
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~~Sahin, Ugur~~

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<210> 16
<211> 1113
<212> DNA
<213> Homo Sapiens

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<211> 731
<212> DNA
<213> Homo Sapiens

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tatnacaaag g 731

<210> 18
<211> 1145
<212> DNA
<213> Homo Sapiens

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<210> 19
<211> 1106
<212> DNA
<213> Homo Sapiens

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gcctggctgt gagctggagt attatttcca ctctcggcca ccacctctcc atcttcttgg 180
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<210> 20
<211> 484
<212> DNA
<213> Homo Sapiens

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gtgggaatcn atgttgaaaa tnaaagaagg acttctaagg cagaaagaaa ttgtantcga 360
tcggcagaag caacnaatta cccacctgcn tnanangata agggataatg aattaccggc 420
tcnncatgcc atgttaggac attatgtnaa ttgtgaggat tcttatgtgg ctagtttgca 480
ccac 484

<210> 21
<211> 355
<212> DNA
<213> Homo Sapiens

<400> 21
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<210> 22
<211> 1070
<212> DNA
<213> Homo Sapiens

<400> 22
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cacacacaag tnaaaaacac aagaagaaaa cccatcactg ttctgaagag aaagaagatg 180
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gtttctgaat tttatataaa tggcaaaang tttacttntg tgactttctt tcatttttat 1020
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<210> 23

<211> 861
<212> DNA
<213> Homo Sapiens

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tgcatcattt ttaggagtat a 861

<210> 24
<211> 985
<212> DNA
<213> Homo Sapiens

<400> 24
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ctctgagccc agggagagcc ttctgcagcc ccatttcctc aaaaatccaa cctgcccagg 120
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<210> 25
<211> 545
<212> DNA
<213> Homo Sapiens

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<210> 26
<211> 374
<212> DNA
<213> Homo Sapiens

<400> 26
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<210> 27
<211> 552
<212> DNA
<213> Homo Sapiens

<400> 27
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<210> 28
<211> 502
<212> DNA
<213> Homo Sapiens

<400> 28
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<210> 29

<211> 537
<212> DNA
<213> Homo Sapiens

<400> 29
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<210> 30
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<212> DNA
<213> Homo Sapiens

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caacgggtta ccnaatgccg nttcnaaggg aaanncaaca aanacccaan ggccgganan 2220
gcccaaagaa acggggggntt aatgttggtt cccacaatta ttacaaggga cccccaaaaa 2280
agctcttgcg aaggaggact ttgganaaan tttgttgacc agggtaaaan tagggcaggg 2340
acccagcaaa aagactgttt tcccagcaaa gcccttcaga ggccaccttc agaccgttca 2400
gagggcagca gccgggacgg ccagggtagc gacgagaacg aggagtcgag cgttgtggat 2460
tacgtggagg tgacggtcgg ggaggaggat gccatcttca gatagatcag atagctggag 2520
tcaggntgcg gcagaaggtg tgtcggaact ggctgaatca gactccgact gcgtccctgc 2580
agaggctggc caggcctaga cagggaagtc tgttagaact gctgtgctga tcaacgggac 2640
gctccgtctt tgaagaaaga agagatggtc tctccccagc catgggccac ccttgccagt 2700
gactccaagt ggaactactt agctcgcgtg tgcctggagg gtgcgggaag tccagcgact 2760
ctcagacgca cctcccagag gaccggtggg aattgttcat agtgccaaag tcctactact 2820
gcgttttcaa tgggtccttg tacatagttt gctcctctgc cctagccctc acctcttgct 2880
atactggaac cgatttgtac aatgtgggaa ttttgttacc ttttaatca agggcaactt 2940
ccttttccag cactaccatt gtaaggtttt tttcaggagg gagggctaac caccttgctt 3000
ttctcttttc tctttttctt ttttttattt ttgttttatt aatttgggga aaggggtgtt 3060
agcattagtg ccatgatatc tactggattt taagtaggga gactttattt ttaaaggtag 3120
gttgaaattt gggagatttc tcggcaggaa gggctgaaat ccaggcccct gtctcaactt 3180
ggagagaggt gacagacggc agatcttcca aatcaaattc ctttccagtt cttcccctgg 3240
ctgccttttt gggggtccct gccttagccc cacacaaggc tttctgaact gccaagaggg 3300
gatctggctt ctcaactgct cggcctcttg ggccaggctg tgcccagcca gccctgggag 3360
aactgggtag caggtggctg acttctttaa gcacctttct aaataccagc agaagaggct 3420
cccgcctctg ttagcatgat cagtactatt gtgacattaa aacaacaaca ataagatctt 3480
cctatctgga gggtacagag gtgaatggct ttggttttca tttctctttc ttcactgctt 3540
ttctcggtgt ggtatttgac aagattttag ntnaaagcct caccatgaat tgattttttt 3600
tgtttgngng ngtgtttgtt ttgggacaat tttagatacc tgngtgcant ttttcagtta 3660
gtcctaantt ttaaaagaag ggnaaccaag nganatattt ggtgtaagtg ttgcagtatg 3720
aanttctggt tgcaatccct ccccgtccca cantgccccc catttgagta caccgcacaa 3780
gtcaaacgnt aggnagtttg nataaaacca atttttctaa nttgttgntc atttgttgta 3840
antcaataaa gcnaaganta aacattttta tt 3872

<210> 31
<211> 655
<212> DNA
<213> Homo Sapiens

<400> 31
gaaatcatgg gagcacaaag aagaaataag tgaagcagag ccaggggggtg gttccttggg 60
agatggaagg ccgccagagg aaagtgccca tgaaatgatg gaggaggaag aggaaatccc 120
aaaacctaag tctgtggttg caccgccagg tgctcctaag aaagagcatg taaatgtagt 180
attcattggg cacgtanatg ctggcaagtc aaccattgga ggacaaataa tgtatttgac 240
tggaatggtt gacaaaagga cgcttgaaaa gtatgaaaga gaagctaaag agaaaaacag 300
agaaacttgg tacttgtctt gggccttaga cacaaatcag gaagaacgag acaagggtaa 360
aacagtagaa gtgggtcgtg cctattttga aaccgaaaag aacatttcac aattctagat 420
atgaatccca gaacactgag ctcaaaaccc aaagcccaga atttgaagct caaagttccn 480
aattccanga aggtgcggag atgcttctga accccgagga aaagatcctt tgaatatctc 540
cgtaggagtt cacccccctgg actccttcac tcaggggttt ggggagcacc cacaggggac 600
ctgcccatag ggccaccttt tgagatgccc acaggggccc tgctgtctac accgc 655

<210> 32
<211> 466
<212> DNA
<213> Homo Sapiens

<400> 32
gaaaggtggc cagaggaagg gacagctgac ctggcacaat ctgggcttga agggggcaca 60
acaagagcgt ctgtgagctg gtgctgtctg gagggatctt ggctcctctc cggctatctg 120
accttcctga agacctgctc gcacactgca tcccttgcag tcagttccag ctcgtgccga 180
attcggcacg agctcgtgcc gaattcggca cgagggaagc actactccca gcgctgggcc 240
caggaggacc tgctggagga gcagaaggat ggggcccggg cagcggctgt ggctgacaag 300
aagaaaggcc tcatggggcc actgaccgaa ctggacacta aagatgtgga tgccctgctg 360
aagaagtctg aggcccagca tgaacagccg gaagatggat gcccctttgg tgccctgacg 420
cagcgcctcc tgcaggccct ggtggaggaa aatattattt tttccc 466

<210> 33
<211> 293
<212> DNA
<213> Homo Sapiens

<400> 33
gtcggcgccc tacatgagaa gcatgatgca gtcgctgagc cagaatccag atttggctgc 60
acagatgatg ctgaatagcc cgctgtttac tgcaaatcct cagctgcagg agcagatgcg 120
gccacagctc ccagccttcc tgcagcagat gcagaatcca gacacactat cagccatgtc 180
aaacccaaga gcaatgcagg ctttaatgca gatccagcag ggctacagaa cattagccac 240
tgaagcacct ggcctgattc cgagcttcac tccaggtgtg ggggtggggn tct 293

<210> 34
<211> 456
<212> DNA
<213> Homo Sapiens

<400> 34
caaagcctta agtcagagcc tgctagaatg tgtccaggtt tacagctata ctgcacagca 60
cttcccatgc tagtctctgt aaaacgcaaa aagccatttt caggagcagt aggcaagtca 120
cattcaattg aaatgcagga tggtgcactg ccattccaag ttccatcttc ctggcagatc 180
agcacagggt tccccagaag ttcatatcct ggattacagg tgtatgaaac catggtacca 240
tacagaaagt ttgatgaatg tgtagcagga gactcctttg tatttcccca ggttttagcc 300
actgctccca aatgataagg agggtgagga gtcacatatg gaacttccat catgtcgtct 360
tcttgctcaa aatatccctg gtcatctttg agtttagtac agtctccaaa atctatatga 420
ggagggaggc cacagtctat tggcatacca aatttt 456

<210> 35
<211> 679
<212> DNA
<213> Homo Sapiens

<400> 35
ggcggcgttc gtgtccgagg tcactagttt cccggtagtt cagctgcaca tgaatagaac 60
agcaatgaga gccagtcaga aggactttga aaattcaata aatcaagtga aactcttgaa 120
aaaggatcca ggaaacgaag tgaagctaaa actctacgcg ctatataagc aggccactga 180
aggaccttgt aacatgccca aaccaggtgt atttgacttg atcaacaagg ccaaatggga 240
cgcatggaat gcccttggca gcctgcccaa ggaagctgcc aggcagaact atgtggattt 300
ggtgtccagt ttgagtcctt cattggaatc ctctagtcag gtggagcctg gaacagacag 360
gaaatcaact gggtttgaaa ctctggtggt gacctccgaa gatggcatca caaagatcat 420
gttcaaccgg cccaaaaaga aaaatgccat aaacactgag atgtatcatg aaattatgcg 480
tgcacttaaa gctgccagca aggatgactc aatcatcact gttttaacag gaaatggtga 540
ctattacagt agtgggaatg atctgactaa cttcactgat attccccctg gtggagtana 600
ggagaaagct aaaaataatg ccgttttact gaagggaatt tgtgggctgt tttatagaat 660
ttcctaagcc tctgattgc 679

<210> 36
<211> 689
<212> DNA
<213> Homo Sapiens

<400> 36
ctaaaccagt ggacatatca ggccatggtc cacgaactac taggcataaa caacaatcgg 60
attgatcttt ccagagtgcc gggaatcagt aaagacttaa gagaagtggt cctatctgct 120
gaaaatgatg aattctatgc taataatatg tacctgaact ttgctgagat tggtagcaat 180
ataaagaatc tcatggaaga ttttcagaag aagaaaccaa aagaacagca aaaactagaa 240
tcaatagcag acatgaaggc gtttgttgag aattatccac agttcaagaa aatgtctggg 300
actgtttcaa agcatgtgac agtggttgga gaactgtctc gattggtcag tgaacggaat 360
ctgctggagg tttcagaggt tgagcaagaa ctggcctgtc aaaatgacca ttctagtgct 420
ctccagaata taaaaaggct tctgcagaac cccaaagtga cagagtttga tgctgcccgc 480
ctggtgatgc tttatgcttt acattatgag cgacacagca gcaatagcct gccaggacta 540
atgatggncc tcaggaataa aggtgtttct gagaagtatc gaaagctcgt gtctgcagtt 600
gttgaatatg gtggtaaaac gagtcagagg aagtgacctc ctcagcccca aagatgctgt 660
tggctatcac caaacaattc ctcaaaggg 689

<210> 37
<211> 443
<212> DNA
<213> Homo Sapiens

<400> 37
ccacgcccgg ccccggagca ggcttttacg catgccccgc gcgccccctt gtgtccggaa 60
tttattcctt ccggtgggtt cgcggtctag ctgaccaaga acggaactgg ggactttcgc 120
agtgagagtt acagctctta aagatggcac cgacccaggc cgggcgcggt ggctcaggcc 180
tgcaatccca gcactttggg aggcggaggc aggtgaatca cgaggtcagg aaatcgagac 240
catcctggct aacatggtga aaccccgtct ccactaaaaa tacaaaaaat tagccaggca 300
tggtggctgg cacctgtagt cccagctact tgggaggctg agccaggaaa gtggcatgaa 360
cccgcgaggc agagcttgca ataagccgag atcgtgccaa tgcactccag cctgggcaac 420
agaaggagac actgtctcaa aaa 443

<210> 38
<211> 442
<212> DNA
<213> Homo Sapiens

<400> 38
ctcgcctcgg agcagccatg atggaaggcc tggacgacgg cccggacttc ctctcagaag 60
aggaccgcgg acttaaagca ataaatgtag atcttcaaag tgatgctgct ctgcaggtgg 120
acatttctga tgctcttagt gagcgggata aagtaaaatt cactgttcac acaaagattc 180
caccagcacc accaagacct gattttgatg cttcaaggga aaaactacag aagcttggtg 240
aaggagaagg gtcaatgacg aaggaagaat tcacaaagat gaaacaggaa ctggaagctg 300
aatatttggc aatattcaag aagacagttg cgatgcatga agtgttcctg tgtcgtgtgg 360
cagcacatcc tattttgaga agagatttaa atttccatgt cttcttggaa tataatcaag 420
atttgagtgt gcgaggaaaa aa 442

<210> 39
<211> 692
<212> DNA
<213> Homo Sapiens

<400> 39

cagggacagg ccctatctta tattttttc catcttcatc atccacttct gcttacagtt 60
tgctgcttac aataacttaa tgatggattg agttatctgg gtggtctcta gccatctggg 120
cagtgtggtt ctgtctaacc aaagggcatt ggcctcaaac cctgcatttg gtttagggc 180
taacagagct cctcagataa tcttcacaca catgtaactg ctggagatct tattctatta 240
tgaataagaa acgagaagtt tttccaaagt gttagtcagg atctgaaggc tgtcattcag 300
ataacccagc ttttcctttt ggcttttagc ccattcagac tttgccagag tcaagccaag 360
gattgctttt ttgctacagt tttctgccaa atggcctagt tcctgagtac ctggaaacca 420
gagagaaaga ggatccagga tgtacttgga tgaggaggcc tggcttatct aggaagtcgt 480
gtctggggtg cttattgctg ctccatacag ctgtacgtca gcccttggc cttctctgta 540
ggttcttggc ancaatgagc agctttcact caagtgacac aagtaattac tgagtcctaa 600
tttgatagcc accaactgta cctgggtang caaagtcaga tttttgagaa nctttttcct 660
gatttgaagt tttaattacc ttaatttcct tt 692

<210> 40
<211> 619
<212> DNA
<213> Homo Sapiens

<400> 40
gaggcaccag attctgctga ggggaccacc cttacagtgc tgcctgaagg tgaggagttg 60
cccctgtgtg tgagtgagag caatggcctg gagctcccac cctcagcagc atctgatgag 120
ccacttcagg agccactgga ggctgacagg acctcggaag agctgacaga ggccaagacc 180
ccaacctcca gcccagagaa gccacaggaa ctcgttacag ctgaggttgc agctccatcc 240
acctcatctt cagccacttc ctcgcctgag ggtccttcac ctgcccgacc tcctcggcgt 300
cgcaccagtg ctgatgtgga aattaggggt caagggactg gtcggccagg acaaccacca 360
ggccccaaag tgcttcgaaa gctgccagga cggctggtaa ctgtggtaga ggaaaaggaa 420
ctggtgcggc ggcggcggca gcagcgggga gctgccaanc accctagtgc ctggggtctc 480
tgagactagt gccagcccgg gaagcccgtc tgtccgcagc atgtcanggc canaatcctc 540
ccctcccatt ggtgggccct gtgaaagctg ctccttcatc cncactgcnc actccanccc 600
agnagccctt cattgcncg 619

<210> 41
<211> 153
<212> PRT
<213> Homo Sapiens

<400> 41
Pro Glu Ser Lys Pro Ile Met Thr Ser Ser Glu Ala Phe Glu Pro Pro
1 5 10 15
Lys Tyr Leu Met Leu Gly Gln Gln Ala Val Gly Gly Val Pro Ile Gln
20 25 30
Pro Ser Val Arg Thr Gln Met Trp Leu Thr Glu Gln Leu Arg Thr Asn
35 40 45
Pro Leu Glu Gly Arg Asn Thr Glu Asp Ser Tyr Ser Leu Ala Pro Trp
50 55 60
Gln Gln Gln Gln Ile Glu Phe Arg Gln Gly Ser Glu Thr Pro Met Gln
65 70 75 80
Val Leu Thr Gly Ser Ser Arg Gln Ser Tyr Ser Pro Gly Tyr Gln Asp
85 90 95
Phe Ser Lys Trp Glu Ser Met Leu Lys Lys Glu Gly Leu Leu Arg Gln
100 105 110
Lys Glu Ile Val Asp Arg Gln Lys Gln Ile Thr His Leu Ile Arg Asp
115 120 125
Asn Glu Leu Pro Ala His Ala Met Leu Gly His Tyr Val Asn Cys Glu
130 135 140

Asp Ser Tyr Val Ala Ser Leu His His
145 150

<210> 42
<211> 95
<212> PRT
<213> Homo Sapiens

<400> 42
Ile Leu Leu Glu Phe Tyr Leu Trp Gln Ile Gly Arg Tyr Ile Phe Val
1 5 10 15
His Val Asn Asn His Ile Tyr Ile Lys Leu Tyr Asn Cys Thr Phe Leu
20 25 30
Thr Ala Leu Ser Gln Val Ala Leu Ser Phe Pro Ser Ile Asn Gly Leu
35 40 45
Ile Phe Val Ser Phe Ala Phe Phe Arg Val Val Asn Ser Tyr Cys Pro
50 55 60
Leu Gln Phe Val Gln Phe Leu Arg Cys Leu Leu Leu Leu Lys Arg Met
65 70 75 80
Leu Gly Glu Phe Ile Phe His Lys Glu Met Glu His Tyr Leu Lys
85 90 95

<210> 43
<211> 114
<212> PRT
<213> Homo Sapiens

<400> 43
Ser Lys Leu Leu Leu Ser Gly Thr Ala Asp Gly Ala Asp Leu Arg Thr
1 5 10 15
Val Asp Pro Glu Thr Gln Ala Arg Leu Glu Ala Leu Leu Glu Ala Ala
20 25 30
Gly Ile Gly Lys Leu Ser Thr Ala Asp Gly Lys Ala Phe Ala Asp Pro
35 40 45
Glu Val Leu Arg Arg Leu Thr Ser Ser Val Ser Cys Ala Leu Asp Glu
50 55 60
Ala Ala Ala Leu Thr Arg Met Arg Ala Glu Ser Thr Ala Asn Ala Gly
65 70 75 80
Gln Ser Asp Asn Arg Ser Leu Ala Glu Ala Cys Ser Gly Asp Val Ala
85 90 95
Val Arg Lys Leu Leu Ile Glu Gly Arg Ser Val Phe Glu Leu Pro Glu
100 105 110
Glu Gly

<210> 44
<211> 132
<212> PRT
<213> Homo Sapiens

<400> 44
Gly Glu Lys Glu Gln Asp Lys Pro Pro Asn Leu Val Leu Lys Asp Lys
1 5 10 15
Val Lys Pro Lys Gln Asp Thr Lys Tyr Asp Leu Ile Leu Asp Glu Gln
20 25 30

Ala Glu Asp Ser Lys Ser Ser His Ser His Thr Ser Lys His Lys Lys
35 40 45
Lys Thr His His Cys Ser Glu Glu Lys Glu Asp Glu Asp Tyr Met Pro
50 55 60
Ile Lys Asn Thr Asn Gln Asp Ile Tyr Arg Glu Met Gly Phe Gly His
65 70 75 80
Tyr Glu Glu Glu Glu Ser Cys Trp Glu Lys Gln Lys Ser Glu Lys Arg
85 90 95
Asp Arg Thr Gln Asn Arg Ser Arg Ser Arg Ser Arg Glu Arg Asp Gly
100 105 110
His Tyr Ser Asn Ser His Lys Ser Lys Tyr Gln Thr Asp Leu Tyr Glu
115 120 125
Arg Glu Arg Ser
130

<210> 45
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 45
Lys Thr Gln Glu Lys Pro Pro Lys Glu Leu Val Asn Glu Trp Ser Leu
1 5 10 15
Lys Ile Arg Lys Glu Met Arg Val Val Asp Arg Gln Ile Arg Asp Ile
20 25 30
Gln Arg Glu Glu Glu Lys Val Lys Arg Ser Val Lys Asp Ala Ala Lys
35 40 45
Lys Gly Gln Lys Asp Val Cys Ile Val Leu Ala Lys Glu Met Ile Arg
50 55 60
Ser Arg Lys Ala Val Ser Lys Leu Ala Ser Lys Ala His Met Asn Ser
65 70 75 80
Val Leu Met Gly Met Lys Asn Gln Leu Ala Val Leu Arg Val Ala Gly
85 90 95
Ser Leu Gln Lys Ser Thr Glu Val Met Lys Ala Met Gln Ser Leu Val
100 105 110
Lys Ile Pro Glu Ile Gln Ala Thr Met Arg Glu Leu Ser Lys Glu Met
115 120 125
Met Lys Ala Gly Ile Ile Glu Glu Met Leu Glu Asp Thr Phe Glu Ser
130 135 140
Met Asp Asp Gln Glu Glu Met Glu Glu Glu Ala Glu Met Glu Ile Asp
145 150 155 160
Arg Ile Leu Phe Glu Ile Thr Ala Gly Ala Leu Gly Lys Ala Pro Ser
165 170 175
Lys Val Thr Asp Ala Leu Pro Glu Pro Glu Pro Pro Gly Ala Met Ala
180 185 190
Ala Ser Glu Asp Glu Glu Glu Glu Glu Glu Leu Glu Ala Met Gln Ser
195 200 205
Arg Leu Ala Thr Arg Ser
210

<210> 46
<211> 248
<212> PRT
<213> Homo Sapiens

<400> 46
Gly Ser Arg Glu Glu Thr Leu Ala Phe Val Pro Leu Leu Arg Leu Leu
1 5 10 15
Glu Ala Thr Leu Ser Pro Gly Arg Ala Phe Cys Ser Pro Ile Ser Ser
20 25 30
Lys Ile Gln Pro Ala Gln Val Ala Gly His Glu Leu Cys Ser Gly Ser
35 40 45
Trp Asn Leu Thr Leu Val Ala Ser Gly Pro Val Ser Met Ala Ala Glu
50 55 60
His Leu Leu Pro Gly Pro Pro Pro Ser Leu Ala Asp Phe Leu Glu Ala
65 70 75 80
Gly Gly Lys Gly Thr Glu Arg Gly Ser Gly Ser Ser Lys Pro Thr Gly
85 90 95
Ser Ser Gly Gly Pro Arg Met Ala Ser Phe Pro Lys Thr Lys Phe Asn
100 105 110
Glu Tyr Lys Asp Val Leu Pro Cys Met Thr Ser Ser Arg Gly Gly Lys
115 120 125
Ile Lys Ala Thr Asp Phe Met Val Ala Met Arg Cys Leu Gly Ala Ser
130 135 140
Pro Thr Pro Gly Glu Val Gln Arg His Leu Gln Thr His Gly Ile Asp
145 150 155 160
Gly Asn Gly Glu Leu Asp Phe Ser Thr Phe Leu Thr Ile Met His Met
165 170 175
Gln Ile Lys Gln Glu Asp Pro Lys Lys Glu Ile Leu Leu Ala Met Leu
180 185 190
Met Val Asp Lys Glu Lys Lys Gly Tyr Val Met Ala Ser Asp Leu Arg
195 200 205
Ser Lys Leu Thr Ser Gly Glu Lys Leu Thr His Lys Glu Val Asp Asp
210 215 220
Leu Phe Arg Glu Ala Asp Ile Glu Pro Asn Gly Lys Val Lys Tyr Asp
225 230 235 240
Glu Phe Ile His Lys Ile Thr Leu
245

<210> 47
<211> 177
<212> PRT
<213> Homo Sapiens

<400> 47
Leu Cys Cys Met His Tyr Cys Cys Lys Ser Cys Trp Asn Glu Tyr Leu
1 5 10 15
Thr Thr Arg Ile Glu Gln Asn Leu Val Leu Asn Cys Thr Cys Pro Ile
20 25 30
Ala Asp Cys Pro Ala Gln Pro Thr Gly Ala Phe Ile Arg Ala Ile Val
35 40 45
Ser Ser Pro Glu Val Ile Ser Lys Tyr Lys Ala Leu Leu Arg Gly Tyr
50 55 60
Val Glu Ser Cys Ser Asn Leu Thr Trp Cys Thr Asn Pro Gln Gly Cys
65 70 75 80
Asp Arg Ile Leu Cys Arg Gln Gly Leu Gly Cys Gly Thr Thr Cys Ser
85 90 95
Lys Cys Gly Trp Ala Ser Cys Phe Asn Cys Ser Phe Pro Glu Ala His
100 105 110
Tyr Pro Ala Ser Cys Gly His Met Ser Gln Trp Val Asp Asp Gly Gly

115 120 125
Tyr Tyr Asp Gly Met Ser Val Glu Ala Lys His Leu Ala Lys Leu Ile
130 135 140
Ser Lys Arg Cys Pro Ser Cys Gln Ala Pro Ile Glu Asn Glu Gly Cys
145 150 155 160
Leu His Met Thr Cys Ala Lys Cys Asn His Gly Phe Cys Trp Arg Cys
165 170 175
Leu

<210> 48
<211> 102
<212> PRT
<213> Homo Sapiens

<400> 48
Glu Lys Gly Leu His Ile Asp Gln Leu Val Cys Leu Val Leu Glu Ala
1 5 10 15
Gln Lys Gly Pro Asn Pro Pro Gly Thr Leu Gly His Thr Val Ala Gly
20 25 30
Gly Val Ala Cys Thr Thr Thr Val Leu Ser Cys Leu His Leu Leu Ser
35 40 45
Gln Gly Tyr Lys Arg Asp Arg Pro Gln Ile Leu Met Tyr Ala Ala Pro
50 55 60
Pro Met Gly Pro Cys Arg Gly Ala His Phe Cys Gly Ser Ser Gln Thr
65 70 75 80
Ser Pro Pro Lys Pro Val Ala Thr Leu Ser Leu Leu Pro Cys Pro Leu
85 90 95
Pro Pro Leu Lys Asn Gly
100

<210> 49
<211> 179
<212> PRT
<213> Homo Sapiens

<400> 49
His Lys Pro Cys Asn Pro Arg Glu Lys Glu Arg Ile Gln Asn Ala Gly
1 5 10 15
Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala Val Ser Arg
20 25 30
Ala Leu Gly Asp Tyr Asp Tyr Lys Cys Val Asp Gly Lys Gly Pro Thr
35 40 45
Glu Gln Leu Val Ser Pro Glu Pro Glu Val Tyr Glu Ile Leu Arg Ala
50 55 60
Glu Glu Asp Glu Phe Ile Ile Leu Ala Cys Asp Gly Ile Trp Asp Val
65 70 75 80
Met Ser Asn Glu Glu Leu Cys Glu Tyr Val Lys Ser Arg Leu Glu Val
85 90 95
Ser Asp Asp Leu Glu Asn Val Cys Asn Trp Val Val Asp Thr Cys Leu
100 105 110
His Lys Gly Ser Arg Asp Asn Met Ser Ile Val Leu Val Cys Phe Ser
115 120 125
Asn Ala Pro Lys Val Ser Asp Glu Ala Val Lys Lys Asp Ser Glu Leu
130 135 140

Asp Lys His Leu Glu Ser Ile Met Glu Asn Leu Ala Lys Glu Cys Leu
145 150 155 160
Ile Leu Pro Met Ser Cys Ala Ser Cys Leu Gln Lys Ile Ser Gln Ile
165 170 175
Cys Leu Leu

<210> 50
<211> 163
<212> PRT
<213> Homo Sapiens

<400> 50
Asp Leu Pro Thr Leu Glu Asp His Gln Lys Gln Ser Gln Gln Leu Lys
1 5 10 15
Asp Ser Glu Leu Lys Ser Thr Glu Leu Gln Glu Lys Val Thr Glu Leu
20 25 30
Glu Ser Leu Leu Glu Glu Thr Gln Ala Ile Cys Arg Glu Lys Glu Ile
35 40 45
Gln Leu Glu Ser Leu Arg Gln Arg Glu Ala Glu Phe Ser Ser Ala Gly
50 55 60
His Ser Leu Gln Asp Lys Gln Ser Val Glu Glu Thr Ser Gly Glu Gly
65 70 75 80
Pro Glu Val Glu Met Glu Ser Trp Gln Lys Arg Tyr Asp Ser Leu Gln
85 90 95
Lys Ile Val Glu Lys Gln Gln Gln Lys Met Asp Gln Leu Arg Ser Gln
100 105 110
Val Gln Ser Leu Glu Gln Glu Val Ala Glu Glu Gly Thr Ser Gln Ala
115 120 125
Leu Arg Glu Glu Ala Gln Arg Arg Asp Ser Ala Leu Gln Gln Leu Arg
130 135 140
Thr Ala Val Lys Leu Ser Val Asn Gln Asp Leu Ile Glu Lys Asn Leu
145 150 155 160
Thr Leu Gln

<210> 51
<211> 164
<212> PRT
<213> Homo Sapiens

<400> 51
Phe Gly Asp Ser Val Asp Cys Ser Asp Cys Trp Leu Pro Val Val Lys
1 5 10 15
Phe Ile Glu Glu Gln Phe Glu Gln Tyr Leu Arg Asp Glu Ser Gly Leu
20 25 30
Asn Arg Lys Asn Ile Gln Asp Ser Arg Val His Cys Cys Leu Tyr Phe
35 40 45
Ile Ser Pro Phe Gly Arg Gly Leu Arg Pro Leu Ala Phe Leu Arg Ala
50 55 60
Val His Lys Val Asn Ile Ile Pro Val Ile Gly Lys Ala Asp Ala Leu
65 70 75 80
Met Pro Gln Glu Thr Gln Ala Leu Lys Gln Lys Ile Arg Asp Gln Leu
85 90 95
Lys Glu Glu Glu Ile His Ile Tyr Gln Phe Pro Glu Cys Asp Ser Asp

100 105 110
Glu Asp Glu Asp Phe Lys Arg Gln Asp Ala Met Lys Glu Ser Ile Pro
115 120 125
Phe Ala Val Val Gly Ser Cys Gln Val Val Arg Asp Gly Gly Asn Arg
130 135 140
Pro Val Arg Gly Arg Arg Tyr Ser Trp Gly Asn Val Glu Val Asn His
145 150 155 160
Ile Ala Ile Ser

<210> 52
<211> 600
<212> PRT
<213> Homo Sapiens

<400> 52
Met Cys Pro Arg Gln Val Asp Arg Ala Lys Glu Lys Gly Ile Gly Thr
1 5 10 15
Pro Gln Pro Asp Val Ala Lys Asp Ser Trp Ala Glu Leu Glu Asn Ser
20 25 30
Ser Lys Glu Asn Glu Val Ile Glu Val Lys Ser Met Gly Glu Ser Gln
35 40 45
Ser Lys Lys Leu Gln Gly Gly Tyr Glu Cys Lys Tyr Cys Pro Tyr Ser
50 55 60
Thr Gln Asn Leu Asn Glu Phe Thr Glu His Val Asp Met Gln His Pro
65 70 75 80
Asn Val Ile Leu Asn Pro Leu Tyr Val Cys Ala Glu Cys Asn Phe Thr
85 90 95
Thr Lys Lys Tyr Asp Ser Leu Ser Asp His Asn Ser Lys Phe His Pro
100 105 110
Gly Glu Ala Asn Phe Lys Leu Lys Leu Ile Lys Arg Asn Asn Gln Thr
115 120 125
Val Leu Glu Gln Ser Ile Glu Thr Thr Asn His Val Val Ser Ile Thr
130 135 140
Thr Ser Gly Pro Gly Thr Gly Asp Ser Asp Ser Gly Ile Ser Val Ser
145 150 155 160
Lys Thr Pro Ile Met Lys Pro Gly Lys Pro Lys Ala Asp Ala Lys Lys
165 170 175
Val Pro Lys Lys Pro Glu Glu Ile Thr Pro Glu Asn His Val Glu Gly
180 185 190
Thr Ala Arg Leu Val Thr Asp Thr Ala Glu Ile Leu Ser Arg Leu Gly
195 200 205
Gly Val Glu Leu Leu Gln Asp Thr Leu Gly His Val Met Pro Ser Val
210 215 220
Gln Leu Pro Pro Asn Ile Asn Leu Val Pro Lys Val Pro Val Pro Leu
225 230 235 240
Asn Thr Thr Lys Tyr Asn Ser Ala Leu Asp Thr Asn Ala Thr Met Ile
245 250 255
Asn Ser Phe Asn Lys Phe Pro Tyr Pro Thr Gln Ala Glu Leu Ser Trp
260 265 270
Leu Thr Ala Ala Ser Lys His Pro Glu Glu His Ile Arg Ile Trp Phe
275 280 285
Ala Thr Gln Arg Leu Lys His Gly Ile Ser Trp Ser Pro Glu Glu Val
290 295 300
Glu Glu Ala Arg Lys Lys Met Phe Asn Gly Thr Ile Gln Ser Val Pro

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305                 310                 315                 320
Pro Thr Ile Thr Val Leu Pro Ala Gln Leu Ala Pro Thr Lys Met Thr
                325                 330                 335
Gln Pro Ile Leu Gln Thr Ala Leu Pro Cys Gln Ile Leu Gly Gln Thr
            340                 345                 350
Ser Leu Val Leu Thr Gln Val Thr Ser Gly Ser Thr Thr Val Ser Cys
        355                 360                 365
Ser Pro Ile Thr Leu Ala Val Ala Gly Val Thr Asn His Gly Gln Lys
    370                 375                 380
Arg Pro Leu Val Thr Pro Gln Ala Ala Pro Glu Pro Lys Arg Pro His
385                 390                 395                 400
Ile Ala Gln Val Pro Glu Pro Pro Pro Lys Val Ala Asn Pro Pro Leu
                405                 410                 415
Thr Pro Ala Ser Asp Arg Lys Lys Thr Lys Glu Gln Ile Ala His Leu
            420                 425                 430
Lys Ala Ser Phe Leu Gln Ser Gln Phe Pro Asp Asp Ala Glu Val Tyr
        435                 440                 445
Arg Leu Ile Glu Val Thr Gly Leu Ala Arg Ser Glu Ile Lys Lys Trp
    450                 455                 460
Phe Ser Asp His Arg Tyr Arg Cys Gln Arg Gly Ile Val His Ile Thr
465                 470                 475                 480
Ser Glu Ser Leu Ala Lys Asp Gln Leu Ala Ile Ala Ala Ser Arg His
            485                 490                 495
Gly Arg Thr Tyr His Ala Tyr Pro Asp Phe Ala Pro Gln Lys Phe Lys
            500                 505                 510
Glu Lys Thr Gln Gly Gln Val Lys Ile Leu Glu Asp Ser Phe Leu Lys
        515                 520                 525
Ser Ser Phe Pro Thr Gln Ala Glu Leu Asp Arg Leu Arg Val Glu Thr
    530                 535                 540
Lys Leu Ser Arg Arg Glu Ile Asp Ser Trp Phe Ser Glu Arg Arg Lys
545                 550                 555                 560
Leu Arg Asp Ser Met Glu Gln Ala Val Leu Asp Ser Met Gly Ser Gly
                565                 570                 575
Gln Lys Arg Pro Arg Cys Gly Lys Pro Pro Met Val Leu Cys Leu Asp
            580                 585                 590
Ser Asn Ser Ser Pro Val Pro Ser
        595                 600

<210> 53
<211> 163
<212> PRT
<213> Homo Sapiens

<400> 53
Arg Lys Ser Trp Glu His Lys Glu Glu Ile Ser Glu Ala Glu Pro Gly
 1               5                  10                  15
Gly Gly Ser Leu Gly Asp Gly Arg Pro Pro Glu Glu Ser Ala His Glu
            20                  25                  30
Met Met Glu Glu Glu Glu Glu Ile Pro Lys Pro Lys Ser Val Val Ala
        35                  40                  45
Pro Pro Gly Ala Pro Lys Lys Glu His Val Asn His Val Ala Gly Lys
    50                  55                  60
Ser Thr Ile Gly Gly Gln Ile Met Tyr Leu Thr Gly Met Val Asp Lys
65                  70                  75                  80
Arg Thr Leu Glu Lys Tyr Glu Arg Glu Ala Lys Glu Lys Asn Arg Glu
```

85 90 95
Thr Trp Tyr Leu Ser Trp Ala Leu Asp Thr Asn Gln Glu Glu Arg Asp
100 105 110
Lys Gly Lys Thr Val Glu Val Gly Arg Ala Tyr Phe Glu Thr Glu Lys
115 120 125
Lys His Phe Thr Ile Leu Asp Met Asn Pro Arg Thr Leu Ser Ser Lys
130 135 140
Pro Lys Ala Gln Asn Leu Lys Leu Lys Val Pro Asn Ser Lys Val Arg
145 150 155 160
Arg Cys Phe

<210> 54
<211> 155
<212> PRT
<213> Homo Sapiens

<400> 54
Glu Arg Trp Pro Glu Glu Gly Thr Ala Asp Leu Ala Gln Ser Gly Leu
1 5 10 15
Glu Gly Gly Thr Thr Arg Ala Ser Val Ser Trp Cys Cys Leu Glu Gly
20 25 30
Ser Trp Leu Leu Ser Gly Tyr Leu Thr Phe Leu Lys Thr Cys Ser His
35 40 45
Thr Ala Ser Leu Ala Val Ser Ser Ser Ser Cys Arg Ile Arg His Glu
50 55 60
Leu Val Pro Asn Ser Ala Arg Gly Lys His Tyr Ser Gln Arg Trp Ala
65 70 75 80
Gln Glu Asp Leu Leu Glu Glu Gln Lys Asp Gly Ala Arg Ala Ala Ala
85 90 95
Val Ala Asp Lys Lys Lys Gly Leu Met Gly Pro Leu Thr Glu Leu Asp
100 105 110
Thr Lys Asp Val Asp Ala Leu Leu Lys Lys Ser Glu Ala Gln His Glu
115 120 125
Gln Pro Glu Asp Gly Cys Pro Phe Gly Ala Leu Thr Gln Arg Leu Leu
130 135 140
Gln Ala Leu Val Glu Glu Asn Ile Ile Phe Ser
145 150 155

<210> 55
<211> 112
<212> PRT
<213> Homo Sapiens

<400> 55
Ser Glu Arg Ala Leu Ala Pro Arg Thr Tyr Arg Met Glu Thr Ala Arg
1 5 10 15
Ser Ala Pro Tyr Met Arg Ser Met Met Gln Ser Leu Ser Gln Asn Pro
20 25 30
Asp Leu Ala Ala Gln Met Met Leu Asn Ser Pro Leu Phe Thr Ala Asn
35 40 45
Pro Gln Leu Gln Glu Gln Met Arg Pro Gln Leu Pro Ala Phe Leu Gln
50 55 60
Gln Met Gln Asn Pro Asp Thr Leu Ser Ala Met Ser Asn Pro Arg Ala
65 70 75 80

Met Gln Ala Leu Met Gln Ile Gln Gln Gly Leu Gln Thr Leu Ala Thr
85 90 95
Glu Ala Pro Gly Leu Ile Pro Ser Phe Thr Pro Gly Val Gly Val Gly
100 105 110

<210> 56
<211> 151
<212> PRT
<213> Homo Sapiens

<400> 56
Lys Phe Gly Met Pro Ile Asp Cys Gly Leu Pro Pro His Ile Asp Phe
1 5 10 15
Gly Asp Cys Thr Lys Leu Lys Asp Asp Gln Gly Tyr Phe Glu Gln Glu
20 25 30
Asp Asp Met Met Glu Val Pro Tyr Val Thr Pro His Pro Pro Tyr His
35 40 45
Leu Gly Ala Val Ala Lys Thr Trp Glu Asn Thr Lys Glu Ser Pro Ala
50 55 60
Thr His Ser Ser Asn Phe Leu Tyr Gly Thr Met Val Ser Tyr Thr Cys
65 70 75 80
Asn Pro Gly Tyr Glu Leu Leu Gly Asn Pro Val Leu Ile Cys Gln Glu
85 90 95
Asp Gly Thr Trp Asn Gly Ser Ala Pro Ser Cys Ile Ser Ile Glu Cys
100 105 110
Asp Leu Pro Thr Ala Pro Glu Asn Gly Phe Leu Arg Phe Thr Glu Thr
115 120 125
Ser Met Gly Ser Ala Val Gln Tyr Ser Cys Lys Pro Gly His Ile Leu
130 135 140
Ala Gly Ser Asp Leu Arg Leu
145 150

<210> 57
<211> 220
<212> PRT
<213> Homo Sapiens

<400> 57
Ala Ala Phe Val Ser Glu Val Thr Ser Phe Pro Val Val Gln Leu His
1 5 10 15
Met Asn Arg Thr Ala Met Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser
20 25 30
Ile Asn Gln Val Lys Leu Leu Lys Lys Asp Pro Gly Asn Glu Val Lys
35 40 45
Leu Lys Leu Tyr Ala Leu Tyr Lys Gln Ala Thr Glu Gly Pro Cys Asn
50 55 60
Met Pro Lys Pro Gly Val Phe Asp Leu Ile Asn Lys Ala Lys Trp Asp
65 70 75 80
Ala Trp Asn Ala Leu Gly Ser Leu Pro Lys Glu Ala Ala Arg Gln Asn
85 90 95
Tyr Val Asp Leu Val Ser Ser Leu Ser Pro Ser Leu Glu Ser Ser Ser
100 105 110
Gln Val Glu Pro Gly Thr Asp Arg Lys Ser Thr Gly Phe Glu Thr Leu
115 120 125
Val Val Thr Ser Glu Asp Gly Ile Thr Lys Ile Met Phe Asn Arg Pro

130 135 140
Lys Lys Lys Asn Ala Ile Asn Thr Glu Met Tyr His Glu Ile Met Arg
145 150 155 160
Ala Leu Lys Ala Ala Ser Lys Asp Asp Ser Ile Ile Thr Val Leu Thr
165 170 175
Gly Asn Gly Asp Tyr Tyr Ser Ser Gly Asn Asp Leu Thr Asn Phe Thr
180 185 190
Asp Ile Pro Pro Gly Gly Val Glu Lys Ala Lys Asn Asn Ala Val Leu
195 200 205
Leu Lys Gly Ile Cys Gly Leu Phe Tyr Arg Ile Ser
210 215 220

<210> 58
<211> 101
<212> PRT
<213> Homo Sapiens

<400> 58
Trp Pro Asp Leu Val His Thr Trp Ser Ser Glu Glu Ala Met Gly Ser
1 5 10 15
Cys Cys Ser Cys Pro Asp Lys Asp Thr Val Pro Asp Asn His Arg Asn
20 25 30
Lys Phe Lys Val Ile Asn Val Asp Asp Asp Gly Asn Glu Leu Gly Ser
35 40 45
Gly Ile Met Glu Leu Thr Asp Thr Glu Leu Ile Leu Tyr Thr Arg Lys
50 55 60
Arg Asp Ser Val Lys Trp His Tyr Leu Cys Leu Arg Arg Tyr Gly Tyr
65 70 75 80
Asp Ser Asn Leu Phe Ser Phe Glu Ser Gly Pro Arg Cys Gln Thr Gly
85 90 95
Thr Arg Asn Leu Cys
100

<210> 59
<211> 43
<212> PRT
<213> Homo Sapiens

<400> 59
Ala His Gly Pro Gly Val Glu Pro Thr Ser Arg His Gln Lys Asn Asn
1 5 10 15
Leu Ser Ser Ser His Thr Val Arg Leu Glu Thr Arg Gly Gln Thr Glu
20 25 30
Asn Gln Glu Cys Leu Leu Cys Pro His Glu Glu
35 40

<210> 60
<211> 210
<212> PRT
<213> Homo Sapiens

<400> 60
Leu Asn Gln Trp Thr Tyr Gln Ala Met Val His Glu Leu Leu Gly Ile
1 5 10 15
Asn Asn Asn Arg Ile Asp Leu Ser Arg Val Pro Gly Ile Ser Lys Asp

```
                20                      25                      30
Leu Arg Glu Val Val Leu Ser Ala Glu Asn Asp Glu Phe Tyr Ala Asn
            35                      40                      45
Asn Met Tyr Leu Asn Phe Ala Glu Ile Gly Ser Asn Ile Lys Asn Leu
        50                      55                      60
Met Glu Asp Phe Gln Lys Lys Lys Pro Lys Glu Gln Gln Lys Leu Glu
65                      70                      75                      80
Ser Ile Ala Asp Met Lys Ala Phe Val Glu Asn Tyr Pro Gln Phe Lys
                    85                      90                      95
Lys Met Ser Gly Thr Val Ser Lys His Val Thr Val Val Gly Glu Leu
                100                     105                     110
Ser Arg Leu Val Ser Glu Arg Asn Leu Leu Glu Val Ser Glu Val Glu
            115                     120                     125
Gln Glu Leu Ala Cys Gln Asn Asp His Ser Ser Ala Leu Gln Asn Ile
        130                     135                     140
Lys Arg Leu Leu Gln Asn Pro Lys Val Thr Glu Phe Asp Ala Ala Arg
145                     150                     155                     160
Leu Val Met Leu Tyr Ala Leu His Tyr Glu Arg His Ser Ser Asn Ser
                    165                     170                     175
Leu Pro Gly Leu Met Met Leu Arg Asn Lys Gly Val Ser Glu Lys Tyr
                180                     185                     190
Arg Lys Leu Val Ser Ala Val Val Glu Tyr Gly Gly Lys Thr Ser Gln
            195                     200                     205
Arg Lys
        210
```

<210> 61
<211> 40
<212> PRT
<213> Homo Sapiens

<400> 61

```
Thr Pro Gly Pro Gly Ala Gly Phe Tyr Ala Cys Pro Ala Arg Pro Leu
 1               5                  10                  15
Val Ser Gly Ile Tyr Ser Phe Arg Trp Val Arg Gly Leu Ala Asp Gln
                20                  25                  30
Glu Arg Asn Trp Gly Leu Ser Gln
            35                  40
```

<210> 62
<211> 238
<212> PRT
<213> Homo Sapiens

<400> 62

```
His Glu Ala Arg Leu Lys Arg Ala Ser Ala Pro Thr Phe Asp Asn Asp
 1               5                  10                  15
Tyr Ser Leu Ser Glu Leu Leu Ser Gln Leu Asp Ser Gly Val Ser Gln
                20                  25                  30
Ala Val Glu Gly Pro Glu Glu Leu Ser Arg Ser Ser Ser Glu Ser Lys
            35                  40                  45
Leu Pro Ser Ser Gly Ser Gly Lys Arg Leu Ser Gly Val Ser Ser Val
        50                  55                  60
Asp Ser Ala Phe Ser Ser Arg Gly Ser Leu Ser Leu Ser Phe Glu Arg
65                  70                  75                  80
```

Glu Pro Ser Thr Ser Asp Leu Gly Thr Thr Asp Val Gln Lys Lys Lys
85 90 95
Leu Val Asp Ala Ile Val Ser Gly Asp Thr Ser Lys Leu Met Lys Ile
100 105 110
Leu Gln Pro Gln Asp Val Asp Leu Ala Leu Asp Ser Gly Ala Ser Leu
115 120 125
Leu His Leu Ala Val Glu Ala Gly Gln Glu Glu Cys Ala Lys Trp Leu
130 135 140
Leu Leu Asn Asn Ala Asn Pro Asn Leu Ser Asn Arg Arg Gly Ser Thr
145 150 155 160
Pro Leu His Met Ala Val Glu Arg Arg Val Arg Gly Val Val Glu Leu
165 170 175
Leu Leu Ala Arg Ile Ser Val Asn Ala Lys Asp Glu Asp Gln Trp Thr
180 185 190
Ala Leu His Phe Ala Asn Gly Gly Val His Thr Ala Ala Val Gly Glu
195 200 205
Arg Leu Gly Gln Thr Lys Val Asp Phe Glu Gly Arg Thr Pro Met Gln
210 215 220
Val Gly Leu Pro Thr Thr Gly Lys Asn Ile Leu Arg Ile Leu
225 230 235

<210> 63
<211> 146
<212> PRT
<213> Homo Sapiens

<400> 63
Arg Leu Gly Ala Ala Met Met Glu Gly Leu Asp Asp Gly Pro Asp Phe
1 5 10 15
Leu Ser Glu Glu Asp Arg Gly Leu Lys Ala Ile Asn Val Asp Leu Gln
20 25 30
Ser Asp Ala Ala Leu Gln Val Asp Ile Ser Asp Ala Leu Ser Glu Arg
35 40 45
Asp Lys Val Lys Phe Thr Val His Thr Lys Ile Pro Pro Ala Pro Pro
50 55 60
Arg Pro Asp Phe Asp Ala Ser Arg Glu Lys Leu Gln Lys Leu Gly Glu
65 70 75 80
Gly Glu Gly Ser Met Thr Lys Glu Glu Phe Thr Lys Met Lys Gln Glu
85 90 95
Leu Glu Ala Glu Tyr Leu Ala Ile Phe Lys Lys Thr Val Ala Met His
100 105 110
Glu Val Phe Leu Cys Arg Val Ala Ala His Pro Ile Leu Arg Arg Asp
115 120 125
Leu Asn Phe His Val Phe Leu Glu Tyr Asn Gln Asp Leu Ser Val Arg
130 135 140
Gly Lys
145

<210> 64
<211> 63
<212> PRT
<213> Homo Sapiens

<400> 64
Glu Arg Gly His Ser Ile Lys Asp Phe Val Ser Phe Ala Arg His Phe

1 5 10 15
Ser Pro Asn Pro Arg Ile Val Ser Val Asn Ala Ser Tyr Ser Leu Ser
20 25 30
Asn Glu Ser Ser Leu Glu Gln Val Tyr Thr Leu Lys Met Ser Phe Ile
35 40 45
Ala Ser Asn Thr Tyr His Asn Gln Leu Tyr Lys Glu Gly Phe Leu
50 55 60

<210> 65
<211> 199
<212> PRT
<213> Homo Sapiens

<400> 65
Glu Ala Pro Asp Ser Ala Glu Gly Thr Thr Leu Thr Val Leu Pro Glu
1 5 10 15
Gly Glu Glu Leu Pro Leu Cys Val Ser Glu Ser Asn Gly Leu Glu Leu
20 25 30
Pro Pro Ser Ala Ala Ser Asp Glu Pro Leu Gln Glu Pro Leu Glu Ala
35 40 45
Asp Arg Thr Ser Glu Glu Leu Thr Glu Ala Lys Thr Pro Thr Ser Ser
50 55 60
Pro Glu Lys Pro Gln Glu Leu Val Thr Ala Glu Val Ala Ala Pro Ser
65 70 75 80
Thr Ser Ser Ser Ala Thr Ser Ser Pro Glu Gly Pro Ser Pro Ala Arg
85 90 95
Pro Pro Arg Arg Arg Thr Ser Ala Asp Val Glu Ile Arg Gly Gln Gly
100 105 110
Thr Gly Arg Pro Gly Gln Pro Pro Gly Pro Lys Val Leu Arg Lys Leu
115 120 125
Pro Gly Arg Leu Val Thr Val Val Glu Glu Lys Glu Leu Val Arg Arg
130 135 140
Arg Arg Gln Gln Arg Gly Ala Ala Ser Thr Leu Val Pro Gly Val Ser
145 150 155 160
Glu Thr Ser Ala Ser Pro Gly Ser Pro Ser Val Arg Ser Met Ser Gly
165 170 175
Pro Glu Ser Ser Pro Pro Ile Gly Gly Pro Cys Glu Ala Ala Pro Ser
180 185 190
Ser Ser Leu Pro Thr Pro Pro
195

<210> 66
<211> 1599
<212> DNA
<213> Homo Sapiens

<400> 66
ttctttgaaa cattattatt cagaacgaag gagaatgata cagatacact ggctgaggtg 60
ttttgaggtg cattgaaatg ttccatgctg ttacttaggt taacatgttc ttgaggtacc 120
atgccatgga ttaaaaggaa atttggtaag tggcttccac ctaaacgact tactagggaa 180
gctatgcgaa attatttaaa agggtaaggg gatcaaatag tacttatcct tcatgcaaaa 240
gttgtacaga agtcatatgg caatcaaaaa atttttttt gccctccccc ttgtgtatat 300
cttatgggca gtggatggaa gaaaaaaaaa gaacaaatga aatgcgatgg ttgttctgaa 360
cacagctctc atccatgtgc atttattggg ataggaaata gtgaccaaga aatgcagcag 420
ctaaacttgg aaggaaagaa ctattgcaca gccaaaacat tgtacatatc tgattcagac 480

aagcaaaagc acttcatttt ttctgtaaag gtgttctatg gcaacggtga tgacattggt 540
gtgttcctca gcaagtagat aaaagtcatc tccaaacctt ccaaaaagaa gcagtcattg 600
aaaaatgctg acttatgcat tgtctcagga acaaaggtgg ctctgtttaa tcgactacga 660
tcccagacag ttagtaccag atacttgcat gtagaaggag gtaattttca tgccagttca 720
cagcagtggg gagcatttta cattcaattc ttggatgatg atggatcaga aggagaagaa 780
ttcacagtct gagatgccta cattcattat ggacaaacat gcaaacttgt gtgctcagtt 840
actggcatgg cactcccaag attgataatt atgaaagttg ataagcatac cgcattattg 900
gatgcagatg atcctgtgtc acaactccat aaatgtgcat tttaccttaa ggatacagaa 960
agaatgtatt tgtgcctttc tcaagaaaga ataattcaat ttcaggccac tccatgtcca 1020
agagaaccaa ataaagagat gataaatgat ggcgcttcct ggacaatcat tagcacagat 1080
aaggcagggt atacatttta tgagggaatg ggccctgtcc ttgccccagt cactcctgtg 1140
cctgtggtag agagccttca gttgaatggc ggtggggacg tagcaatgct tgaacttaca 1200
ggacagaatt tcactccaaa tttacgagtg tggtttgggg gggtagaagc tgaaactatg 1260
tacaggtgtg gagagagtat gctctgtgtc gtcccagaca tttctgcatt ccgagaaggt 1320
tggagatggg tccggcaacc agtccaggtt ccagtaactt tggtccgaaa tgatggaatc 1380
atttattcca ccagccttac ctttacctac acaccagaac cagggccgcg gccacattgc 1440
agtgcagcag gagcaatcct tctagccaat tcaagccagg tgccccctaa cgaatcaaac 1500
acaaacagcg agggaagtta cacaaacgcc agcacaaatt caaccagtgt cacatcatct 1560
acagccacag tggtatccta actaccgtct ttttgctag 1599

<210> 67
<211> 729
<212> PRT
<213> Homo Sapiens

<400> 67

Met Gly Lys Lys Tyr Lys Asn Ile Val Leu Leu Lys Gly Leu Glu Val
1 5 10 15
Ile Asn Asp Tyr His Phe Arg Met Val Lys Ser Leu Leu Ser Asn Asp
20 25 30
Leu Lys Leu Asn Leu Lys Met Arg Glu Glu Tyr Asp Lys Ile Gln Ile
35 40 45
Ala Asp Leu Met Glu Glu Lys Phe Arg Gly Asp Ala Gly Leu Gly Lys
50 55 60
Leu Ile Lys Ile Phe Glu Asp Ile Pro Thr Leu Glu Asp Leu Ala Glu
65 70 75 80
Thr Leu Lys Lys Glu Lys Leu Lys Val Lys Gly Pro Ala Leu Ser Arg
85 90 95
Lys Arg Lys Lys Glu Val His Ala Thr Ser Pro Ala Pro Ser Thr Ser
100 105 110
Ser Thr Val Lys Thr Glu Gly Ala Glu Ala Thr Pro Gly Ala Gln Lys
115 120 125
Arg Lys Lys Ser Thr Lys Glu Lys Ala Gly Pro Lys Gly Ser Lys Val
130 135 140
Ser Glu Glu Gln Thr Gln Pro Pro Ser Pro Ala Gly Ala Gly Met Ser
145 150 155 160
Thr Ala Met Gly Arg Ser Pro Ser Pro Lys Thr Ser Leu Ser Ala Pro
165 170 175
Pro Asn Ser Ser Ser Thr Glu Asn Pro Lys Thr Val Ala Lys Cys Gln
180 185 190
Val Thr Pro Arg Arg Asn Val Leu Gln Lys Arg Pro Val Ile Val Lys
195 200 205
Val Leu Ser Thr Thr Lys Pro Phe Glu Tyr Glu Thr Pro Glu Met Glu
210 215 220
Lys Lys Ile Met Phe His Ala Thr Val Ala Thr Gln Thr Gln Phe Phe

225 230 235 240
His Val Lys Val Leu Asn Thr Ser Leu Lys Glu Lys Phe Asn Gly Lys
245 250 255
Lys Ile Ile Ile Ile Ser Asp Tyr Leu Glu Tyr Asp Ser Leu Leu Glu
260 265 270
Val Asn Glu Glu Ser Thr Val Ser Glu Ala Gly Pro Asn Gln Thr Phe
275 280 285
Glu Val Pro Asn Lys Ile Ile Asn Arg Ala Lys Glu Thr Leu Lys Ile
290 295 300
Asp Ile Leu His Lys Gln Ala Ser Gly Asn Ile Val Tyr Gly Val Phe
305 310 315 320
Met Leu His Lys Lys Thr Val Asn Gln Lys Thr Thr Ile Tyr Glu Ile
325 330 335
Gln Asp Asp Arg Gly Lys Met Asp Val Val Gly Thr Gly Gln Cys His
340 345 350
Asn Ile Pro Cys Glu Glu Gly Asp Lys Leu Gln Leu Phe Cys Phe Arg
355 360 365
Leu Arg Lys Lys Asn Gln Met Ser Lys Leu Ile Ser Glu Met His Ser
370 375 380
Phe Ile Gln Ile Lys Lys Lys Thr Asn Pro Arg Asn Asn Asp Pro Lys
385 390 395 400
Ser Met Lys Leu Pro Gln Glu Gln Arg Gln Leu Pro Tyr Pro Ser Glu
405 410 415
Ala Ser Thr Thr Phe Pro Glu Ser His Leu Arg Thr Pro Gln Met Pro
420 425 430
Pro Thr Thr Pro Ser Ser Ser Phe Phe Thr Lys Lys Ser Glu Asp Thr
435 440 445
Ile Ser Lys Met Asn Asp Phe Met Arg Met Gln Ile Leu Lys Glu Gly
450 455 460
Ser His Phe Pro Gly Pro Phe Met Thr Ser Ile Gly Pro Ala Glu Ser
465 470 475 480
His Pro His Thr Pro Gln Met Pro Pro Ser Thr Pro Ser Ser Ser Phe
485 490 495
Leu Thr Thr Leu Lys Pro Arg Leu Lys Thr Glu Pro Glu Glu Val Ser
500 505 510
Ile Glu Asp Ser Ala Gln Ser Asp Leu Lys Glu Val Met Val Leu Asn
515 520 525
Ala Thr Glu Ser Phe Val Tyr Glu Pro Lys Glu Gln Lys Lys Met Phe
530 535 540
His Ala Thr Val Ala Thr Glu Asn Glu Val Phe Arg Val Lys Val Phe
545 550 555 560
Asn Ile Asp Leu Lys Glu Lys Phe Thr Pro Lys Lys Ile Ile Ala Ile
565 570 575
Ala Asn Tyr Val Cys Arg Asn Gly Phe Leu Glu Val Tyr Pro Phe Thr
580 585 590
Leu Val Ala Asp Val Asn Ala Asp Ala Asn Met Glu Ile Pro Lys Gly
595 600 605
Leu Ile Arg Ser Ala Ser Val Thr Pro Lys Ile Asn Gln Leu Cys Ser
610 615 620
Gln Thr Lys Gly Ser Phe Val Asn Gly Val Phe Glu Val His Lys Lys
625 630 635 640
Asn Val Arg Gly Glu Phe Thr Tyr Tyr Glu Ile Gln Asp Asn Thr Gly
645 650 655
Lys Met Glu Val Val Val His Gly Arg Leu Asn Thr Ile Asn Cys Glu
660 665 670

Glu Gly Asp Lys Leu Lys Leu Thr Ser Phe Glu Leu Ala Pro Lys Ser
675 680 685
Gly Asn Thr Gly Glu Leu Arg Ser Val Ile His Ser His Ile Lys Val
690 695 700
Ile Lys Thr Lys Lys Asn Lys Lys Asp Ile Leu Asn Pro Asp Ser Ser
705 710 715 720
Met Glu Thr Ser Pro Asp Phe Phe Phe
725

<210> 68
<211> 754
<212> PRT
<213> Homo Sapiens

<400> 68
Met Ala Ser Val Pro Ala Leu Gln Leu Thr Pro Ala Asn Pro Pro Pro
1 5 10 15
Pro Glu Val Ser Asn Pro Lys Lys Pro Gly Arg Val Thr Asn Gln Leu
20 25 30
Gln Tyr Leu His Lys Val Val Met Lys Ala Leu Trp Lys His Gln Phe
35 40 45
Ala Trp Pro Phe Arg Gln Pro Val Asp Ala Val Lys Leu Gly Leu Pro
50 55 60
Asp Tyr His Lys Ile Ile Lys Gln Pro Met Asp Met Gly Thr Ile Lys
65 70 75 80
Arg Arg Leu Glu Asn Asn Tyr Tyr Trp Ala Ala Ser Glu Cys Met Gln
85 90 95
Asp Phe Asn Thr Met Phe Thr Asn Cys Tyr Ile Tyr Asn Lys Pro Thr
100 105 110
Asp Asp Ile Val Leu Met Ala Gln Thr Leu Glu Lys Ile Phe Leu Gln
115 120 125
Lys Val Ala Ser Met Pro Gln Glu Glu Gln Glu Leu Val Val Thr Ile
130 135 140
Pro Lys Asn Ser His Lys Lys Gly Ala Lys Leu Ala Ala Leu Gln Gly
145 150 155 160
Ser Val Thr Ser Ala His Gln Val Pro Ala Val Ser Ser Val Ser His
165 170 175
Thr Ala Leu Tyr Thr Pro Pro Pro Glu Ile Pro Thr Thr Val Leu Asn
180 185 190
Ile Pro His Pro Ser Val Ile Ser Ser Pro Leu Leu Lys Ser Leu His
195 200 205
Ser Ala Gly Pro Pro Leu Leu Ala Val Thr Ala Ala Pro Pro Ala Gln
210 215 220
Pro Leu Ala Lys Lys Lys Gly Val Lys Arg Lys Ala Asp Thr Thr Thr
225 230 235 240
Pro Thr Pro Thr Ala Ile Leu Ala Pro Gly Ser Pro Ala Ser Pro Pro
245 250 255
Gly Ser Leu Glu Pro Lys Ala Ala Arg Leu Pro Pro Met Arg Arg Glu
260 265 270
Ser Gly Arg Pro Ile Lys Pro Pro Arg Lys Asp Leu Pro Asp Ser Gln
275 280 285
Gln Gln His Gln Ser Ser Lys Lys Gly Lys Leu Ser Glu Gln Leu Lys
290 295 300
His Cys Asn Gly Ile Leu Lys Glu Leu Leu Ser Lys Lys His Ala Ala
305 310 315 320

Tyr Ala Trp Pro Phe Tyr Lys Pro Val Asp Ala Ser Ala Leu Gly Leu
325 330 335
His Asp Tyr His Asp Ile Ile Lys His Pro Met Asp Leu Ser Thr Val
340 345 350
Lys Arg Lys Met Glu Asn Arg Asp Tyr Arg Asp Ala Gln Glu Phe Ala
355 360 365
Ala Asp Val Arg Leu Met Phe Ser Asn Cys Tyr Lys Tyr Asn Pro Pro
370 375 380
Asp His Asp Val Val Ala Met Ala Arg Lys Leu Gln Asp Val Phe Glu
385 390 395 400
Phe Arg Tyr Ala Lys Met Pro Asp Glu Pro Leu Glu Pro Gly Pro Leu
405 410 415
Pro Val Ser Thr Ala Met Pro Pro Gly Leu Ala Lys Ser Ser Ser Glu
420 425 430
Ser Ser Ser Glu Glu Ser Ser Ser Glu Ser Ser Ser Glu Glu Glu Glu
435 440 445
Glu Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Ser Glu Ser Ser Asp
450 455 460
Ser Glu Glu Glu Arg Ala His Arg Leu Ala Glu Leu Gln Glu Gln Leu
465 470 475 480
Arg Ala Val His Glu Gln Leu Ala Ala Leu Ser Gln Gly Pro Ile Ser
485 490 495
Lys Pro Lys Arg Lys Arg Glu Lys Lys Glu Lys Lys Lys Lys Arg Lys
500 505 510
Ala Glu Lys His Arg Gly Arg Ala Gly Ala Asp Glu Asp Asp Lys Gly
515 520 525
Pro Arg Ala Pro Arg Pro Pro Gln Pro Lys Lys Ser Lys Lys Ala Ser
530 535 540
Gly Ser Gly Gly Gly Ser Ala Ala Leu Gly Pro Ser Gly Phe Gly Pro
545 550 555 560
Ser Gly Gly Ser Gly Thr Lys Leu Pro Lys Lys Ala Thr Lys Thr Ala
565 570 575
Pro Pro Ala Leu Pro Thr Gly Tyr Asp Ser Glu Glu Glu Glu Glu Ser
580 585 590
Arg Pro Met Ser Tyr Asp Glu Lys Arg Gln Leu Ser Leu Asp Ile Asn
595 600 605
Lys Leu Pro Gly Glu Lys Leu Gly Arg Val Val His Ile Ile Gln Ala
610 615 620
Arg Glu Pro Ser Leu Arg Asp Ser Asn Pro Glu Glu Ile Glu Ile Asp
625 630 635 640
Phe Glu Thr Leu Lys Pro Ser Thr Leu Arg Glu Leu Glu Arg Tyr Val
645 650 655
Leu Ser Cys Leu Arg Lys Lys Pro Arg Lys Pro Tyr Thr Ile Lys Lys
660 665 670
Pro Val Gly Lys Thr Lys Glu Glu Leu Ala Leu Glu Lys Lys Arg Glu
675 680 685
Leu Glu Lys Arg Leu Gln Asp Val Ser Gly Gln Leu Asn Ser Thr Lys
690 695 700
Lys Pro Pro Lys Lys Ala Asn Glu Lys Thr Glu Ser Ser Ser Ala Gln
705 710 715 720
Gln Val Ala Val Ser Arg Leu Ser Ala Ser Ser Ser Ser Ser Asp Ser
725 730 735
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Thr Ser Asp Ser Asp
740 745 750
Ser Gly

<210> 69
<211> 210
<212> PRT
<213> Homo Sapiens

<400> 69
Met Asp Asp Glu Glu Glu Thr Tyr Arg Leu Trp Lys Ile Arg Lys Thr
1 5 10 15
Ile Met Gln Leu Cys His Asp Arg Gly Tyr Leu Val Thr Gln Asp Glu
20 25 30
Leu Asp Gln Thr Leu Glu Glu Phe Lys Ala Gln Phe Gly Asp Lys Pro
35 40 45
Ser Glu Gly Arg Pro Arg Arg Thr Asp Leu Thr Val Leu Val Ala His
50 55 60
Asn Asp Asp Pro Thr Asp Gln Met Phe Val Phe Phe Pro Glu Glu Pro
65 70 75 80
Lys Val Gly Ile Lys Thr Ile Lys Val Tyr Cys Gln Arg Met Gln Glu
85 90 95
Glu Asn Ile Thr Arg Ala Leu Ile Val Val Gln Gln Gly Met Thr Pro
100 105 110
Ser Ala Lys Gln Ser Leu Val Asp Met Ala Pro Lys Tyr Ile Leu Glu
115 120 125
Gln Phe Leu Gln Gln Glu Leu Leu Ile Asn Ile Thr Glu His Glu Leu
130 135 140
Val Pro Glu His Val Val Met Thr Lys Glu Glu Val Thr Glu Leu Leu
145 150 155 160
Ala Arg Tyr Lys Leu Arg Glu Asn Gln Leu Pro Arg Ile Gln Ala Gly
165 170 175
Asp Pro Val Ala Arg Tyr Phe Gly Ile Lys Arg Gly Gln Val Val Lys
180 185 190
Ile Ile Arg Pro Ser Glu Thr Ala Gly Arg Tyr Ile Thr Tyr Arg Leu
195 200 205
Val Gln
210

<210> 70
<211> 621
<212> PRT
<213> Homo Sapiens

<400> 70
Met Leu Leu Leu Pro Ser Ala Ala Glu Gly Gln Gly Thr Ala Ile Thr
1 5 10 15
His Ala Leu Thr Ser Ala Ser Ser Val Cys Gln Val Glu Pro Val Gly
20 25 30
Arg Trp Phe Glu Ala Phe Val Lys Arg Arg Asn Arg Asn Ala Ser Thr
35 40 45
Ser Phe Gln Glu Leu Glu Asp Lys Lys Glu Leu Ser Glu Glu Ser Glu
50 55 60
Asp Glu Glu Leu Gln Leu Glu Glu Phe Pro Met Leu Lys Thr Leu Asp
65 70 75 80
Pro Lys Asp Trp Lys Asn Gln Asp His Tyr Ala Val Leu Gly Leu Gly
85 90 95

His Val Arg Tyr Thr Ala Thr Gln Arg Gln Ile Lys Ala Ala His Lys
100 105 110
Ala Met Val Leu Lys His His Pro Asp Lys Arg Lys Ala Ala Gly Glu
115 120 125
Pro Ile Lys Glu Gly Asp Asn Asp Tyr Phe Thr Cys Ile Thr Lys Ala
130 135 140
Tyr Glu Met Leu Ser Asp Pro Val Lys Arg Arg Ala Phe Asn Ser Val
145 150 155 160
Asp Pro Thr Phe Asp Asn Ser Val Pro Ser Lys Ser Glu Ala Lys Asp
165 170 175
Asn Phe Phe Gln Val Phe Ser Pro Val Phe Glu Arg Asn Ser Arg Trp
180 185 190
Ser Asn Lys Lys Asn Val Pro Lys Leu Gly Asp Met Asn Ser Ser Phe
195 200 205
Glu Asp Val Asp Ala Phe Tyr Ser Phe Trp Tyr Asn Phe Asp Ser Trp
210 215 220
Arg Glu Phe Ser Tyr Leu Asp Glu Glu Glu Lys Glu Lys Ala Glu Cys
225 230 235 240
Arg Asp Glu Arg Lys Trp Ile Glu Lys Gln Asn Arg Ala Thr Arg Ala
245 250 255
Gln Arg Lys Lys Glu Glu Met Asn Arg Ile Arg Thr Leu Val Asp Asn
260 265 270
Ala Tyr Ser Cys Asp Pro Arg Ile Lys Lys Phe Lys Glu Glu Glu Lys
275 280 285
Ala Lys Lys Glu Ala Glu Lys Lys Ala Lys Ala Glu Ala Arg Arg Lys
290 295 300
Glu Gln Glu Ala Lys Glu Lys Gln Arg Gln Ala Glu Leu Glu Ala Val
305 310 315 320
Arg Leu Ala Lys Glu Lys Glu Glu Glu Glu Val Arg Gln Gln Ala Leu
325 330 335
Leu Ala Lys Lys Glu Lys Asp Ile Gln Lys Lys Ala Ile Lys Lys Glu
340 345 350
Arg Gln Lys Leu Arg Asn Ser Cys Lys Ser Trp Asn His Phe Ser Asp
355 360 365
Asn Glu Ala Asp Arg Val Lys Met Met Glu Glu Val Glu Lys Leu Cys
370 375 380
Asp Arg Leu Glu Leu Ala Ser Leu Gln Gly Leu Asn Glu Ile Leu Ala
385 390 395 400
Ser Ser Thr Arg Glu Val Gly Lys Ala Ala Leu Glu Lys Gln Ile Glu
405 410 415
Glu Val Asn Glu Gln Met Arg Arg Glu Lys Glu Glu Ala Asp Ala Arg
420 425 430
Met Arg Gln Ala Ser Lys Asn Ala Glu Lys Ser Thr Gly Gly Ser Gly
435 440 445
Ser Gly Ser Lys Asn Trp Ser Glu Asp Asp Leu Gln Leu Leu Ile Lys
450 455 460
Ala Val Asn Leu Phe Pro Ala Gly Thr Asn Ser Arg Trp Glu Val Ile
465 470 475 480
Ala Asn Tyr Met Asn Ile His Ser Ser Ser Gly Val Lys Arg Thr Ala
485 490 495
Lys Asp Val Ile Ser Lys Ala Lys Ser Leu Gln Lys Leu Asp Pro His
500 505 510
Gln Lys Asp Asp Ile Asn Lys Lys Ala Phe Asp Lys Phe Lys Lys Glu
515 520 525
His Gly Val Ala Ser Gln Ala Asp Ser Ala Ala Pro Ser Glu Arg Phe

530 535 540
Glu Gly Pro Cys Ile Asp Ser Thr Pro Trp Thr Thr Glu Glu Gln Lys
545 550 555 560
Leu Leu Glu Gln Ala Leu Lys Thr Tyr Pro Val Asn Thr Pro Glu Arg
565 570 575
Trp Glu Lys Ile Ala Glu Ala Val Pro Gly Arg Thr Lys Lys Asp Cys
580 585 590
Met Arg Arg Tyr Lys Glu Leu Val Glu Met Val Lys Ala Lys Lys Ala
595 600 605
Ala Gln Glu Gln Val Leu Asn Ala Ser Arg Ala Arg Lys
610 615 620

<210> 71
<211> 267
<212> PRT
<213> Homo Sapiens

<400> 71
Met Ala Ser Leu Leu Lys Val Asp Gln Glu Val Lys Leu Lys Val Asp
1 5 10 15
Ser Phe Arg Glu Arg Ile Thr Ser Lys Ala Glu Asp Leu Val Ala Asn
20 25 30
Phe Phe Pro Lys Lys Leu Leu Glu Leu Asp Ser Phe Leu Lys Glu Pro
35 40 45
Ile Leu Asn Ile His Asp Leu Thr Gln Ile His Ser Asp Met Asn Leu
50 55 60
Pro Val Pro Asp Pro Ile Leu Leu Thr Asn Ser His Asp Gly Leu Asp
65 70 75 80
Gly Pro Thr Tyr Lys Lys Arg Arg Leu Asp Glu Cys Glu Glu Ala Phe
85 90 95
Gln Gly Thr Lys Val Phe Val Met Pro Asn Gly Met Leu Lys Ser Asn
100 105 110
Gln Gln Leu Val Asp Ile Ile Glu Lys Val Lys Pro Glu Ile Arg Leu
115 120 125
Leu Ile Glu Lys Cys Asn Thr Pro Ser Gly Lys Gly Pro His Ile Cys
130 135 140
Phe Asp Leu Gln Val Lys Met Trp Val Gln Leu Leu Ile Pro Arg Ile
145 150 155 160
Glu Asp Gly Asn Asn Phe Gly Val Ser Ile Gln Glu Glu Thr Val Ala
165 170 175
Glu Leu Arg Thr Val Glu Ser Glu Ala Ala Ser Tyr Leu Asp Gln Ile
180 185 190
Ser Arg Tyr Tyr Ile Thr Arg Ala Lys Leu Val Ser Lys Ile Ala Lys
195 200 205
Tyr Pro His Val Glu Asp Tyr Arg Arg Thr Val Thr Glu Ile Asp Glu
210 215 220
Lys Glu Tyr Ile Ser Leu Arg Leu Ile Ile Ser Glu Leu Arg Asn Gln
225 230 235 240
Tyr Val Thr Leu His Asp Met Ile Leu Lys Asn Ile Glu Lys Ile Lys
245 250 255
Arg Pro Arg Ser Ser Asn Ala Glu Thr Leu Tyr
260 265

<210> 72
<211> 1752

<212> PRT
<213> Homo Sapiens

<400> 72
Arg Glu Lys Arg Arg Arg Lys Ser Val Glu Asp Arg Phe Asp Gln Gln
1 5 10 15
Lys Asn Asp Tyr Asp Gln Leu Gln Lys Ala Arg Gln Cys Glu Lys Glu
20 25 30
Asn Leu Gly Trp Gln Lys Leu Glu Ser Glu Lys Ala Ile Lys Glu Lys
35 40 45
Glu Tyr Glu Ile Glu Arg Leu Arg Val Leu Leu Gln Glu Glu Gly Thr
50 55 60
Arg Lys Arg Glu Tyr Glu Asn Glu Leu Ala Lys Val Arg Asn His Tyr
65 70 75 80
Asn Glu Glu Met Ser Asn Leu Arg Asn Lys Tyr Glu Thr Glu Ile Asn
85 90 95
Ile Thr Lys Thr Thr Ile Lys Glu Ile Ser Met Gln Lys Glu Asp Asp
100 105 110
Ser Lys Asn Leu Arg Asn Gln Leu Asp Arg Leu Ser Arg Glu Asn Arg
115 120 125
Asp Leu Lys Asp Glu Ile Val Arg Leu Asn Asp Ser Ile Leu Gln Ala
130 135 140
Thr Glu Gln Arg Arg Arg Ala Glu Glu Asn Ala Leu Gln Gln Lys Ala
145 150 155 160
Cys Gly Ser Glu Ile Met Gln Lys Lys Gln His Leu Glu Ile Glu Leu
165 170 175
Lys Gln Val Met Gln Gln Arg Ser Glu Asp Asn Ala Arg His Lys Gln
180 185 190
Ser Leu Glu Glu Ala Ala Lys Thr Ile Gln Asp Lys Asn Lys Glu Ile
195 200 205
Glu Arg Leu Lys Ala Glu Phe Gln Glu Glu Ala Lys Arg Arg Trp Glu
210 215 220
Tyr Glu Asn Glu Leu Ser Lys Val Arg Asn Asn Tyr Asp Glu Glu Ile
225 230 235 240
Ile Ser Leu Lys Asn Gln Phe Glu Thr Glu Ile Asn Ile Thr Lys Thr
245 250 255
Thr Ile His Gln Leu Thr Met Gln Lys Glu Glu Asp Thr Ser Gly Tyr
260 265 270
Arg Ala Gln Ile Asp Asn Leu Thr Arg Glu Asn Arg Ser Leu Ser Glu
275 280 285
Glu Ile Lys Arg Leu Lys Asn Thr Leu Thr Gln Thr Thr Glu Asn Leu
290 295 300
Arg Arg Val Glu Glu Asp Ile Gln Gln Gln Lys Ala Thr Gly Ser Glu
305 310 315 320
Val Ser Gln Arg Lys Gln Gln Leu Glu Val Glu Leu Arg Gln Val Thr
325 330 335
Gln Met Arg Thr Glu Glu Ser Val Arg Tyr Lys Gln Ser Leu Asp Asp
340 345 350
Ala Ala Lys Thr Ile Gln Asp Lys Asn Lys Glu Ile Glu Arg Leu Lys
355 360 365
Gln Leu Ile Asp Lys Glu Thr Asn Asp Arg Lys Cys Leu Glu Asp Glu
370 375 380
Asn Ala Arg Leu Gln Arg Val Gln Tyr Asp Leu Gln Lys Ala Asn Ser
385 390 395 400
Ser Ala Thr Glu Thr Ile Asn Lys Leu Lys Val Gln Glu Gln Glu Leu

405 410 415
Thr Arg Leu Arg Ile Asp Tyr Glu Arg Val Ser Gln Glu Arg Thr Val
420 425 430
Lys Asp Gln Asp Ile Thr Arg Phe Gln Asn Ser Leu Lys Glu Leu Gln
435 440 445
Leu Gln Lys Gln Lys Val Glu Glu Glu Leu Asn Arg Leu Lys Arg Thr
450 455 460
Ala Ser Glu Asp Ser Cys Lys Arg Lys Lys Leu Glu Glu Glu Leu Glu
465 470 475 480
Gly Met Arg Arg Ser Leu Lys Glu Gln Ala Ile Lys Ile Thr Asn Leu
485 490 495
Thr Gln Gln Leu Glu Gln Ala Ser Ile Val Lys Lys Arg Ser Glu Asp
500 505 510
Asp Leu Arg Gln Gln Arg Asp Val Leu Asp Gly His Leu Arg Glu Lys
515 520 525
Gln Arg Thr Gln Glu Glu Leu Arg Arg Leu Ser Ser Glu Val Glu Ala
530 535 540
Leu Arg Arg Gln Leu Leu Gln Glu Gln Glu Ser Val Lys Gln Ala His
545 550 555 560
Leu Arg Asn Glu His Phe Gln Lys Ala Ile Glu Asp Lys Ser Arg Ser
565 570 575
Leu Asn Glu Ser Lys Ile Glu Ile Glu Arg Leu Gln Ser Leu Thr Glu
580 585 590
Asn Leu Thr Lys Glu His Leu Met Leu Glu Glu Glu Leu Arg Asn Leu
595 600 605
Arg Leu Glu Tyr Asp Asp Leu Arg Arg Gly Arg Ser Glu Ala Asp Ser
610 615 620
Asp Lys Asn Ala Thr Ile Leu Glu Leu Arg Ser Gln Leu Gln Ile Ser
625 630 635 640
Asn Asn Arg Thr Leu Glu Leu Gln Gly Leu Ile Asn Asp Leu Gln Arg
645 650 655
Glu Arg Glu Asn Leu Arg Gln Glu Ile Glu Lys Phe Gln Lys Gln Ala
660 665 670
Leu Glu Ala Ser Asn Arg Ile Gln Glu Ser Lys Asn Gln Cys Thr Gln
675 680 685
Val Val Gln Glu Arg Glu Ser Leu Leu Val Lys Ile Lys Val Leu Glu
690 695 700
Gln Asp Lys Ala Arg Leu Gln Arg Leu Glu Asp Glu Leu Asn Arg Ala
705 710 715 720
Lys Ser Thr Leu Glu Ala Glu Thr Arg Val Lys Gln Arg Leu Glu Cys
725 730 735
Glu Lys Gln Gln Ile Gln Asn Asp Leu Asn Gln Trp Lys Thr Gln Tyr
740 745 750
Ser Arg Lys Glu Glu Ala Ile Arg Lys Ile Glu Ser Glu Arg Glu Lys
755 760 765
Ser Glu Arg Glu Lys Asn Ser Leu Arg Ser Glu Ile Glu Arg Leu Gln
770 775 780
Ala Glu Ile Lys Arg Ile Glu Glu Arg Cys Arg Arg Lys Leu Glu Asp
785 790 795 800
Ser Thr Arg Glu Thr Gln Ser Gln Leu Glu Thr Glu Arg Ser Arg Tyr
805 810 815
Gln Arg Glu Ile Asp Lys Leu Arg Gln Arg Pro Tyr Gly Ser His Arg
820 825 830
Glu Thr Gln Thr Glu Cys Glu Trp Thr Val Asp Thr Ser Lys Leu Val
835 840 845

Phe Asp Gly Leu Arg Lys Lys Val Thr Ala Met Gln Leu Tyr Glu Cys
850 855 860
Gln Leu Ile Asp Lys Thr Thr Leu Asp Lys Leu Leu Lys Gly Lys Lys
865 870 875 880
Ser Val Glu Glu Val Ala Ser Glu Ile Gln Pro Phe Leu Arg Gly Ala
885 890 895
Gly Ser Ile Ala Gly Ala Ser Ala Ser Pro Lys Glu Lys Tyr Ser Leu
900 905 910
Val Glu Ala Lys Arg Lys Lys Leu Ile Ser Pro Glu Ser Thr Val Met
915 920 925
Leu Leu Glu Ala Gln Ala Ala Thr Gly Gly Ile Ile Asp Pro His Arg
930 935 940
Asn Glu Lys Leu Thr Val Asp Ser Ala Ile Ala Arg Asp Leu Ile Asp
945 950 955 960
Phe Asp Asp Arg Gln Gln Ile Tyr Ala Ala Glu Lys Ala Ile Thr Gly
965 970 975
Phe Asp Asp Pro Phe Ser Gly Lys Thr Val Ser Val Ser Glu Ala Ile
980 985 990
Lys Lys Asn Leu Ile Asp Arg Glu Thr Gly Met Arg Leu Leu Glu Ala
995 1000 1005
Gln Ile Ala Ser Gly Gly Val Val Asp Pro Val Asn Ser Val Phe Leu
1010 1015 1020
Pro Lys Asp Val Ala Leu Ala Arg Gly Leu Ile Asp Arg Asp Leu Tyr
1025 1030 1035 104
Arg Ser Leu Asn Asp Pro Arg Asp Ser Gln Lys Asn Phe Val Asp Pro
1045 1050 1055
Val Thr Lys Lys Lys Val Ser Tyr Val Gln Leu Lys Glu Arg Cys Arg
1060 1065 1070
Ile Glu Pro His Thr Gly Leu Leu Leu Leu Ser Val Gln Lys Arg Ser
1075 1080 1085
Met Ser Phe Gln Gly Ile Arg Gln Pro Val Thr Val Thr Glu Leu Val
1090 1095 1100
Asp Ser Gly Ile Leu Arg Pro Ser Thr Val Asn Glu Leu Glu Ser Gly
1105 1110 1115 112
Gln Ile Ser Tyr Asp Glu Val Gly Glu Arg Ile Lys Asp Phe Leu Gln
1125 1130 1135
Gly Ser Ser Cys Ile Ala Gly Ile Tyr Asn Glu Thr Thr Lys Gln Lys
1140 1145 1150
Leu Gly Ile Tyr Glu Ala Met Lys Ile Gly Leu Val Arg Pro Gly Thr
1155 1160 1165
Ala Leu Glu Leu Leu Glu Ala Gln Ala Ala Thr Gly Phe Ile Val Asp
1170 1175 1180
Pro Val Ser Asn Leu Arg Leu Pro Val Glu Glu Ala Tyr Lys Arg Gly
1185 1190 1195 120
Leu Val Gly Ile Glu Phe Lys Glu Lys Leu Leu Ser Ala Glu Arg Ala
1205 1210 1215
Val Thr Gly Tyr Asn Asp Pro Glu Thr Gly Asn Ile Ile Ser Leu Phe
1220 1225 1230
Gln Ala Met Asn Lys Glu Leu Ile Glu Lys Gly His Gly Ile Arg Leu
1235 1240 1245
Leu Glu Ala Gln Ile Ala Thr Gly Gly Ile Ile Asp Pro Lys Glu Ser
1250 1255 1260
His Arg Leu Pro Val Asp Ile Ala Tyr Lys Arg Gly Tyr Phe Asn Glu
1265 1270 1275 128
Glu Leu Ser Glu Ile Leu Ser Asp Pro Ser Asp Asp Thr Lys Gly Phe

1285 1290 1295
Phe Asp Pro Asn Thr Glu Glu Asn Leu Thr Tyr Leu Gln Leu Lys Glu
1300 1305 1310
Arg Cys Ile Lys Asp Glu Glu Thr Gly Leu Cys Leu Leu Pro Leu Lys
1315 1320 1325
Glu Lys Lys Lys Gln Val Gln Thr Ser Gln Lys Asn Thr Leu Arg Lys
1330 1335 1340
Arg Arg Val Val Ile Val Asp Pro Glu Thr Asn Lys Glu Met Ser Val
1345 1350 1355 136
Gln Glu Ala Tyr Lys Lys Gly Leu Ile Asp Tyr Glu Thr Phe Lys Glu
1365 1370 1375
Leu Cys Glu Gln Glu Cys Glu Trp Glu Glu Ile Thr Ile Thr Gly Ser
1380 1385 1390
Asp Gly Ser Thr Arg Val Val Leu Val Asp Arg Lys Thr Gly Ser Gln
1395 1400 1405
Tyr Asp Ile Gln Asp Ala Ile Asp Lys Gly Leu Val Asp Arg Lys Phe
1410 1415 1420
Phe Asp Gln Tyr Arg Ser Gly Ser Leu Ser Leu Thr Gln Phe Ala Asp
1425 1430 1435 144
Met Ile Ser Leu Lys Asn Gly Val Gly Thr Ser Ser Ser Met Gly Ser
1445 1450 1455
Gly Val Ser Asp Asp Val Phe Ser Ser Ser Arg His Glu Ser Val Ser
1460 1465 1470
Lys Ile Ser Thr Ile Ser Ser Val Arg Asn Leu Thr Ile Arg Ser Ser
1475 1480 1485
Ser Phe Ser Asp Thr Leu Glu Glu Ser Ser Pro Ile Ala Ala Ile Phe
1490 1495 1500
Asp Thr Glu Asn Leu Glu Lys Ile Ser Ile Thr Glu Gly Ile Glu Arg
1505 1510 1515 152
Gly Ile Val Asp Ser Ile Thr Gly Gln Arg Leu Leu Glu Ala Gln Ala
1525 1530 1535
Cys Thr Gly Gly Ile Ile His Pro Thr Thr Gly Gln Lys Leu Ser Leu
1540 1545 1550
Gln Asp Ala Val Ser Gln Gly Val Ile Asp Gln Asp Met Ala Thr Ser
1555 1560 1565
Val Lys Pro Ala Gln Lys Ala Phe Ile Gly Phe Glu Gly Val Lys Gly
1570 1575 1580
Lys Lys Lys Met Ser Ala Ala Glu Ala Val Lys Glu Lys Trp Leu Pro
1585 1590 1595 160
Tyr Glu Ala Gly Gln Arg Phe Leu Glu Phe Gln Tyr Leu Thr Gly Gly
1605 1610 1615
Leu Val Asp Pro Glu Val His Gly Arg Ile Ser Thr Glu Glu Ala Ile
1620 1625 1630
Arg Lys Gly Phe Ile Asp Gly Arg Ala Ala Gln Arg Leu Gln Asp Thr
1635 1640 1645
Ser Ser Tyr Ala Lys Ile Leu Thr Cys Pro Lys Thr Lys Leu Lys Ile
1650 1655 1660
Ser Tyr Lys Asp Ala Ile Asn Arg Ser Met Val Glu Asp Ile Thr Gly
1665 1670 1675 168
Leu Arg Leu Leu Glu Ala Ala Ser Val Ser Ser Lys Gly Leu Pro Ser
1685 1690 1695
Pro Tyr Asn Met Ser Ser Ala Pro Gly Ser Arg Ser Gly Ser Arg Ser
1700 1705 1710
Gly Ser Arg Ser Gly Ser Arg Ser Gly Ser Arg Ser Gly Ser Arg Arg
1715 1720 1725

Gly Ser Phe Asp Ala Thr Gly Asn Ser Ser Tyr Ser Tyr Ser Tyr Ser
1730 1735 1740
Phe Ser Ser Ser Ser Ile Gly His
1745 1750

<210> 73
<211> 1978
<212> PRT
<213> Homo Sapiens

<400> 73
Met Ser Arg Pro Arg Phe Asn Pro Arg Gly Asp Phe Pro Leu Gln Arg
1 5 10 15
Pro Arg Ala Pro Asn Pro Ser Gly Met Arg Pro Pro Gly Pro Phe Met
20 25 30
Arg Pro Gly Ser Met Gly Leu Pro Arg Phe Tyr Pro Ala Gly Arg Ala
35 40 45
Arg Gly Ile Pro His Arg Phe Ala Gly Leu Glu Ser Tyr Gln Asn Met
50 55 60
Gly Pro Gln Arg Met Asn Val Gln Val Thr Gln His Arg Thr Asp Pro
65 70 75 80
Arg Leu Thr Lys Glu Lys Leu Asp Phe His Glu Ala Gln Gln Lys Lys
85 90 95
Gly Lys Pro His Gly Ser Arg Trp Asp Asp Glu Pro His Ile Ser Ala
100 105 110
Ser Val Ala Val Lys Gln Ser Ser Val Thr Gln Val Thr Glu Gln Ser
115 120 125
Pro Lys Val Gln Ser Arg Tyr Thr Lys Glu Ser Ala Ser Ser Ile Leu
130 135 140
Ala Ser Phe Gly Leu Ser Asn Glu Asp Leu Glu Glu Leu Ser Arg Tyr
145 150 155 160
Pro Asp Glu Gln Leu Thr Pro Glu Asn Met Pro Leu Ile Leu Arg Asp
165 170 175
Ile Arg Met Arg Lys Met Gly Arg Arg Leu Pro Asn Leu Pro Ser Gln
180 185 190
Ser Arg Asn Lys Glu Thr Leu Gly Ser Glu Ala Val Ser Ser Asn Val
195 200 205
Ile Asp Tyr Gly His Ala Ser Lys Tyr Gly Tyr Thr Glu Asp Pro Leu
210 215 220
Glu Val Arg Ile Tyr Asp Pro Glu Ile Pro Thr Asp Glu Val Glu Asn
225 230 235 240
Glu Phe Gln Ser Gln Gln Asn Ile Ser Ala Ser Val Pro Asn Pro Asn
245 250 255
Val Ile Cys Asn Ser Met Phe Pro Val Glu Asp Val Phe Arg Gln Met
260 265 270
Asp Phe Pro Gly Glu Ser Ser Asn Asn Arg Ser Phe Phe Ser Val Glu
275 280 285
Ser Gly Thr Lys Met Ser Gly Leu His Ile Ser Gly Gly Gln Ser Val
290 295 300
Leu Glu Pro Ile Lys Ser Val Asn Gln Ser Ile Asn Gln Thr Val Ser
305 310 315 320
Gln Thr Met Ser Gln Ser Leu Ile Pro Pro Ser Met Asn Gln Gln Pro
325 330 335
Phe Ser Ser Glu Leu Ile Ser Ser Val Ser Gln Gln Glu Arg Ile Pro
340 345 350

His Glu Pro Val Ile Asn Ser Ser Asn Val His Val Gly Ser Arg Gly
355 360 365
Ser Lys Lys Asn Tyr Gln Ser Gln Ala Asp Ile Pro Ile Arg Ser Pro
370 375 380
Phe Gly Ile Val Lys Ala Ser Trp Leu Pro Lys Phe Ser His Ala Asp
385 390 395 400
Ala Gln Lys Met Lys Arg Leu Pro Thr Pro Ser Met Met Asn Asp Tyr
405 410 415
Tyr Ala Ala Ser Pro Arg Ile Phe Pro His Leu Cys Ser Leu Cys Asn
420 425 430
Val Glu Cys Ser His Leu Lys Asp Trp Ile Gln His Gln Asn Thr Ser
435 440 445
Thr His Ile Glu Ser Cys Arg Gln Leu Arg Gln Gln Tyr Pro Asp Trp
450 455 460
Asn Pro Glu Ile Leu Pro Ser Arg Arg Asn Glu Gly Asn Arg Lys Glu
465 470 475 480
Asn Glu Thr Pro Arg Arg Arg Ser His Ser Pro Ser Pro Arg Arg Ser
485 490 495
Arg Arg Ser Ser Ser Ser His Arg Phe Arg Arg Ser Arg Ser Pro Met
500 505 510
His Tyr Met Tyr Arg Pro Arg Ser Arg Ser Pro Arg Ile Cys His Arg
515 520 525
Phe Ile Ser Arg Tyr Arg Ser Arg Ser Arg Ser Arg Ser Pro Tyr Arg
530 535 540
Ile Arg Asn Pro Phe Arg Gly Ser Pro Lys Cys Phe Arg Ser Val Ser
545 550 555 560
Pro Glu Arg Met Ser Arg Arg Ser Val Arg Ser Ser Asp Arg Lys Lys
565 570 575
Ala Leu Glu Asp Val Val Gln Arg Ser Gly His Gly Thr Glu Phe Asn
580 585 590
Lys Gln Lys His Leu Glu Ala Ala Asp Lys Gly His Ser Pro Ala Gln
595 600 605
Lys Pro Lys Thr Ser Ser Gly Thr Lys Pro Ser Val Lys Pro Thr Ser
610 615 620
Ala Thr Lys Ser Asp Ser Asn Leu Gly Gly His Ser Ile Arg Cys Lys
625 630 635 640
Ser Lys Asn Leu Glu Asp Asp Thr Leu Ser Glu Cys Lys Gln Val Ser
645 650 655
Asp Lys Ala Val Ser Leu Gln Arg Lys Leu Arg Lys Glu Gln Ser Leu
660 665 670
His Tyr Gly Ser Val Leu Leu Ile Thr Glu Leu Pro Glu Asp Gly Cys
675 680 685
Thr Glu Glu Asp Val Arg Lys Leu Phe Gln Pro Phe Gly Lys Val Asn
690 695 700
Asp Val Leu Ile Val Pro Tyr Arg Lys Glu Ala Tyr Leu Glu Met Glu
705 710 715 720
Phe Lys Glu Ala Ile Thr Ala Ile Met Lys Tyr Ile Glu Thr Thr Pro
725 730 735
Leu Thr Ile Lys Gly Lys Ser Val Lys Ile Cys Val Pro Gly Lys Lys
740 745 750
Lys Ala Gln Asn Lys Glu Val Lys Lys Lys Thr Leu Glu Ser Lys Lys
755 760 765
Val Ser Ala Ser Thr Leu Lys Arg Asp Ala Asp Ala Ser Lys Ala Val
770 775 780
Glu Ile Val Thr Ser Thr Ser Ala Ala Lys Thr Gly Gln Ala Lys Ala

785 790 795 800
Cys Val Ala Lys Val Asn Lys Ser Thr Gly Lys Ser Ala Ser Ser Val
805 810 815
Lys Ser Val Val Thr Val Ala Val Lys Gly Asn Lys Ala Ser Ile Lys
820 825 830
Thr Ala Lys Ser Gly Gly Lys Lys Ser Leu Glu Ala Lys Lys Thr Gly
835 840 845
Asn Val Lys Asn Lys Asp Ser Asn Lys Pro Val Thr Ile Pro Glu Asn
850 855 860
Ser Glu Ile Lys Thr Ser Ile Glu Val Lys Ala Thr Glu Asn Cys Ala
865 870 875 880
Lys Glu Ala Ile Ser Asp Ala Ala Leu Glu Ala Thr Glu Asn Glu Pro
885 890 895
Leu Asn Lys Glu Thr Glu Glu Met Cys Val Met Leu Val Ser Asn Leu
900 905 910
Pro Asn Lys Gly Tyr Ser Val Glu Glu Val Tyr Asp Leu Ala Lys Pro
915 920 925
Phe Gly Gly Leu Lys Asp Ile Leu Ile Leu Ser Ser His Lys Lys Ala
930 935 940
Tyr Ile Glu Ile Asn Arg Lys Ala Ala Glu Ser Met Val Lys Phe Tyr
945 950 955 960
Thr Cys Phe Pro Val Leu Met Asp Gly Asn Gln Leu Ser Ile Ser Met
965 970 975
Ala Pro Glu Asn Met Asn Ile Lys Asp Glu Glu Ala Ile Phe Ile Thr
980 985 990
Leu Val Lys Glu Asn Asp Pro Glu Ala Asn Ile Asp Thr Ile Tyr Asp
995 1000 1005
Arg Phe Val His Leu Asp Asn Leu Pro Glu Asp Gly Leu Gln Cys Val
1010 1015 1020
Leu Cys Val Gly Leu Gln Phe Gly Lys Val Asp His His Val Phe Ile
1025 1030 1035 104
Ser Asn Arg Asn Lys Ala Ile Leu Gln Leu Asp Ser Pro Glu Ser Ala
1045 1050 1055
Gln Ser Met Tyr Ser Phe Leu Lys Gln Asn Pro Gln Asn Ile Gly Asp
1060 1065 1070
His Met Leu Thr Cys Ser Leu Ser Pro Lys Ile Asp Leu Pro Glu Val
1075 1080 1085
Gln Ile Glu His Asp Pro Glu Leu Glu Lys Glu Ser Pro Gly Leu Lys
1090 1095 1100
Asn Ser Pro Ile Asp Glu Ser Glu Val Gln Thr Ala Thr Asp Ser Pro
1105 1110 1115 112
Ser Val Lys Pro Asn Glu Leu Glu Glu Glu Ser Thr Pro Ser Ile Gln
1125 1130 1135
Thr Glu Thr Leu Val Gln Gln Glu Glu Pro Cys Glu Glu Glu Ala Glu
1140 1145 1150
Lys Ala Thr Cys Asp Ser Asp Phe Ala Val Glu Thr Leu Glu Leu Glu
1155 1160 1165
Thr Gln Gly Glu Glu Val Lys Glu Glu Ile Pro Leu Val Ala Ser Ala
1170 1175 1180
Ser Val Ser Ile Glu Gln Phe Thr Glu Asn Ala Glu Glu Cys Ala Leu
1185 1190 1195 120
Asn Gln Gln Met Phe Asn Ser Asp Leu Glu Lys Lys Gly Ala Glu Ile
1205 1210 1215
Ile Asn Pro Lys Thr Ala Leu Leu Pro Ser Asp Ser Val Phe Ala Glu
1220 1225 1230

Glu Arg Asn Leu Lys Gly Ile Leu Glu Glu Ser Pro Ser Glu Ala Glu
1235 1240 1245

Asp Phe Ile Ser Gly Ile Thr Gln Thr Met Val Glu Ala Val Ala Glu
1250 1255 1260

Val Glu Lys Asn Glu Thr Val Ser Glu Ile Leu Pro Ser Thr Cys Ile
1265 1270 1275 128

Val Thr Leu Val Pro Gly Ile Pro Thr Gly Asp Glu Lys Thr Val Asp
1285 1290 1295

Lys Lys Asn Ile Ser Glu Lys Lys Gly Asn Met Asp Glu Lys Glu Glu
1300 1305 1310

Lys Glu Phe Asn Thr Lys Glu Thr Arg Met Asp Leu Gln Ile Gly Thr
1315 1320 1325

Glu Lys Ala Glu Lys Asn Glu Gly Arg Met Asp Ala Glu Lys Val Glu
1330 1335 1340

Lys Met Ala Ala Met Lys Glu Lys Pro Ala Glu Asn Thr Leu Phe Lys
1345 1350 1355 136

Ala Tyr Pro Asn Lys Gly Val Gly Gln Ala Asn Lys Pro Asp Glu Thr
1365 1370 1375

Ser Lys Thr Ser Ile Leu Ala Val Ser Asp Val Ser Ser Ser Lys Pro
1380 1385 1390

Ser Ile Lys Ala Val Ile Val Ser Ser Pro Lys Ala Lys Ala Thr Val
1395 1400 1405

Ser Lys Thr Glu Asn Gln Lys Ser Phe Pro Lys Ser Val Pro Arg Asp
1410 1415 1420

Gln Ile Asn Ala Glu Lys Lys Leu Ser Ala Lys Glu Phe Gly Leu Leu
1425 1430 1435 144

Lys Pro Thr Ser Ala Arg Ser Gly Leu Ala Glu Ser Ser Ser Lys Phe
1445 1450 1455

Lys Pro Thr Gln Ser Ser Leu Thr Arg Gly Gly Ser Gly Arg Ile Ser
1460 1465 1470

Ala Leu Gln Gly Lys Leu Ser Lys Leu Asp Tyr Arg Asp Ile Thr Lys
1475 1480 1485

Gln Ser Gln Glu Thr Glu Ala Arg Pro Ser Ile Met Lys Arg Asp Asp
1490 1495 1500

Ser Asn Asn Lys Thr Leu Ala Glu Gln Asn Thr Lys Asn Pro Lys Ser
1505 1510 1515 152

Thr Thr Gly Arg Ser Ser Lys Ser Lys Glu Glu Pro Leu Phe Pro Phe
1525 1530 1535

Asn Leu Asp Glu Phe Val Thr Val Asp Glu Val Ile Glu Glu Val Asn
1540 1545 1550

Pro Ser Gln Ala Lys Gln Asn Pro Leu Lys Gly Lys Arg Lys Glu Thr
1555 1560 1565

Leu Lys Asn Val Pro Phe Ser Glu Leu Asn Leu Lys Lys Lys Lys Gly
1570 1575 1580

Lys Thr Ser Thr Pro Arg Gly Val Glu Gly Glu Leu Ser Phe Val Thr
1585 1590 1595 160

Leu Asp Glu Ile Gly Glu Glu Glu Asp Ala Ala Ala His Leu Ala Gln
1605 1610 1615

Ala Leu Val Thr Val Asp Glu Val Ile Asp Glu Glu Glu Leu Asn Met
1620 1625 1630

Glu Glu Met Val Lys Asn Ser Asn Ser Leu Phe Thr Leu Asp Glu Leu
1635 1640 1645

Ile Asp Gln Asp Asp Cys Ile Ser His Ser Glu Pro Lys Asp Val Thr
1650 1655 1660

Val Leu Ser Val Ala Glu Glu Gln Asp Leu Leu Lys Gln Glu Arg Leu

1665 1670 1675 168
Val Thr Val Asp Glu Ile Gly Glu Val Glu Glu Leu Pro Leu Asn Glu
1685 1690 1695
Ser Ala Asp Ile Thr Phe Ala Thr Leu Asn Thr Lys Gly Asn Glu Gly
1700 1705 1710
Asp Ile Val Arg Asp Ser Ile Gly Phe Ile Ser Ser Gln Val Pro Glu
1715 1720 1725
Asp Pro Ser Thr Leu Val Thr Val Asp Glu Ile Gln Asp Asp Ser Ser
1730 1735 1740
Asp Leu His Leu Val Thr Leu Asp Glu Val Thr Glu Glu Asp Glu Asp
1745 1750 1755 176
Ser Leu Ala Asp Phe Asn Asn Leu Lys Glu Glu Leu Asn Phe Val Thr
1765 1770 1775
Val Asp Glu Val Gly Glu Glu Glu Asp Gly Asp Asn Asp Leu Lys Val
1780 1785 1790
Glu Leu Ala Gln Ser Lys Asn Asp His Pro Thr Asp Lys Lys Gly Asn
1795 1800 1805
Arg Lys Lys Arg Ala Val Asp Thr Lys Lys Thr Lys Leu Glu Ser Leu
1810 1815 1820
Ser Gln Val Gly Pro Val Asn Glu Asn Val Met Glu Glu Asp Leu Lys
1825 1830 1835 184
Thr Met Ile Glu Arg His Leu Thr Ala Lys Thr Pro Thr Lys Arg Val
1845 1850 1855
Arg Ile Gly Lys Thr Leu Pro Ser Glu Lys Ala Val Val Thr Glu Pro
1860 1865 1870
Ala Lys Gly Glu Glu Ala Phe Gln Met Ser Glu Val Asp Glu Glu Ser
1875 1880 1885
Gly Leu Lys Asp Ser Glu Pro Glu Arg Lys Arg Lys Lys Thr Glu Asp
1890 1895 1900
Ser Ser Ser Gly Lys Ser Val Ala Ser Asp Val Pro Glu Glu Leu Asp
1905 1910 1915 192
Phe Leu Val Pro Lys Ala Gly Phe Phe Cys Pro Ile Cys Ser Leu Phe
1925 1930 1935
Tyr Ser Gly Glu Lys Ala Met Thr Asn His Cys Lys Ser Thr Arg His
1940 1945 1950
Lys Gln Asn Thr Glu Lys Phe Met Ala Lys Gln Arg Lys Glu Lys Glu
1955 1960 1965
Gln Asn Glu Ala Glu Glu Arg Ser Ser Arg
1970 1975

<210> 74
<211> 366
<212> PRT
<213> Homo Sapiens

<400> 74
Met Arg Val Met Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala
1 5 10 15
Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser His Ser Met Arg Tyr Phe
20 25 30
Tyr Thr Ala Val Ser Arg Pro Gly Arg Gly Glu Pro His Phe Ile Ala
35 40 45
Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala
50 55 60
Ala Ser Pro Arg Gly Glu Pro Arg Ala Pro Trp Val Glu Gln Glu Gly

65 70 75 80
Pro Glu Tyr Trp Asp Arg Glu Thr Gln Lys Tyr Lys Arg Gln Ala Gln
85 90 95
Thr Asp Arg Val Ser Leu Arg Asn Leu Arg Gly Tyr Tyr Asn Gln Ser
100 105 110
Glu Ala Gly Ser His Ile Ile Gln Arg Met Tyr Gly Cys Asp Val Gly
115 120 125
Pro Asp Gly Arg Leu Leu Arg Gly Tyr Asp Gln Tyr Ala Tyr Asp Gly
130 135 140
Lys Asp Tyr Ile Ala Leu Asn Glu Asp Leu Arg Ser Trp Thr Ala Ala
145 150 155 160
Asp Thr Ala Ala Gln Ile Thr Gln Arg Lys Trp Glu Ala Ala Arg Glu
165 170 175
Ala Glu Gln Leu Arg Ala Tyr Leu Glu Gly Leu Cys Val Glu Trp Leu
180 185 190
Arg Arg Tyr Leu Lys Asn Gly Lys Glu Thr Leu Gln Arg Ala Glu His
195 200 205
Pro Lys Thr His Val Thr His His Pro Val Ser Asp His Glu Ala Thr
210 215 220
Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala Glu Ile Thr Leu Thr
225 230 235 240
Trp Gln Trp Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu
245 250 255
Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val
260 265 270
Val Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu
275 280 285
Gly Leu Pro Glu Pro Leu Thr Leu Arg Trp Glu Pro Ser Ser Gln Pro
290 295 300
Thr Ile Pro Ile Val Gly Ile Val Ala Gly Leu Ala Val Leu Ala Val
305 310 315 320
Leu Ala Val Leu Gly Ala Val Val Ala Val Val Met Cys Arg Arg Lys
325 330 335
Ser Ser Gly Gly Lys Gly Gly Ser Cys Ser Gln Ala Ala Ser Ser Asn
340 345 350
Ser Ala Gln Gly Ser Asp Glu Ser Leu Ile Ala Cys Lys Ala
355 360 365

<210> 75
<211> 240
<212> PRT
<213> Homo Sapiens

<400> 75
Met Gly Leu Glu Leu Tyr Leu Asp Leu Leu Ser Gln Pro Cys Arg Ala
1 5 10 15
Val Tyr Ile Phe Ala Lys Lys Asn Asp Ile Pro Phe Glu Leu Arg Ile
20 25 30
Val Asp Leu Ile Lys Gly Gln His Leu Ser Asp Ala Phe Ala Gln Val
35 40 45
Asn Pro Leu Lys Lys Val Pro Ala Leu Lys Asp Gly Asp Phe Thr Leu
50 55 60
Thr Glu Ser Val Ala Ile Leu Leu Tyr Leu Thr Arg Lys Tyr Lys Val
65 70 75 80
Pro Asp Tyr Trp Tyr Pro Gln Asp Leu Gln Ala Arg Ala Arg Val Asp

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                    85                  90                  95
Glu Tyr Leu Ala Trp Gln His Thr Thr Leu Arg Arg Ser Cys Leu Arg
            100                 105                 110
Ala Leu Trp His Lys Val Met Phe Pro Val Phe Leu Gly Gly Pro Val
        115                 120                 125
Ser Pro Gln Thr Leu Ala Ala Thr Leu Ala Glu Leu Asp Val Thr Leu
    130                 135                 140
Gln Leu Leu Glu Asp Lys Phe Leu Gln Asn Lys Ala Phe Leu Thr Gly
145                 150                 155                 160
Pro His Ile Ser Leu Ala Asp Leu Val Ala Ile Thr Glu Leu Met His
                165                 170                 175
Pro Val Gly Ala Gly Cys Gln Val Phe Glu Gly Arg Pro Lys Leu Ala
            180                 185                 190
Thr Trp Arg Gln Arg Val Glu Ala Ala Val Gly Glu Asp Leu Phe Gln
        195                 200                 205
Glu Ala His Glu Val Ile Leu Lys Ala Lys Asp Phe Pro Pro Ala Asp
    210                 215                 220
Pro Thr Ile Lys Gln Lys Leu Met Pro Trp Val Leu Ala Met Ile Arg
225                 230                 235                 240

<210> 76
<211> 953
<212> PRT
<213> Homo Sapiens

<400> 76
Met Ile Thr Ser Ala Ala Gly Ile Ile Ser Leu Leu Asp Glu Asp Glu
1               5                   10                  15
Pro Gln Leu Lys Glu Phe Ala Leu His Lys Leu Asn Ala Val Val Asn
            20                  25                  30
Asp Phe Trp Ala Glu Ile Ser Glu Ser Val Asp Lys Ile Glu Val Leu
        35                  40                  45
Tyr Glu Asp Glu Gly Phe Arg Ser Arg Gln Phe Ala Ala Leu Val Ala
    50                  55                  60
Ser Lys Val Phe Tyr His Leu Gly Ala Phe Glu Glu Ser Leu Asn Tyr
65                  70                  75                  80
Ala Leu Gly Ala Arg Asp Leu Phe Asn Val Asn Asp Asn Ser Glu Tyr
                85                  90                  95
Val Glu Thr Ile Ile Ala Lys Cys Ile Asp His Tyr Thr Lys Gln Cys
            100                 105                 110
Val Glu Asn Ala Asp Leu Pro Glu Gly Glu Lys Lys Pro Ile Asp Gln
        115                 120                 125
Arg Leu Glu Gly Ile Val Asn Lys Met Phe Gln Arg Cys Leu Asp Asp
    130                 135                 140
His Lys Tyr Lys Gln Ala Ile Gly Ile Ala Leu Glu Thr Arg Arg Leu
145                 150                 155                 160
Asp Val Phe Glu Lys Thr Ile Leu Glu Ser Asn Asp Val Pro Gly Met
                165                 170                 175
Leu Ala Tyr Ser Leu Lys Leu Cys Met Ser Leu Met Gln Asn Lys Gln
            180                 185                 190
Phe Arg Asn Lys Val Leu Arg Val Leu Val Lys Ile Tyr Met Asn Leu
        195                 200                 205
Glu Lys Pro Asp Phe Ile Asn Val Cys Gln Cys Leu Ile Phe Leu Asp
    210                 215                 220
Asp Pro Gln Ala Val Ser Asp Ile Leu Glu Lys Leu Val Lys Glu Asp
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225 230 235 240
Asn Leu Leu Met Ala Tyr Gln Ile Cys Phe Asp Leu Tyr Glu Ser Ala
245 250 255
Ser Gln Gln Phe Leu Ser Ser Val Ile Gln Asn Leu Arg Thr Val Gly
260 265 270
Thr Pro Ile Ala Ser Val Pro Gly Ser Thr Asn Thr Gly Thr Val Pro
275 280 285
Gly Ser Glu Lys Asp Ser Asp Ser Met Glu Thr Glu Glu Lys Thr Ser
290 295 300
Ser Ala Phe Val Gly Lys Thr Pro Glu Ala Ser Pro Glu Pro Lys Asp
305 310 315 320
Gln Thr Leu Lys Met Ile Lys Ile Leu Ser Gly Glu Met Ala Ile Glu
325 330 335
Leu His Leu Gln Phe Leu Ile Arg Asn Asn Asn Thr Asp Leu Met Ile
340 345 350
Leu Lys Asn Thr Lys Asp Ala Val Arg Asn Ser Val Cys His Thr Ala
355 360 365
Thr Val Ile Ala Asn Ser Phe Met His Cys Gly Thr Thr Ser Asp Gln
370 375 380
Phe Leu Arg Asp Asn Leu Glu Trp Leu Ala Arg Ala Thr Asn Trp Ala
385 390 395 400
Lys Phe Thr Ala Thr Ala Ser Leu Gly Val Ile His Lys Gly His Glu
405 410 415
Lys Glu Ala Leu Gln Leu Met Ala Thr Tyr Leu Pro Lys Asp Thr Ser
420 425 430
Pro Gly Ser Ala Tyr Gln Glu Gly Gly Gly Leu Tyr Ala Leu Gly Leu
435 440 445
Ile His Ala Asn His Gly Gly Asp Ile Ile Asp Tyr Leu Leu Asn Gln
450 455 460
Leu Lys Asn Ala Ser Asn Asp Ile Val Arg His Gly Gly Ser Leu Gly
465 470 475 480
Leu Gly Leu Ala Ala Met Gly Thr Ala Arg Gln Asp Val Tyr Asp Leu
485 490 495
Leu Lys Thr Asn Leu Tyr Gln Asp Asp Ala Val Thr Gly Glu Ala Ala
500 505 510
Gly Leu Ala Leu Gly Leu Val Met Leu Gly Ser Lys Asn Ala Gln Ala
515 520 525
Ile Glu Asp Met Val Gly Tyr Ala Gln Glu Thr Gln His Glu Lys Ile
530 535 540
Leu Arg Gly Leu Ala Val Gly Ile Ala Leu Val Met Tyr Gly Arg Met
545 550 555 560
Glu Glu Ala Asp Ala Leu Ile Glu Ser Leu Cys Arg Asp Lys Asp Pro
565 570 575
Ile Leu Arg Arg Ser Gly Met Tyr Thr Val Ala Met Ala Tyr Cys Gly
580 585 590
Ser Gly Asn Asn Lys Ala Ile Arg Arg Leu Leu His Val Ala Val Ser
595 600 605
Asp Val Asn Asp Asp Val Arg Ser Ala Ala Val Glu Ser Leu Gly Phe
610 615 620
Ile Leu Phe Arg Thr Pro Glu Gln Cys Pro Ser Val Val Ser Leu Leu
625 630 635 640
Ser Glu Ser Tyr Asn Pro His Val Arg Tyr Gly Ala Ala Met Ala Leu
645 650 655
Gly Ile Cys Cys Ala Gly Thr Gly Asn Lys Glu Ala Ile Asn Leu Leu
660 665 670

Glu Pro Met Thr Asn Asp Pro Val Asn Tyr Val Arg Gln Gly Ala Leu
675 680 685
Ile Ala Ser Ala Leu Ile Met Ile Gln Gln Thr Glu Ile Thr Cys Pro
690 695 700
Lys Val Asn Gln Phe Arg Gln Leu Tyr Ser Lys Val Ile Asn Asp Lys
705 710 715 720
His Asp Asp Val Met Ala Lys Phe Gly Ala Ile Leu Ala Gln Gly Ile
725 730 735
Leu Asp Ala Gly Gly His Asn Val Thr Ile Ser Leu Gln Ser Arg Thr
740 745 750
Gly His Thr His Met Pro Ser Val Val Gly Val Leu Val Phe Thr Gln
755 760 765
Phe Trp Phe Trp Phe Pro Leu Ser His Phe Leu Ser Leu Ala Tyr Thr
770 775 780
Pro Thr Cys Val Ile Gly Leu Asn Lys Asp Leu Lys Met Pro Lys Val
785 790 795 800
Gln Tyr Lys Ser Asn Cys Lys Pro Ser Thr Phe Ala Tyr Pro Ala Pro
805 810 815
Leu Glu Val Pro Lys Glu Lys Glu Lys Glu Lys Val Ser Thr Ala Val
820 825 830
Leu Ser Ile Thr Ala Lys Ala Lys Lys Lys Glu Lys Glu Lys Glu Lys
835 840 845
Lys Glu Glu Glu Lys Met Glu Val Asp Glu Ala Glu Lys Lys Glu Glu
850 855 860
Lys Glu Lys Lys Lys Glu Pro Glu Pro Asn Phe Gln Leu Leu Asp Asn
865 870 875 880
Pro Ala Arg Val Met Pro Ala Gln Leu Lys Val Leu Thr Met Pro Glu
885 890 895
Thr Cys Arg Tyr Gln Pro Phe Lys Pro Leu Ser Ile Gly Gly Ile Ile
900 905 910
Ile Leu Lys Asp Thr Ser Glu Asp Ile Glu Glu Leu Val Glu Pro Val
915 920 925
Ala Ala His Gly Pro Lys Ile Glu Glu Glu Glu Gln Glu Pro Glu Pro
930 935 940
Pro Glu Pro Phe Glu Tyr Ile Asp Asp
945 950

<210> 77
<211> 335
<212> PRT
<213> Homo Sapiens

<400> 77
Met Gly Lys Val Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg
1 5 10 15
Leu Val Thr Arg Ala Ala Phe Asn Ser Gly Lys Val Asp Ile Val Ala
20 25 30
Ile Asn Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln
35 40 45
Tyr Asp Ser Thr His Gly Lys Phe His Gly Thr Val Lys Ala Glu Asn
50 55 60
Gly Lys Leu Val Ile Asn Gly Asn Pro Ile Thr Ile Phe Gln Glu Arg
65 70 75 80
Asp Pro Ser Lys Ile Lys Trp Gly Asp Ala Gly Ala Glu Tyr Val Val
85 90 95

Glu Ser Thr Gly Val Phe Thr Thr Met Glu Lys Ala Gly Ala His Leu
100 105 110
Gln Gly Gly Ala Lys Arg Val Ile Ile Ser Ala Pro Ser Ala Asp Ala
115 120 125
Pro Met Phe Val Met Gly Val Asn His Glu Lys Tyr Asp Asn Ser Leu
130 135 140
Lys Ile Ile Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu
145 150 155 160
Ala Lys Val Ile His Asp Asn Phe Gly Ile Val Glu Gly Leu Met Thr
165 170 175
Thr Val His Ala Ile Thr Ala Thr Gln Lys Thr Val Asp Gly Pro Ser
180 185 190
Gly Lys Leu Trp Arg Asp Gly Arg Gly Ala Leu Gln Asn Ile Ile Pro
195 200 205
Ala Ser Thr Gly Ala Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu
210 215 220
Asn Gly Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Ala Asn Val
225 230 235 240
Ser Val Val Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp
245 250 255
Asp Ile Lys Lys Val Val Lys Gln Ala Ser Glu Gly Pro Leu Lys Gly
260 265 270
Ile Leu Gly Tyr Thr Glu His Gln Val Val Ser Ser Asp Phe Asn Ser
275 280 285
Asp Thr His Ser Ser Thr Phe Asp Ala Gly Ala Gly Ile Ala Leu Asn
290 295 300
Asp His Phe Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Phe Gly Tyr
305 310 315 320
Ser Asn Arg Val Val Asp Leu Met Ala His Met Ala Ser Lys Glu
325 330 335

<210> 78
<211> 117
<212> PRT
<213> Homo Sapiens

<400> 78
Met Val Gln Arg Leu Thr Tyr Arg Arg Arg Leu Ser Tyr Asn Thr Ala
1 5 10 15
Ser Asn Lys Thr Arg Leu Ser Arg Thr Pro Gly Asn Arg Ile Val Tyr
20 25 30
Leu Tyr Thr Lys Lys Val Gly Lys Ala Pro Lys Ser Ala Cys Gly Val
35 40 45
Cys Pro Gly Lys Leu Arg Gly Val Arg Pro Val Arg Pro Lys Val Leu
50 55 60
Met Arg Leu Ser Lys Thr Lys Lys His Val Ser Arg Ala Tyr Gly Gly
65 70 75 80
Ser Met Cys Ala Lys Cys Val Arg Asp Arg Ile Lys Arg Ala Phe Leu
85 90 95
Ile Glu Glu Gln Lys Ile Ile Val Lys Val Leu Lys Ala Gln Ala Gln
100 105 110
Ser Gln Lys Ala Lys
115

<210> 79

<211> 614
<212> PRT
<213> Homo Sapiens

<400> 79

Arg Ser Gly Gln Pro Arg Ala Glu Gly Leu Gly Ala Gly Ala Ala Gly
1 5 10 15
Pro Leu Arg Ala Met Ala Ala Pro Val Lys Gly Asn Arg Lys Gln Ser
20 25 30
Thr Glu Gly Asp Ala Leu Asp Pro Pro Ala Ser Pro Lys Pro Ala Gly
35 40 45
Lys Gln Asn Gly Ile Gln Asn Pro Ile Ser Leu Glu Asp Ser Pro Glu
50 55 60
Ala Gly Gly Glu Arg Glu Glu Glu Gln Glu Arg Glu Glu Glu Gln Ala
65 70 75 80
Phe Leu Val Ser Leu Tyr Lys Phe Met Lys Glu Arg His Thr Pro Ile
85 90 95
Glu Arg Val Pro His Leu Gly Phe Lys Gln Ile Asn Leu Trp Lys Ile
100 105 110
Tyr Lys Ala Val Glu Lys Leu Gly Ala Tyr Glu Leu Val Thr Gly Arg
115 120 125
Arg Leu Trp Lys Asn Val Tyr Asp Glu Leu Gly Gly Ser Pro Gly Ser
130 135 140
Thr Ser Ala Ala Thr Cys Thr Arg Arg His Tyr Glu Arg Leu Val Leu
145 150 155 160
Pro Tyr Val Arg His Leu Lys Gly Glu Asp Asp Lys Pro Leu Pro Thr
165 170 175
Ser Lys Pro Arg Lys Gln Tyr Lys Met Ala Lys Glu Asn Arg Gly Asp
180 185 190
Asp Gly Ala Thr Glu Arg Pro Lys Lys Ala Lys Glu Glu Arg Arg Met
195 200 205
Asp Gln Met Met Pro Gly Lys Thr Lys Ala Asp Ala Ala Asp Pro Ala
210 215 220
Pro Leu Pro Ser Gln Glu Pro Pro Arg Asn Ser Thr Glu Gln Gln Gly
225 230 235 240
Leu Ala Ser Gly Ser Ser Val Ser Phe Val Gly Ala Ser Gly Cys Pro
245 250 255
Glu Ala Tyr Lys Arg Leu Leu Ser Ser Phe Tyr Cys Lys Gly Thr His
260 265 270
Gly Ile Met Ser Pro Leu Ala Lys Lys Lys Leu Leu Ala Gln Val Ser
275 280 285
Lys Val Glu Ala Leu Gln Cys Gln Glu Glu Gly Cys Arg His Gly Ala
290 295 300
Glu Pro Gln Ala Ser Pro Ala Val His Leu Pro Glu Ser Pro Gln Ser
305 310 315 320
Pro Lys Gly Leu Thr Glu Asn Ser Arg His Arg Leu Thr Pro Gln Glu
325 330 335
Gly Leu Gln Ala Pro Gly Gly Ser Leu Arg Glu Glu Ala Gln Ala Gly
340 345 350
Pro Cys Pro Ala Ala Pro Ile Phe Lys Gly Cys Phe Tyr Thr His Pro
355 360 365
Thr Glu Val Leu Lys Pro Val Ser Gln His Pro Arg Asp Phe Phe Ser
370 375 380
Arg Leu Lys Asp Gly Val Leu Leu Gly Pro Pro Gly Lys Glu Gly Leu
385 390 395 400

Ser Val Lys Glu Pro Gln Leu Val Trp Gly Gly Asp Ala Asn Arg Pro
405 410 415
Ser Ala Phe His Lys Gly Gly Ser Arg Lys Gly Ile Leu Tyr Pro Lys
420 425 430
Pro Lys Ala Cys Trp Val Ser Pro Met Ala Lys Val Pro Ala Glu Ser
435 440 445
Pro Thr Leu Pro Pro Thr Phe Pro Ser Ser Pro Gly Leu Gly Ser Lys
450 455 460
Arg Ser Leu Glu Glu Glu Gly Ala Ala His Ser Gly Lys Arg Leu Arg
465 470 475 480
Ala Val Ser Pro Phe Leu Lys Glu Ala Asp Ala Lys Lys Cys Gly Ala
485 490 495
Lys Pro Ala Gly Ser Gly Leu Val Ser Cys Leu Leu Gly Pro Ala Leu
500 505 510
Gly Pro Val Pro Pro Glu Ala Tyr Arg Gly Thr Met Leu His Cys Pro
515 520 525
Leu Asn Phe Thr Gly Thr Pro Gly Pro Leu Lys Gly Gln Ala Ala Leu
530 535 540
Pro Phe Ser Pro Leu Val Ile Pro Ala Phe Pro Ala His Phe Leu Ala
545 550 555 560
Thr Ala Gly Pro Ser Pro Met Ala Ala Gly Leu Met His Phe Pro Pro
565 570 575
Thr Ser Phe Asp Ser Ala Leu Arg His Arg Leu Cys Pro Ala Ser Ser
580 585 590
Ala Trp His Ala Pro Pro Val Thr Thr Tyr Ala Ala Pro His Phe Phe
595 600 605
His Leu Asn Thr Lys Leu
610

<210> 80
<211> 114
<212> PRT
<213> Homo Sapiens

<400> 80
Met Ala Ser Val Ser Glu Leu Ala Cys Ile Tyr Ser Ala Leu Ile Leu
1 5 10 15
His Asp Asp Glu Val Thr Val Thr Glu Asp Lys Ile Asn Ala Leu Ile
20 25 30
Lys Ala Ala Gly Val Asn Val Glu Pro Phe Trp Pro Gly Leu Phe Ala
35 40 45
Lys Ala Leu Ala Asn Val Asn Ile Gly Ser Leu Ile Cys Asn Val Gly
50 55 60
Ala Gly Gly Pro Ala Pro Ala Ala Gly Ala Ala Pro Ala Gly Gly Pro
65 70 75 80
Ala Pro Ser Thr Ala Ala Ala Pro Ala Glu Glu Lys Lys Val Glu Ala
85 90 95
Lys Lys Glu Glu Ser Glu Glu Ser Asp Asp Asp Met Gly Phe Gly Leu
100 105 110
Phe Asp

<210> 81
<211> 596
<212> PRT

<213> Homo Sapiens

<400> 81

Met Arg Arg Ala His Glu Gly Arg Glu Ile Pro Ser Leu Gly Gly Ala
1   5   10   15
Arg Arg Arg Glu Val Leu Gln Ala Gly Arg Ser Gln Arg Ala Ala Gly
            20   25   30
Arg Arg Arg Arg Arg Gln Glu Leu Glu Leu Gly Val Gly Ser Gly Arg
        35   40   45
Pro Gly Gly Pro Pro Pro Gly Pro Gly Arg Arg Gly Thr Cys Ala Ala
    50   55   60
Ala Leu Pro Pro Glu Trp Pro Arg Arg Arg Thr Gly Leu Pro Arg Arg
65   70   75   80
Gly Pro Arg Pro Pro Leu Ala Met Ala Lys Trp Leu Asn Lys Tyr Phe
                85   90   95
Ser Leu Gly Asn Ser Lys Thr Lys Ser Pro Pro Gln Pro Pro Arg Pro
            100   105   110
Asp Tyr Arg Glu Gln Arg Arg Arg Gly Glu Arg Pro Ser Gln Pro Pro
        115   120   125
Gln Ala Val Pro Gln Ala Ser Ser Ala Ala Ser Ala Ser Cys Gly Pro
    130   135   140
Ala Thr Ala Ser Cys Phe Ser Ala Ser Ser Gly Ser Leu Pro Asp Asp
145   150   155   160
Ser Gly Ser Thr Ser Asp Leu Ile Arg Ala Tyr Arg Ala Gln Lys Glu
                165   170   175
Arg His Phe Gln Asp Pro Tyr Asn Gly Pro Gly Ser Ser Leu Arg Lys
            180   185   190
Leu Arg Ala Met Cys Arg Leu Asp Tyr Cys Gly Gly Ser Gly Glu Pro
        195   200   205
Gly Gly Val Gln Arg Ala Phe Ser Ala Ser Ser Ala Ser Gly Ala Ala
    210   215   220
Gly Cys Cys Cys Ala Ser Ser Gly Ala Gly Ala Ala Ala Ser Ser Ser
225   230   235   240
Ser Ser Ser Gly Ser Pro His Leu Tyr Arg Ser Ser Ser Glu Arg Arg
                245   250   255
Pro Ala Thr Pro Ala Glu Val Arg Tyr Ile Ser Pro Lys His Arg Leu
            260   265   270
Ile Lys Val Glu Ser Ala Ala Gly Gly Gly Ala Gly Asp Pro Leu Gly
        275   280   285
Gly Ala Cys Ala Gly Gly Arg Thr Trp Ser Pro Thr Ala Cys Gly Gly
    290   295   300
Lys Lys Leu Leu Asn Lys Cys Ala Ala Ser Ala Ala Glu Glu Ser Gly
305   310   315   320
Ala Gly Lys Lys Asp Lys Val Thr Ile Ala Asp Asp Tyr Ser Asp Pro
                325   330   335
Phe Asp Ala Lys Asn Asp Leu Lys Ser Lys Ala Gly Lys Gly Glu Ser
            340   345   350
Ala Gly Tyr Met Glu Pro Tyr Glu Ala Gln Arg Ile Met Thr Glu Phe
        355   360   365
Gln Arg Gln Glu Ser Val Arg Ser Gln His Lys Gly Ile Gln Leu Tyr
    370   375   380
Asp Thr Pro Tyr Glu Pro Glu Gly Gln Ser Val Asp Ser Asp Ser Glu
385   390   395   400
Ser Thr Val Ser Pro Arg Leu Arg Glu Ser Lys Leu Pro Gln Asp Asp
                405   410   415

Asp Arg Pro Ala Asp Glu Tyr Asp Gln Pro Trp Glu Trp Asn Arg Val
420 425 430
Thr Ser Pro Ala Leu Ala Ala Gln Phe Asn Gly Asn Glu Lys Arg Gln
435 440 445
Ser Ser Pro Ser Pro Ser Arg Asp Arg Arg Arg Gln Leu Arg Ala Pro
450 455 460
Gly Gly Gly Phe Lys Pro Ile Lys His Gly Ser Pro Glu Phe Cys Gly
465 470 475 480
Ile Leu Gly Glu Arg Val Asp Pro Ala Val Pro Leu Glu Lys Gln Ile
485 490 495
Trp Tyr His Gly Ala Ile Ser Arg Gly Asp Ala Glu Asn Leu Leu Arg
500 505 510
Leu Cys Lys Glu Cys Ser Tyr Leu Val Arg Asn Ser Gln Thr Ser Lys
515 520 525
His Asp Tyr Pro Leu Ser Leu Arg Ser Asn Gln Gly Phe Met His Met
530 535 540
Lys Leu Ala Lys Thr Lys Glu Lys Tyr Val Leu Gly Gln Asn Ser Pro
545 550 555 560
Pro Phe Asp Ser Val Pro Glu Val Ile His Tyr Tyr Thr Thr Arg Lys
565 570 575
Leu Pro Ile Lys Gly Ala Glu His Leu Ser Leu Leu Tyr Pro Val Ala
580 585 590
Val Arg Thr Leu
595

<210> 82
<211> 207
<212> PRT
<213> Homo Sapiens

<400> 82
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
1 5 10 15
Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30
Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45
Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60
Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95
Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
100 105 110
Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115 120 125
Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
130 135 140
Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
145 150 155 160
Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
165 170 175
His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
180 185 190

Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
195 200 205

<210> 83
<211> 429
<212> PRT
<213> Homo Sapiens

<400> 83
Glu Cys Asp Val Met Thr Tyr Val Arg Glu Thr Cys Gly Cys Cys Asp
1 5 10 15
Cys Glu Lys Arg Cys Gly Ala Leu Asp Val Val Phe Val Ile Asp Ser
20 25 30
Ser Glu Ser Ile Gly Tyr Thr Asn Phe Thr Leu Glu Lys Asn Phe Val
35 40 45
Ile Asn Val Val Asn Arg Leu Gly Ala Ile Ala Lys Asp Pro Lys Ser
50 55 60
Glu Thr Gly Thr Arg Val Gly Val Val Gln Tyr Ser His Glu Gly Thr
65 70 75 80
Phe Glu Ala Ile Gln Leu Asp Asp Glu His Ile Asp Ser Leu Ser Ser
85 90 95
Phe Lys Glu Ala Val Lys Asn Leu Glu Trp Ile Ala Gly Gly Thr Trp
100 105 110
Thr Pro Ser Ala Leu Lys Phe Ala Tyr Asp Arg Leu Ile Lys Glu Ser
115 120 125
Arg Arg Gln Lys Thr Arg Val Phe Ala Val Val Ile Thr Asp Gly Arg
130 135 140
His Asp Pro Arg Asp Asp Asp Leu Asn Leu Arg Ala Leu Cys Asp Arg
145 150 155 160
Asp Val Thr Val Thr Ala Ile Gly Ile Gly Asp Met Phe His Glu Lys
165 170 175
His Glu Ser Glu Asn Leu Tyr Ser Ile Ala Cys Asp Lys Pro Gln Gln
180 185 190
Val Arg Asn Met Thr Leu Phe Ser Asp Leu Val Ala Glu Lys Phe Ile
195 200 205
Asp Asp Met Glu Asp Val Leu Cys Pro Asp Pro Gln Ile Val Cys Pro
210 215 220
Asp Leu Pro Cys Gln Thr Glu Leu Ser Val Ala Gln Cys Thr Gln Arg
225 230 235 240
Pro Val Asp Ile Val Phe Leu Leu Asp Gly Ser Glu Arg Leu Gly Glu
245 250 255
Gln Asn Phe His Lys Ala Arg Arg Phe Val Glu Gln Val Ala Arg Arg
260 265 270
Leu Thr Leu Ala Arg Arg Asp Asp Asp Pro Leu Asn Ala Arg Val Ala
275 280 285
Leu Leu Gln Phe Gly Gly Pro Gly Glu Gln Gln Val Ala Phe Pro Leu
290 295 300
Ser His Asn Leu Thr Ala Ile His Glu Ala Leu Glu Thr Thr Gln Tyr
305 310 315 320
Leu Asn Ser Phe Ser His Val Gly Ala Gly Val Val His Ala Ile Asn
325 330 335
Ala Ile Val Arg Ser Pro Arg Gly Gly Ala Arg Arg His Ala Glu Leu
340 345 350
Ser Phe Val Phe Leu Thr Asp Gly Val Thr Gly Asn Asp Ser Leu His
355 360 365

Glu Ser Ala His Ser Met Arg Asn Glu Asn Val Val Pro Thr Val Leu
370 375 380
Ala Leu Gly Ser Asp Val Asp Met Asp Val Leu Thr Thr Leu Ser Leu
385 390 395 400
Gly Asp Arg Ala Ala Val Phe His Glu Lys Asp Tyr Asp Ser Leu Ala
405 410 415
Gln Pro Gly Phe Phe Asp Arg Phe Ile Arg Trp Ile Cys
420 425

<210> 84
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 84
Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu Glu Tyr
1 5 10 15
Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr Leu Leu
20 25 30
Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu Leu Val
35 40 45
Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser Cys Val
50 55 60
Gly Ser Phe Ile Leu Ala Val Cys Leu Arg Ile Gln Ile Asn Pro Gln
65 70 75 80
Asn Lys Ala Asp Phe Gln Gly Ile Ser Pro Glu Arg Ala Phe Ala Asp
85 90 95
Phe Leu Phe Ala Ser Thr Ile Leu His Leu Val Val Met Asn Phe Val
100 105 110
Gly

<210> 85
<211> 258
<212> PRT
<213> Homo Sapiens

<400> 85
Met Ile Asn Ile Glu Ser Met Asp Thr Asp Lys Asp Asp Pro His Gly
1 5 10 15
Arg Leu Glu Tyr Thr Glu His Gln Gly Arg Ile Lys Asn Ala Arg Glu
20 25 30
Ala His Ser Gln Ile Glu Lys Arg Arg Arg Asp Lys Met Asn Ser Phe
35 40 45
Ile Asp Glu Leu Ala Ser Leu Val Pro Thr Cys Asn Ala Met Ser Arg
50 55 60
Lys Leu Asp Lys Leu Thr Val Leu Arg Met Ala Val Gln His Met Lys
65 70 75 80
Thr Leu Arg Gly Ala Thr Asn Pro Tyr Thr Glu Ala Asn Tyr Lys Pro
85 90 95
Thr Phe Leu Ser Asp Asp Glu Leu Lys His Leu Ile Leu Arg Ala Ala
100 105 110
Asp Gly Phe Leu Phe Val Val Gly Cys Asp Arg Gly Lys Ile Leu Phe
115 120 125
Val Ser Glu Ser Val Phe Lys Ile Leu Asn Tyr Ser Gln Asn Asp Leu

130 135 140
Ile Gly Gln Ser Leu Phe Asp Tyr Leu His Pro Lys Asp Ile Ala Lys
145 150 155 160
Val Lys Glu Gln Leu Ser Ser Ser Asp Thr Ala Pro Arg Glu Arg Leu
165 170 175
Ile Asp Ala Lys Thr Gly Leu Pro Val Lys Thr Asp Ile Thr Pro Gly
180 185 190
Pro Ser Arg Leu Cys Ser Gly Ala Arg Arg Ser Phe Phe Cys Arg Met
195 200 205
Lys Cys Asn Arg Pro Ser Val Asn Val Glu Asp Lys Asn Phe Pro Ser
210 215 220
Thr Cys Ser Lys Lys Lys Ala Asp Arg Lys Ala Phe Cys Thr Ile His
225 230 235 240
Ser Thr Gly Tyr Phe Gly Ile Phe Thr Thr Arg Thr Ser Arg His Ile
245 250 255
Val Leu

<210> 86
<211> 569
<212> PRT
<213> Homo Sapiens

<400> 86
Met Ser Thr Met Val Tyr Ile Lys Glu Asp Lys Leu Glu Lys Leu Thr
1 5 10 15
Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu
20 25 30
Ala Leu Lys Asn Glu His Asn Ser Ile Leu Gln Ser Leu Leu Glu Thr
35 40 45
Leu Lys Cys Leu Lys Lys Asp Asp Glu Ser Asn Leu Val Glu Glu Lys
50 55 60
Ser Asn Met Ile Arg Lys Ser Leu Glu Met Leu Glu Leu Gly Leu Ser
65 70 75 80
Glu Ala Gln Val Met Met Ala Leu Ser Asn His Leu Asn Ala Val Glu
85 90 95
Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg Leu Cys Gln Glu
100 105 110
Asn Gln Trp Leu Arg Asp Glu Leu Ala Asn Thr Gln Gln Lys Leu Gln
115 120 125
Lys Ser Glu Gln Ser Val Ala Gln Leu Glu Glu Glu Lys Lys His Leu
130 135 140
Glu Phe Met Asn Gln Leu Lys Lys Tyr Asp Asp Asp Ile Ser Pro Ser
145 150 155 160
Glu Asp Lys Asp Thr Asp Ser Thr Lys Glu Pro Leu Asp Asp Leu Phe
165 170 175
Pro Asn Asp Glu Asp Asp Pro Gly Gln Gly Ile Gln Gln Gln His Ser
180 185 190
Ser Ala Ala Ala Ala Ala Gln Gln Gly Gly Tyr Glu Ile Pro Ala Arg
195 200 205
Leu Arg Thr Leu His Asn Leu Val Ile Gln Tyr Ala Ser Gln Gly Arg
210 215 220
Tyr Glu Val Ala Val Pro Leu Cys Lys Gln Ala Leu Glu Asp Leu Glu
225 230 235 240
Lys Thr Ser Gly His Asp His Pro Asp Val Ala Thr Met Leu Asn Ile

245 250 255
Leu Ala Leu Val Tyr Arg Asp Gln Asn Lys Tyr Lys Asp Ala Ala Asn
260 265 270
Leu Leu Asn Asp Ala Leu Ala Ile Arg Glu Lys Thr Leu Gly Lys Asp
275 280 285
His Pro Ala Val Ala Ala Thr Leu Asn Asn Leu Ala Val Leu Tyr Gly
290 295 300
Lys Arg Gly Lys Tyr Lys Glu Ala Glu Pro Leu Cys Lys Arg Ala Leu
305 310 315 320
Glu Ile Arg Glu Lys Val Leu Gly Lys Asp His Pro Asp Val Ala Lys
325 330 335
Gln Leu Asn Asn Leu Ala Leu Leu Cys Gln Asn Gln Gly Lys Tyr Glu
340 345 350
Glu Val Glu Tyr Tyr Tyr Gln Arg Ala Leu Glu Ile Tyr Gln Thr Lys
355 360 365
Leu Gly Pro Asp Asp Pro Asn Val Ala Lys Thr Lys Asn Asn Leu Ala
370 375 380
Ser Cys Tyr Leu Lys Gln Gly Lys Phe Lys Gln Ala Glu Thr Leu Tyr
385 390 395 400
Lys Glu Ile Leu Thr Arg Ala His Glu Arg Glu Phe Gly Ser Val Asp
405 410 415
Asp Glu Asn Lys Pro Ile Trp Met His Ala Glu Glu Arg Glu Glu Cys
420 425 430
Lys Gly Lys Gln Lys Asp Gly Thr Ser Phe Gly Glu Tyr Gly Gly Trp
435 440 445
Tyr Lys Ala Cys Lys Val Asp Ser Pro Thr Val Thr Thr Thr Leu Lys
450 455 460
Asn Leu Gly Ala Leu Tyr Arg Arg Gln Gly Lys Phe Glu Ala Ala Glu
465 470 475 480
Thr Leu Glu Glu Ala Ala Met Arg Ser Arg Lys Gln Gly Leu Asp Asn
485 490 495
Val His Lys Gln Arg Val Ala Glu Val Leu Asn Asp Pro Glu Asn Met
500 505 510
Glu Lys Arg Arg Ser Arg Glu Ser Leu Asn Val Asp Val Val Lys Tyr
515 520 525
Glu Ser Gly Pro Asp Gly Gly Glu Glu Val Ser Met Ser Val Glu Trp
530 535 540
Asn Gly Gly Val Ser Gly Arg Ala Ser Phe Cys Gly Lys Arg Gln Gln
545 550 555 560
Gln Gln Trp Pro Gly Arg Arg His Arg
565

<210> 87
<211> 736
<212> PRT
<213> Homo Sapiens

<400> 87
Met Glu Ala Leu Ile Pro Val Ile Asn Lys Leu Gln Asp Val Phe Asn
1 5 10 15
Thr Val Gly Ala Asp Ile Ile Gln Leu Pro Gln Ile Val Val Val Gly
20 25 30
Thr Gln Ser Ser Gly Lys Ser Ser Val Leu Glu Ser Leu Val Gly Arg
35 40 45
Asp Leu Leu Pro Arg Gly Thr Gly Ile Val Thr Arg Arg Pro Leu Ile

50 55 60
Leu Gln Leu Val His Val Thr Gln Glu Asp Lys Arg Lys Thr Thr Gly
65 70 75 80
Glu Glu Asn Gly Val Glu Ala Glu Glu Trp Gly Lys Phe Leu His Thr
85 90 95
Lys Asn Lys Leu Tyr Thr Asp Phe Asp Glu Ile Arg Gln Glu Ile Glu
100 105 110
Asn Glu Thr Glu Arg Ile Ser Gly Asn Asn Lys Gly Val Ser Pro Glu
115 120 125
Pro Ile His Leu Lys Ile Phe Ser Pro Asn Val Val Asn Leu Thr Leu
130 135 140
Val Asp Leu Pro Gly Met Thr Lys Val Pro Val Gly Asp Gln Pro Lys
145 150 155 160
Asp Ile Glu Leu Gln Ile Arg Glu Leu Ile Leu Arg Phe Ile Ser Asn
165 170 175
Pro Asn Ser Ile Ile Leu Ala Val Thr Ala Ala Asn Thr Asp Met Ala
180 185 190
Thr Ser Glu Ala Leu Lys Ile Ser Arg Glu Val Asp Pro Asp Gly Arg
195 200 205
Arg Thr Leu Ala Val Ile Thr Lys Leu Asp Leu Met Asp Ala Gly Thr
210 215 220
Asp Ala Met Asp Val Leu Met Gly Arg Val Ile Pro Val Lys Leu Gly
225 230 235 240
Ile Ile Gly Val Val Asn Arg Ser Gln Leu Asp Ile Asn Asn Lys Lys
245 250 255
Ser Val Thr Asp Ser Ile Arg Asp Glu Tyr Ala Phe Leu Gln Lys Lys
260 265 270
Tyr Pro Ser Leu Ala Asn Arg Asn Gly Thr Lys Tyr Leu Ala Arg Thr
275 280 285
Leu Asn Arg Leu Leu Met His His Ile Arg Asp Cys Leu Pro Glu Leu
290 295 300
Lys Thr Arg Ile Asn Val Leu Ala Ala Gln Tyr Gln Ser Leu Leu Asn
305 310 315 320
Ser Tyr Gly Glu Pro Val Asp Asp Lys Ser Ala Thr Leu Leu Gln Leu
325 330 335
Ile Thr Lys Phe Ala Thr Glu Tyr Cys Asn Thr Ile Glu Gly Thr Ala
340 345 350
Lys Tyr Ile Glu Thr Ser Glu Leu Cys Gly Gly Ala Arg Ile Cys Tyr
355 360 365
Ile Phe His Glu Thr Phe Gly Arg Thr Leu Glu Ser Val Asp Pro Leu
370 375 380
Gly Gly Leu Asn Thr Ile Asp Ile Leu Thr Ala Ile Arg Asn Ala Thr
385 390 395 400
Gly Pro Arg Pro Ala Leu Phe Val Pro Glu Val Ser Phe Glu Leu Leu
405 410 415
Val Lys Arg Gln Ile Lys Arg Leu Glu Glu Pro Ser Leu Arg Cys Val
420 425 430
Glu Leu Val His Glu Glu Met Gln Arg Ile Ile Gln His Cys Ser Asn
435 440 445
Tyr Ser Thr Gln Glu Leu Leu Arg Phe Pro Lys Leu His Asp Ala Ile
450 455 460
Val Glu Val Val Thr Cys Leu Leu Arg Lys Arg Leu Pro Val Thr Asn
465 470 475 480
Glu Met Val His Asn Leu Val Ala Ile Glu Leu Ala Tyr Ile Asn Thr
485 490 495

Lys His Pro Asp Phe Ala Asp Ala Cys Gly Leu Met Asn Asn Asn Ile
500 505 510
Glu Glu Gln Arg Arg Asn Arg Leu Ala Arg Glu Leu Pro Ser Ala Val
515 520 525
Ser Arg Asp Lys Ser Ser Lys Val Pro Ser Ala Leu Ala Pro Ala Ser
530 535 540
Gln Glu Pro Ser Pro Ala Ala Ser Ala Glu Ala Asp Gly Lys Leu Ile
545 550 555 560
Gln Asp Ser Arg Arg Glu Thr Lys Asn Val Ala Ser Gly Gly Gly Gly
565 570 575
Val Gly Asp Gly Val Gln Glu Pro Thr Thr Gly Asn Trp Arg Gly Met
580 585 590
Leu Lys Thr Ser Lys Ala Glu Glu Leu Leu Ala Glu Glu Lys Ser Lys
595 600 605
Pro Ile Pro Ile Met Pro Ala Ser Pro Gln Lys Gly His Ala Val Asn
610 615 620
Leu Leu Asp Val Pro Val Pro Val Ala Arg Lys Leu Ser Ala Arg Glu
625 630 635 640
Gln Arg Asp Cys Glu Val Ile Glu Arg Leu Ile Lys Ser Tyr Phe Leu
645 650 655
Ile Val Arg Lys Asn Ile Gln Asp Ser Val Pro Lys Ala Val Met His
660 665 670
Phe Leu Val Asn His Val Lys Asp Thr Leu Gln Ser Glu Leu Val Gly
675 680 685
Gln Leu Tyr Lys Ser Ser Leu Leu Asp Asp Leu Leu Thr Glu Ser Glu
690 695 700
Asp Met Ala Gln Arg Arg Lys Glu Ala Ala Asp Met Leu Lys Ala Leu
705 710 715 720
Gln Gly Ala Ser Gln Ile Ile Ala Glu Ile Arg Glu Thr His Leu Trp
725 730 735

<210> 88
<211> 37
<212> PRT
<213> Homo Sapiens

<400> 88
Met Gly Asp His Ala Trp Ser Phe Leu Lys Asp Phe Leu Ala Gly Gly
1 5 10 15
Val Ala Ala Ala Val Ser Lys Thr Ala Val Ala Pro Ile Glu Arg Val
20 25 30
Lys Leu Leu Leu Gln
35

<210> 89
<211> 1381
<212> DNA
<213> Homo Sapiens

<400> 89
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gcgttcgtgt ccgagttctc tgcaggtcnc tantttcccg gtagttcanc tgcncatgaa 120
tanaacagca atgagagccn ctcncaaaga ctttgaaaat tcactgaatc nagtgaaact 180
ctngaaaaag gatccangaa acgaaatgaa nctnaaactc tncgcgctat atnancangc 240
cnctgaanga cttgtntcat gcccnaacca ngtgtntttg acttgatcna caaggggcca 300

atgggacaca tggaatgccc ttggcancct gcccnaagaa ctgccaggca naactatgtg 360
gatttggtgt ccantttgan tccntccttg gaatcctcna atcnngtgga ncctggaaca 420
nacaggaaat ccactgggtt tgaaactctg gtggtgacct ccgaagatgg catcacaaag 480
atcatgttca accggcccaa aaagaaaaat gccataaaca ctgagatgta tcatgaaatt 540
atgcgtgcac ttaaagctgc cagcaaggat gactcaatca tcactgtttt aacaggaaat 600
ggtgactatt acagtagtgg gaatgatctg actaacttca ctgatattcc ccctggtgga 660
gtagaggaga aagctaaaaa taatgccgtt ttactgaggg aatttgtggg ctgttttata 720
gattttccta agcctctgat tgcagtggtc aatggtccag ctgtgggcat ctccgtcacc 780
ctccttgggc tattcgatgc cgtgtatgca tctgacaggg caacatttca tacaccattt 840
agtcacctag gccaaagtcc ggaaggatgc tcctcttaca cttttccgaa gataatgagc 900
ccagccaagg caacagagat gcttattttt ggaaagaagt taacagcggg agaggcatgt 960
gctcaaggac ttgttactga agttttccct gatagcactt ttcagaaaga agtctggacc 1020
aggctgaagg catttgcaaa gcttccccca aatgccttga gaatttcaaa agaggtaatc 1080
aggaaaagag agagagaaaa actacacgct gttaatgctg aagaatgcaa tgtccttcag 1140
ggaagatggc tatcagatga atgcacaaat gctgtggtga acttcttatc cagaaaatca 1200
aaactgtgat gaccactaca gcagagtaaa gcatgtccaa ggaaggatgt gctgttacct 1260
ctgatttcca gtactggaac taaataagct tcattgtgcc ttttgtagtg ctagaatatc 1320
aattacaatg atgatatttc actacagctc tgatgaataa aaagttttgt aaaacaagaa 1380
a 1381

<210> 90
<211> 298
<212> PRT
<213> Homo Sapiens

<400> 90
Thr Cys Met Pro Pro Val Phe Asp Leu Ile Lys Gly Pro Met Gly His
1 5 10 15
Met Glu Cys Pro Trp Pro Ala Arg Thr Ala Arg Asn Tyr Val Asp Leu
20 25 30
Val Ser Leu Pro Ser Leu Glu Ser Ser Asn Val Pro Gly Thr Arg Lys
35 40 45
Ser Thr Gly Phe Glu Thr Leu Val Val Thr Ser Glu Asp Gly Ile Thr
50 55 60
Lys Ile Met Phe Asn Arg Pro Lys Lys Lys Asn Ala Ile Asn Thr Glu
65 70 75 80
Met Tyr His Glu Ile Met Arg Ala Leu Lys Ala Ala Ser Lys Asp Asp
85 90 95
Ser Ile Ile Thr Val Leu Thr Gly Asn Gly Asp Tyr Tyr Ser Ser Gly
100 105 110
Asn Asp Leu Thr Asn Phe Thr Asp Ile Pro Pro Gly Gly Val Glu Glu
115 120 125
Lys Ala Lys Asn Asn Ala Val Leu Leu Arg Glu Phe Val Gly Cys Phe
130 135 140
Ile Asp Phe Pro Lys Pro Leu Ile Ala Val Val Asn Gly Pro Ala Val
145 150 155 160
Gly Ile Ser Val Thr Leu Leu Gly Leu Phe Asp Ala Val Tyr Ala Ser
165 170 175
Asp Arg Ala Thr Phe His Thr Pro Phe Ser His Leu Gly Gln Ser Pro
180 185 190
Glu Gly Cys Ser Ser Tyr Thr Phe Pro Lys Ile Met Ser Pro Ala Lys
195 200 205
Ala Thr Glu Met Leu Ile Phe Gly Lys Lys Leu Thr Ala Gly Glu Ala
210 215 220
Cys Ala Gln Leu Val Thr Glu Val Phe Pro Asp Ser Thr Phe Gln Lys

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225                 230                 235                 240
Glu Val Trp Thr Lys Leu Lys Ala Phe Ala Lys Ala Ser Pro Lys Cys
                245                 250                 255
Leu Glu Asn Phe Lys Arg Gly Asn Gln Gly Lys Glu Arg Glu Lys Asn
            260                 265                 270
Tyr Thr Pro Leu Met Leu Lys Lys Cys Asn Val Pro Ser Arg Lys Gly
        275                 280                 285
Tyr Gln Asp Glu Cys Thr Lys Cys Leu Trp
    290                 295
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<210> 91
<211> 1514
<212> DNA
<213> Homo Sapiens

<400> 91

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gccgcgcgct gtgtctccgc tgcgtccgcc gaggcccccg agtgtcaggg acaaaagcct      60
ccgcctgctc ccgcagccgg ggctcatctg ccgccgccgc cgcgctgagg agagttcgcc     120
gccgtcgccg cccgtgagga tctgagagcc atgtcggcca gcagcctctt ggagcagaga     180
ccaaaaggtc aaggaaacaa agtacaaaat ggatctgtac atcaaaagga tggattaaac     240
gatgatgatt ttgaacctta cttgagtcca caggcaaggc ccaataatgc atatactgcc     300
atgtcagatt cctacttacc cagttactac agtccctcca ttggcttctc ctattctttg     360
ggtgaagctg cttggtctac ggggggtgac acagccatgc cctacttaac ttcttatgga     420
cagctgagca acggagagcc ccacttccta ccagatgcaa tgtttgggca accaggagcc     480
ctaggtagca ctccatttct tggtcagcat ggttttaatt tctttcccag tgggattgac     540
ttctcagcat ggggaaataa cagttctcag ggacagtcta ctcagagctc tggatatagt     600
agcaattatg cttatgcacc tagctcctta ggtggagcca tgattgatgg acagtcagct     660
tttgccaatg agaccctcaa taaggctcct ggcatgaata ctatagacca agggatggca     720
gcactgaagt tgggtagcac agaagttgca agcaatgttc caaaagttgt aggttctgct     780
gttggtagcg ggtccattac tagtaacatc gtggcttcca atagtttgcc tccagccacc     840
attgctcctc caaaaccagc atcttgggct gatattgcta gcaagcctgc aaaacagcaa     900
cctaaactga agaccaagaa tggcattgca gggtcaagtc ttccgccacc cccgataaag     960
cataacatgg atattggaac ttgggataac aagggtcccg ttgcaaaagc cccctcacag    1020
gctttggttc agaatatagg tcagccaacc caggggtctc ctcagcctgt aggtcagcag    1080
gctaacaata gcccaccagt ggctcaggca tcagtagggc aacagacaca gccattgcct    1140
ccacctccac cacagcctgc ccagctttca gtccagcaac aggcagctca gccaacccgc    1200
tgggtagcac ctcggaaccg tggcagtggg ttcggtcata atggggtgga tggtaatgga    1260
gtaggacagt ctcaggctgg ttctggatct actccttcag aaccccaccc agtgttggag    1320
aagcttcggt ccattaataa ctataacccc aaagattttg actgggaaat ctgaaacatg    1380
ggcgggtttt catcattaaa gaactactct gangacgata ttcaccgttc catttaagtt    1440
ataatatttg gtggancaca anagcaatgg taacaagaga atgggatgcc ngcttatcgt    1500
ttccatgaac gggg                                                      1514
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<210> 92
<211> 407
<212> PRT
<213> Homo Sapiens

<400> 92

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Met Ser Ala Ser Ser Leu Leu Glu Gln Arg Pro Lys Gly Gln Gly Asn
 1               5                  10                  15
Lys Val Gln Asn Gly Ser Val His Gln Lys Asp Gly Leu Asn Asp Asp
            20                  25                  30
Asp Phe Glu Pro Tyr Leu Ser Pro Gln Ala Arg Pro Asn Asn Ala Tyr
        35                  40                  45
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Thr Ala Met Ser Asp Ser Tyr Leu Pro Ser Tyr Tyr Ser Pro Ser Ile
50 55 60
Gly Phe Ser Tyr Ser Leu Gly Glu Ala Ala Trp Ser Thr Gly Gly Asp
65 70 75 80
Thr Ala Met Pro Tyr Leu Thr Ser Tyr Gly Gln Leu Ser Asn Gly Glu
85 90 95
Pro His Phe Leu Pro Asp Ala Met Phe Gly Gln Pro Gly Ala Leu Gly
100 105 110
Ser Thr Pro Phe Leu Gly Gln His Gly Phe Asn Phe Phe Pro Ser Gly
115 120 125
Ile Asp Phe Ser Ala Trp Gly Asn Asn Ser Ser Gln Gly Gln Ser Thr
130 135 140
Gln Ser Ser Gly Tyr Ser Ser Asn Tyr Ala Tyr Ala Pro Ser Ser Leu
145 150 155 160
Gly Gly Ala Met Ile Asp Gly Gln Ser Ala Phe Ala Asn Glu Thr Leu
165 170 175
Asn Lys Ala Pro Gly Met Asn Thr Ile Asp Gln Gly Met Ala Ala Leu
180 185 190
Lys Leu Gly Ser Thr Glu Val Ala Ser Asn Val Pro Lys Val Val Gly
195 200 205
Ser Ala Val Gly Ser Gly Ser Ile Thr Ser Asn Ile Val Ala Ser Asn
210 215 220
Ser Leu Pro Pro Ala Thr Ile Ala Pro Pro Lys Pro Ala Ser Trp Ala
225 230 235 240
Asp Ile Ala Ser Lys Pro Ala Lys Gln Gln Pro Lys Leu Lys Thr Lys
245 250 255
Asn Gly Ile Ala Gly Ser Ser Leu Pro Pro Pro Pro Ile Lys His Asn
260 265 270
Met Asp Ile Gly Thr Trp Asp Asn Lys Gly Pro Val Ala Lys Ala Pro
275 280 285
Ser Gln Ala Leu Val Gln Asn Ile Gly Gln Pro Thr Gln Gly Ser Pro
290 295 300
Gln Pro Val Gly Gln Gln Ala Asn Asn Ser Pro Pro Val Ala Gln Ala
305 310 315 320
Ser Val Gly Gln Gln Thr Gln Pro Leu Pro Pro Pro Pro Pro Gln Pro
325 330 335
Ala Gln Leu Ser Val Gln Gln Gln Ala Ala Gln Pro Thr Arg Trp Val
340 345 350
Ala Pro Arg Asn Arg Gly Ser Gly Phe Gly His Asn Gly Val Asp Gly
355 360 365
Asn Gly Val Gly Gln Ser Gln Ala Gly Ser Gly Ser Thr Pro Ser Glu
370 375 380
Pro His Pro Val Leu Glu Lys Leu Arg Ser Ile Asn Asn Tyr Asn Pro
385 390 395 400
Lys Asp Phe Asp Trp Glu Ile
405

<210> 93
<211> 2236
<212> DNA
<213> Homo Sapiens

<400> 93
cctggcccgg tcgcggtcgc ggctctttcc agctcctggc agccgggcac ccgaaggaac 60
gggtcgtgca acgacgcagc tggacctggc ccagccatgg accgaaaagt ggcccgagaa 120

ttccggcata aggtggattt tctgattgaa aatgatgcag agaaggacta tctctatgat 180
gtgctgcgaa tgtaccacca gaccatggac gtggccgtgc tcgtgggaga cctgaagctg 240
gtcatcaatg aacccagccg tctgcctctg tttgatgcca ttcggccgct gatcccactg 300
aagcaccagg tggaatatga tcagctgacc ccccggcgct ccaggaagct gaaggaggtg 360
cgtctggacc gtctgcaccc cgaaggcctc ggcctgagtg tgcgtggtgg cctggagttt 420
ggctgtgggc tcttcatctc ccacctcatc aaaggcggtc aggcagacag cgtcgggctc 480
caggtagggg acgagatcgt ccggatcaat ggatattcca tctcctcctg tacccatgag 540
gaggtcatca acctcattcg aaccaagaaa actgtgtcca tcaaagtgag acacatcggc 600
ctgatccccg tgaaaagctc tcctgatgag cccctcactt ggcagtatgt ggatcagttt 660
gtgtcggaat ctgggggcgt gcgaggcagc ctgggctccc ctggaaatcg ggaaaacaag 720
gagaagaagg tcttcatcag cctggtaggc tcccgaggcc ttggctgcag catttccagc 780
ggccccatcc agaagcctgg catctttatc agccatgtga aacctggctc cctgtctgct 840
gaggtgggat tggagatagg ggaccagatt gtcgaagtca atggcgtcga cttctctaac 900
ctggatcaca aggaggctgt aaatgtgctg aaaaatagcc gcagcctgac catctccatt 960
gtagctgcag ctggccggga gctgttcatg acagaccggg agcggctggc agaggcgcgg 1020
cagcgtgagc tgcagcggca ggagcttctc atgcagaagc ggctggcgat ggagtccaac 1080
aagatcctcc aggagcagca ggagatggag cggcaaagga gaaaagaaat tgcccagaag 1140
gcagcagagg aaaatgagag ataccggaag gagatggaac agattgtaga ggaggaagag 1200
aagtttaaga agcaatggga agaagactgg ggctcaaagg aacagctact cttgcctaaa 1260
accatcactg ctgaggtaca cccagtaccc cttcgcaagc caaagtatga tcagggagtg 1320
gaacctgagc tcgagcccgc agatgacctg gatggaggca cggaggagca gggagagcag 1380
gatttccgga aatatgagga aggctttgac ccctactcta tgttcacccc agagcagatc 1440
atggggaagg atgtccggct cctacgcatc aagaaggagg gatccttaga cctggccctg 1500
gaaggcggtg tggactcccc cattgggaag gtggtcgttt ctgctgtgta tgagcgggga 1560
gctgctgagc ggcatggtgg cattgtgaaa ggggacgaga tcatggcaat caacggcaag 1620
attgtgacag actacaccct ggctgaggct gacgctgccc tgcagaaggc ctggaatcag 1680
ggcggggact ggatcgacct tgtggttgcc gtctgccccc caaaggagta tgacgatgag 1740
ctgaccttct tgctgaagtc caaaagggga aaccaaattc acgcgttagg aaacagtgag 1800
ctccggcccc acctcgtgaa cacaaagcct cggaccagcc ttgagagagg ccacatgaca 1860
cacaccagat ggcatccttg ggacctgaat ctatcaccca ggaatctcaa actccctttg 1920
gccctgaacc agggccagat aaggaacagc tcgggccact tttttgaagg ccaatgtgga 1980
ggaaagggag cagccagccg tttgggagaa gatctcaagg atccagactc tcattccttt 2040
cctctggccc agtgaatttg gtctctccca gctttggggg actccttcct tgaaccctaa 2100
taagacccca ctggagtctc tctctctcca tccctctcct ctgccctctg ctctaattgc 2160
tgccaggatt gtcactccaa accttactct gagctcatta ataaaataaa cagatttatt 2220
ttccagctta aaaaaa 2236

<210> 94
<211> 652
<212> PRT
<213> Homo Sapiens

<400> 94
Met Asp Arg Lys Val Ala Arg Glu Phe Arg His Lys Val Asp Phe Leu
1 5 10 15
Ile Glu Asn Asp Ala Glu Lys Asp Tyr Leu Tyr Asp Val Leu Arg Met
20 25 30
Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
35 40 45
Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
50 55 60
Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
65 70 75 80
Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
85 90 95

Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
100 105 110
Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu
115 120 125
Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser
130 135 140
Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
145 150 155 160
Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
165 170 175
Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
180 185 190
Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
195 200 205
Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
210 215 220
Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
225 230 235 240
Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
245 250 255
Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys
260 265 270
Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile
275 280 285
Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu
290 295 300
Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln
305 310 315 320
Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu
325 330 335
Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu
340 345 350
Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu
355 360 365
Lys Phe Lys Lys Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu
370 375 380
Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg
385 390 395 400
Lys Pro Lys Tyr Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp
405 410 415
Asp Leu Asp Gly Gly Thr Glu Glu Gln Gly Glu Gln Asp Phe Arg Lys
420 425 430
Tyr Glu Glu Gly Phe Asp Pro Tyr Ser Met Phe Thr Pro Glu Gln Ile
435 440 445
Met Gly Lys Asp Val Arg Leu Leu Arg Ile Lys Lys Glu Gly Ser Leu
450 455 460
Asp Leu Ala Leu Glu Gly Gly Val Asp Ser Pro Ile Gly Lys Val Val
465 470 475 480
Val Ser Ala Val Tyr Glu Arg Gly Ala Ala Glu Arg His Gly Gly Ile
485 490 495
Val Lys Gly Asp Glu Ile Met Ala Ile Asn Gly Lys Ile Val Thr Asp
500 505 510
Tyr Thr Leu Ala Glu Ala Asp Ala Ala Leu Gln Lys Ala Trp Asn Gln
515 520 525
Gly Gly Asp Trp Ile Asp Leu Val Val Ala Val Cys Pro Pro Lys Glu

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    530                 535                 540
Tyr Asp Asp Glu Leu Thr Phe Leu Leu Lys Ser Lys Arg Gly Asn Gln
545                 550                 555                 560
Ile His Ala Leu Gly Asn Ser Glu Leu Arg Pro His Leu Val Asn Thr
                565                 570                 575
Lys Pro Arg Thr Ser Leu Glu Arg Gly His Met Thr His Thr Arg Trp
            580                 585                 590
His Pro Trp Asp Leu Asn Leu Ser Pro Arg Asn Leu Lys Leu Pro Leu
        595                 600                 605
Ala Leu Asn Gln Gly Gln Ile Arg Asn Ser Ser Gly His Phe Phe Glu
    610                 615                 620
Gly Gln Cys Gly Gly Lys Gly Ala Ala Ser Arg Leu Gly Glu Asp Leu
625                 630                 635                 640
Lys Asp Pro Asp Ser His Ser Phe Pro Leu Ala Gln
                645                 650
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<210> 95
<211> 831
<212> DNA
<213> Homo Sapiens

<400> 95

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cataactggg actcgcgcgc ctgcaggtcg acactagtgg gatccaaaga attcggcacg      60
agaaaccaca atgcccagat ctcaagtaga tgaagagttt ttgaagcaaa gtttaaagga     120
aaaacnattg cagaaaacat ttagattnta tgaaatatat aatnanancc aaaanccatt     180
tgaanttaat nganccttac ctgtcntcac taaatcaggg ttntctgcgc caccnaaggg     240
cngcccancg cctgctgtgt tggcttanta ggcctnagca tangggcagn tgcaatcctt     300
tcctcctnng gcggcanatg ggcttctgga anaacccttn ccttatcccc ancgcaaggc     360
ggcccctccc ctgccctnaa aggaaacctc ntggacncag ggaatatang gccaccttga     420
agggtggact ggctatcntg gaagatcaga taccaccaag caatttggag acagttcctg     480
ttgagaataa ccacggtttc catgaaaaga cagcagcgct gaagcttgag gccgagggcg     540
aggccatgga agatgcagcc gcgccaggga acgaccgagg cggcacacag gagccagccc     600
cagtgcctgc tgagccgttt gacaacacta cctacaagaa cctgcagcat catgactaca     660
gcacgtacac cttcttagac ctcaacctcg aactctcaaa attcaggatg cctcagccct     720
cctcaggccg ggagtcacct cgacactgag ggccctcggt gtgaagatga accttccacc     780
gtcttcactg catcctggag tgcaaaaata aaatccactc aagagtcaaa a              831
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<210> 96
<211> 184
<212> PRT
<213> Homo Sapiens

<400> 96

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Arg Lys Asn Cys Arg Lys His Leu Asp Met Lys Tyr Ile Lys His Leu
 1               5                  10                  15
Leu Pro Tyr Leu Ser Ser Leu Asn Gln Gly Leu Arg His Arg Ala Ala
            20                  25                  30
Arg Leu Leu Cys Trp Leu Arg Pro His Gly Cys Asn Pro Phe Leu Leu
        35                  40                  45
Arg Met Gly Phe Trp Asn Pro Leu Ile Pro Ala Arg Arg Pro Leu Pro
    50                  55                  60
Cys Pro Arg Lys Pro Gly Arg Glu Tyr Ala Thr Leu Lys Gly Gly Leu
65                  70                  75                  80
Ala Ile Glu Asp Gln Ile Pro Pro Ser Asn Leu Glu Thr Val Pro Val
                85                  90                  95
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Glu Asn Asn His Gly Phe His Glu Lys Thr Ala Ala Leu Lys Leu Glu
100 105 110
Ala Glu Gly Glu Ala Met Glu Asp Ala Ala Ala Pro Gly Asn Asp Arg
115 120 125
Gly Gly Thr Gln Glu Pro Ala Pro Val Pro Ala Glu Pro Phe Asp Asn
130 135 140
Thr Thr Tyr Lys Asn Leu Gln His His Asp Tyr Ser Thr Tyr Thr Phe
145 150 155 160
Leu Asp Leu Asn Leu Glu Leu Ser Lys Phe Arg Met Pro Gln Pro Ser
165 170 175
Ser Gly Arg Glu Ser Pro Arg His
180

<210> 97
<211> 1008
<212> DNA
<213> Homo Sapiens

<400> 97
gcaaggtctc caagtcccag ctcaaggtcc tttcccataa cctgtgcacg gtgctgaagg 60
ttcctcatga cccagttgcc cttgaagagc acttcaggga tgatgatgag ggtccagtgt 120
ccaaccaggg ctacatgcct tatttaaaca ggttcatttt ggaaaaggtc caagacaact 180
ttgacaagat tgaattcaat aggatgtgtt ggaccctctg tgtcaaaaaa aacctcacaa 240
agaatcccct gctcattaca gaagaanatg catttaaaat atgggttatt ttcaactttt 300
tatctgagga caagtatcca ttaattattg tgtcagaana gattgaatac ctgcttaaga 360
agcttacaga agctatggga ggaggttggc agcaagaaca atttgaacat tataaaatca 420
actttgatga cagtaaaaat ggcctttctg catgggaact tattgagctt attggaaatg 480
gacagtttag caaaggcatg gaccggcaga ctgtgtctat ggcaattaat gaagtcttta 540
atgaacttat attagatgtg ttaaagcagg gttacatgat gaaaaagggc cacagacgga 600
aaaactggac tgaacgatgg tttgtactaa aacccaacat aatttcttac tatgtgagtg 660
aggatctgaa ggataagaaa ggagacattc tcttggatga aaattgctgt gtagagtcct 720
tgcctgacaa agatggaaag aaatgccttt ttctcgtaaa atgttttgat aagacttttg 780
aaatcagtgc ttcagataag aanaanaaac aggagtggat tcaagccatt cattctacta 840
ttcatctgtt gaagctgngc agccctccac canacaaaga agccnnccag cttctnaaan 900
aactccggna gaatcatctg gctgaacaag angaactgga gcgacaaatg aangaactcc 960
aagcccgcca atgaaagcaa ncagcaagag ctggaaggcc ttncggaa 1008

<210> 98
<211> 312
<212> PRT
<213> Homo Sapiens

<400> 98
Lys Val Ser Lys Ser Gln Leu Lys Val Leu Ser His Asn Leu Cys Thr
1 5 10 15
Val Leu Lys Val Pro His Asp Pro Val Ala Leu Glu Glu His Phe Arg
20 25 30
Asp Asp Asp Glu Gly Pro Val Ser Asn Gln Gly Tyr Met Pro Tyr Leu
35 40 45
Asn Arg Phe Ile Leu Glu Lys Val Gln Asp Asn Phe Asp Lys Ile Glu
50 55 60
Phe Asn Arg Met Cys Trp Thr Leu Cys Val Lys Lys Asn Leu Thr Lys
65 70 75 80
Asn Pro Leu Leu Ile Thr Glu Glu Ala Phe Lys Ile Trp Val Ile Phe
85 90 95

Asn Phe Leu Ser Glu Asp Lys Tyr Pro Leu Ile Ile Val Ser Glu Ile
100 105 110
Glu Tyr Leu Leu Lys Lys Leu Thr Glu Ala Met Gly Gly Gly Trp Gln
115 120 125
Gln Glu Gln Phe Glu His Tyr Lys Ile Asn Phe Asp Asp Ser Lys Asn
130 135 140
Gly Leu Ser Ala Trp Glu Leu Ile Glu Leu Ile Gly Asn Gly Gln Phe
145 150 155 160
Ser Lys Gly Met Asp Arg Gln Thr Val Ser Met Ala Ile Asn Glu Val
165 170 175
Phe Asn Glu Leu Ile Leu Asp Val Leu Lys Gln Gly Tyr Met Met Lys
180 185 190
Lys Gly His Arg Arg Lys Asn Trp Thr Glu Arg Trp Phe Val Leu Lys
195 200 205
Pro Asn Ile Ile Ser Tyr Tyr Val Ser Glu Asp Leu Lys Asp Lys Lys
210 215 220
Gly Asp Ile Leu Leu Asp Glu Asn Cys Cys Val Glu Ser Leu Pro Asp
225 230 235 240
Lys Asp Gly Lys Lys Cys Leu Phe Leu Val Lys Cys Phe Asp Lys Thr
245 250 255
Phe Glu Ile Ser Ala Ser Asp Lys Lys Gln Glu Trp Ile Gln Ala Ile
260 265 270
His Ser Thr Ile His Leu Leu Lys Leu Ser Pro Pro Pro Lys Glu Ala
275 280 285
Gln Leu Leu Lys Leu Arg Asn His Leu Ala Glu Gln Glu Leu Glu Arg
290 295 300
Gln Met Glu Leu Gln Ala Arg Gln
305 310

<210> 99
<211> 1009
<212> DNA
<213> Homo Sapiens

<400> 99
ggctaatgta acatactcta ccacttggtc tgaagcccag cagtatctga tggataatcc 60
aacttttgca gaagatgagg agttacaaaa tatggacaaa gaagatgcat taatttgctt 120
tgaagaacac attcgggctt tagaaaagga ggaagaagaa gaaaaacaga agagtttgct 180
gagagaaagg agacgacagc gaaaaaatag ggaatctttc cagatatttt tagatgaatt 240
acatgaacat ggacaactgc attctatgtc atcttggatg gaattgtatc caactattag 300
ttctgatatt agattcacta atatgcttgg tcagcctgga tcaactgcac ttgatctttt 360
caagttttat gttgaggatc ttaaagcacg ttatcatgac gagaagaaga taataaaaga 420
cattctaaag gataaaggat ttgtagttga agtaaacact acttttgaag attttgtggc 480
gataatcagt tcaactaaaa gatcaactac attagatgct ggaaatatca aattggcttt 540
caatagttta ctagaaaagg cagaagcccg tgaacgtgaa agagaaaaag aagaggctcg 600
gaagatgaaa cgaaaagaat ctgcatttaa gagtatgtta aaacaagctg ctcctccgat 660
agaattggat gctgtctggg aagatatccg tgagagattt gtaaaagagc cagcatttga 720
ggacataact ctagaatctg aaagaaaacg aatatttaaa gattttatgc atgtgcttga 780
gcatgaatgt cagcatcatc attcaaagaa caagaaacat tctaagaaat ctaaaaaaca 840
tcataggaaa cgttcccgct ctcgatcggg gtcagattca ngatgatgat gatagccatt 900
caaagaaaaa aagacagcga tgagaagtct cggtctgntt canaacattc ttccantngc 960
agagtctgag agaagtntaa aaagtcaaaa nagcatagan aggaaagtt 1009

<210> 100
<211> 292

<212> PRT
<213> Homo Sapiens

<400> 100
Ala Asn Val Thr Tyr Ser Thr Thr Trp Ser Glu Ala Gln Gln Tyr Leu
1 5 10 15
Met Asp Asn Pro Thr Phe Ala Glu Asp Glu Glu Leu Gln Asn Met Asp
20 25 30
Lys Glu Asp Ala Leu Ile Cys Phe Glu Glu His Ile Arg Ala Leu Glu
35 40 45
Lys Glu Glu Glu Glu Glu Lys Gln Lys Ser Leu Leu Arg Glu Arg Arg
50 55 60
Arg Gln Arg Lys Asn Arg Glu Ser Phe Gln Ile Phe Leu Asp Glu Leu
65 70 75 80
His Glu His Gly Gln Leu His Ser Met Ser Ser Trp Met Glu Leu Tyr
85 90 95
Pro Thr Ile Ser Ser Asp Ile Arg Phe Thr Asn Met Leu Gly Gln Pro
100 105 110
Gly Ser Thr Ala Leu Asp Leu Phe Lys Phe Tyr Val Glu Asp Leu Lys
115 120 125
Ala Arg Tyr His Asp Glu Lys Lys Ile Ile Lys Asp Ile Leu Lys Asp
130 135 140
Lys Gly Phe Val Val Glu Val Asn Thr Thr Phe Glu Asp Phe Val Ala
145 150 155 160
Ile Ile Ser Ser Thr Lys Arg Ser Thr Thr Leu Asp Ala Gly Asn Ile
165 170 175
Lys Leu Ala Phe Asn Ser Leu Leu Glu Lys Ala Glu Ala Arg Glu Arg
180 185 190
Glu Arg Glu Lys Glu Glu Ala Arg Lys Met Lys Arg Lys Glu Ser Ala
195 200 205
Phe Lys Ser Met Leu Lys Gln Ala Ala Pro Pro Ile Glu Leu Asp Ala
210 215 220
Val Trp Glu Asp Ile Arg Glu Arg Phe Val Lys Glu Pro Ala Phe Glu
225 230 235 240
Asp Ile Thr Leu Glu Ser Glu Arg Lys Arg Ile Phe Lys Asp Phe Met
245 250 255
His Val Leu Glu His Glu Cys Gln His His His Ser Lys Asn Lys Lys
260 265 270
His Ser Lys Lys Ser Lys Lys His His Arg Lys Arg Ser Arg Ser Arg
275 280 285
Ser Gly Ser Asp
290

<210> 101
<211> 983
<212> DNA
<213> Homo Sapiens

<400> 101
aggtgacaat agatatagaa gtacgttgat gtgcgaagat gtattttgtt ttagccagcg 60
aggaaaaaag aatcagtttg attatacatt taccaaacat taagaattta atatggtaac 120
ttttatttca gtattaaaat agcaatttta tttattactt ttttatatat agaatttgac 180
accaaatttt ggaacttaaa aagaagattc ttaaaactta caatccagat tacgatgagg 240
acctggtgca ggaagcttca tctgaagatg tcctgggcgt tcatatggtg gacaaagaca 300
cagagagaga cattgagatg aaacggcaac tacggcgact acgggagctc cacctataca 360

gcacatggaa gaagtaccaa gaggcgatga agacatcctt gggagttcca caacgtgagc 420
gtgacgaagg ctccttgggc aagccattgt gtccacccga gatactctcg gagacgttgc 480
caggctctgt gaagaaaagg gtatgctttc catcagaaga tcatctagag gagtttatag 540
cagaacatct ccctgaagca tccaatcaga gtctcctcac tgttgcccat gcagacgcag 600
gcacccaaac caacggtgac ctggaagacc tggaggagca tgggccaggg cagacagtct 660
ctgaggaagc cacagaagtt cacatgatgg agggggaccc agacacactg gccgaacttc 720
tgatcaggga tgtacttcag gagctgtcca gttacaacgg cgaggaggag gacccanagg 780
aggtgaagac atccttggga gttccacaac gtggtgacct ggaagacctg gaggagcatg 840
tgncagggca gnnnttctct gaggaagcca caggggttca catgatgcag gtggacccag 900
ccacgctggc aaagagtgac ctggaagacc tggaggagca tgtgccagag cagacagtct 960
ctgaggaagc cacaggggtt cac 983

<210> 102
<211> 230
<212> PRT
<213> Homo Sapiens

<400> 102

Met Val Asp Lys Asp Thr Glu Arg Asp Ile Glu Met Lys Arg Gln Leu
1 5 10 15
Arg Arg Leu Arg Glu Leu His Leu Tyr Ser Thr Trp Lys Lys Tyr Gln
20 25 30
Glu Ala Met Lys Thr Ser Leu Gly Val Pro Gln Arg Glu Arg Asp Glu
35 40 45
Gly Ser Leu Gly Lys Pro Leu Cys Pro Pro Glu Ile Leu Ser Glu Thr
50 55 60
Leu Pro Gly Ser Val Lys Lys Arg Val Cys Phe Pro Ser Glu Asp His
65 70 75 80
Leu Glu Glu Phe Ile Ala Glu His Leu Pro Glu Ala Ser Asn Gln Ser
85 90 95
Leu Leu Thr Val Ala His Ala Asp Ala Gly Thr Gln Thr Asn Gly Asp
100 105 110
Leu Glu Asp Leu Glu Glu His Gly Pro Gly Gln Thr Val Ser Glu Glu
115 120 125
Ala Thr Glu Val His Met Met Glu Gly Asp Pro Asp Thr Leu Ala Glu
130 135 140
Leu Leu Ile Arg Asp Val Leu Gln Glu Leu Ser Ser Tyr Asn Gly Glu
145 150 155 160
Glu Glu Asp Pro Glu Val Lys Thr Ser Leu Gly Val Pro Gln Arg Gly
165 170 175
Asp Leu Glu Asp Leu Glu Glu His Val Gly Gln Phe Ser Glu Glu Ala
180 185 190
Thr Gly Val His Met Met Gln Val Asp Pro Ala Thr Leu Ala Lys Ser
195 200 205
Asp Leu Glu Asp Leu Glu Glu His Val Pro Glu Gln Thr Val Ser Glu
210 215 220
Glu Ala Thr Gly Val His
225 230

<210> 103
<211> 843
<212> DNA
<213> Homo Sapiens

<400> 103

aatnccccgct gcaggtcgac actagtggat ccaaagaatt cggcacgagg caagttctgg 60
gagctggaca cggaccacga cctgctcatc gacgcggacg acctggcgcg gcacaatgac 120
cacgcccttt ctaccaagat gatagacagg atcttctcag gagcagtcac acgaggcaga 180
aaagtgcaga aggaagggaa gatcagctat gccgactttg tctggttttt gatctctgag 240
gaagacaaaa aaacaccgac cagcatcgag tactggttcc gctgcatgga cctggacggg 300
gacggcgccc tgtccatgtt cgagctcgag tacttctacg aggagcagtg ccgaaggctg 360
gacagcatgg ccatcgaggc cctgcccttc caggactgcc tctgccagat gctggacctg 420
gtcaagccga ggactgaagg gaagatcacg ctgcaggacc tgaagcgctg caagctggcc 480
aacgtcttct tcgacacctt cttcaacatc gagaagtncc tcgaccacga gcagaaagag 540
cagatctccc tgctcaggga cggtgacagc ggcgggcccg agctctcgga ctgggagaag 600
tnccggccga agagtncgac atcctggtgg ccgangaaac cgtggggana nccctgggga 660
agacgggttc naaggcgaac tcacccccnt gganncanaaa ctgantgcgc tgcgctcccc 720
gctgggccan aggccttctt ccaagcgcct cccgctgggg cgccgtggaa ctgttncaaa 780
ttcccctgcg gggacaagaa cttgaaaccg ctgtgannc ccccncnana acccnccccg 840
gnt 843

<210> 104
<211> 197
<212> PRT
<213> Homo Sapiens

<400> 104

Arg Cys Arg Ser Thr Leu Val Asp Pro Lys Asn Ser Ala Arg Gly Lys
1 5 10 15
Phe Trp Glu Leu Asp Thr Asp His Asp Leu Leu Ile Asp Ala Asp Asp
20 25 30
Leu Ala Arg His Asn Asp His Ala Leu Ser Thr Lys Met Ile Asp Arg
35 40 45
Ile Phe Ser Gly Ala Val Thr Arg Gly Arg Lys Val Gln Lys Glu Gly
50 55 60
Lys Ile Ser Tyr Ala Asp Phe Val Trp Phe Leu Ile Ser Glu Glu Asp
65 70 75 80
Lys Lys Thr Pro Thr Ser Ile Glu Tyr Trp Phe Arg Cys Met Asp Leu
85 90 95
Asp Gly Asp Gly Ala Leu Ser Met Phe Glu Leu Glu Tyr Phe Tyr Glu
100 105 110
Glu Gln Cys Arg Arg Leu Asp Ser Met Ala Ile Glu Ala Leu Pro Phe
115 120 125
Gln Asp Cys Leu Cys Gln Met Leu Asp Leu Val Lys Pro Arg Thr Glu
130 135 140
Gly Lys Ile Thr Leu Gln Asp Leu Lys Arg Cys Lys Leu Ala Asn Val
145 150 155 160
Phe Phe Asp Thr Phe Phe Asn Ile Glu Lys Leu Asp His Glu Gln Lys
165 170 175
Glu Gln Ile Ser Leu Leu Arg Asp Gly Asp Ser Gly Gly Pro Glu Leu
180 185 190
Ser Asp Trp Glu Lys
195

<210> 105
<211> 2264
<212> DNA
<213> Homo Sapiens

<400> 105

ctagcacaag tacacaggcc ccagccgctt cccctactgg tgtagttcct ggtaccaaat 60
atgcagtacc tgacacgtcc acttaccagt atgatgaatc ttcaggatat tactatgatc 120
cgacaacagg gctctattat gaccccaact cgcaatacta ctataattcc ttgacccagc 180
agtaccttta ctgggatggg gaaaaagaga cctacgtgcc agctgcagag tctagctccc 240
accagcagtc gggcctgcct cctgcaaaag aggggaaaga gaagaaggag aaacccaaga 300
gcaaaacagc ccagcagatt gccaaagaca tggaacgctg ggctaagagt ttgaataagc 360
agaaagaaaa ctttaaaaat agctttcagc ctgtcaattc cttgagggaa gaagaaagga 420
gagaatctgc tgcagcagac gctggctttg ctctctttga gaagaaggga gccttagctg 480
aaaggcagca gctcatccca gaattggtgc gaaatggaga tgaggagaat cccctcaaaa 540
ggggtctggt tgctgcttac agtggtgaca gtgacaatga ggaggagctg gtggagagac 600
ttgagagtga ggaagagaag ctagctgact ggaagaagat ggcctgtctg ctctgccggc 660
gccagttccc gaacaaagat gccctagtca ggcaccagca actctcagac cttcacaagc 720
aaaacatgga catctaccga cgatccaggc tgagcgagca ggagctggaa gccttggagc 780
taagggagag agagatgaaa taccgagacc gagctgcaga aagacgggag aagtacggca 840
ttccagaacc tccagagccc aagcgcaaga agcagtttga tgccggcact gtgaattacg 900
agcaacccac caaagatggc attgaccaca gtaacattgg caacaagatg ctgcaggcca 960
tgggctggcg ggaaggctct ggcttgggac gaaagtgtca aggcattacg gctcccattg 1020
aggctcaagt tcggctaaag ggagctggcc taggagccaa aggcagcgca tatggtttgt 1080
cgggcgccga ttcctacaaa gatgctgtcc ggaaagccat gtttgcccgg ttcactgaga 1140
tggagtgaga gagagagaga gagagagatg acaaggagca caagaagtgg tccatctccc 1200
gaattcgctg ttaccgcctg tctctttaag ggcatgcctt gtgctgttaa tagatcttag 1260
ggtgaaccac ttcattctgc agggttctcc ctcccacctt aaagaagttc cccttatgtg 1320
ggttgcctgg tgaatggcct tccttcccgc cagagggctt gtgaacagac cggagaggac 1380
agtggattgt ttatactcca gtgtacatag tgtaatgtag cgtgtttaca tgtgtagcct 1440
atgttgtggt ccatcagccc ctcacattcc taggggtttg agatgctgta ggtggtatgt 1500
gacaccaaag ccacctctgt catttgttgt gatgtctttt cttggcaaaa gccttgtgta 1560
tatttgtata ttacacattt gtacagaatt ttggaagatt ttcaatccaa gttgccaaat 1620
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nnnttttaa aangggncgg gggccaannn ttttccnncc ggggngggna nnaagtaaan 1740
ngtcccaaat ncccccaaaa nggagcccnn ttaaaattaa angggccgcn nttttaaaan 1800
nttcngaatn gggnaaaccc tnggggtttn ccaaatttaa ccccttgaa aaaaaanccc 1860
ctttcncaaa annggggntaa tanccaaaaa gggcccccan ccatttttgc ccnttccaaa 1920
aaaatttgnc caanccnnaa atgggnaaan ggggaatcca atttttaaa gggnnaaaan 1980
gggtttaaac nnacgggntt ccaaanttgn ttgggggaat ttttaaattc ccaannnccc 2040
aagggggnca atttagnggn ccccnaatcc cccaaaaant ggttcnnggn tnaaancngc 2100
cnnnnccnaa tttntanggg tttacttngn tttaaaaaac ccncccaaaa actcccccnn 2160
gaaccnaaaa aanaaaagga ngccattttt ngnngnaaac ttttttaann nnccnnttaa 2220
angggttaaa aaannnnnnn tnnncccnaa tttttcaaan aang 2264

<210> 106
<211> 381
<212> PRT
<213> Homo Sapiens

<400> 106
Ser Thr Ser Thr Gln Ala Pro Ala Ala Ser Pro Thr Gly Val Val Pro
1 5 10 15
Gly Thr Lys Tyr Ala Val Pro Asp Thr Ser Thr Tyr Gln Tyr Asp Glu
20 25 30
Ser Ser Gly Tyr Tyr Tyr Asp Pro Thr Thr Gly Leu Tyr Tyr Asp Pro
35 40 45
Asn Ser Gln Tyr Tyr Tyr Asn Ser Leu Thr Gln Gln Tyr Leu Tyr Trp
50 55 60
Asp Gly Glu Lys Glu Thr Tyr Val Pro Ala Ala Glu Ser Ser Ser His
65 70 75 80

Gln Gln Ser Gly Leu Pro Pro Ala Lys Glu Gly Lys Glu Lys Lys Glu
85 90 95
Lys Pro Lys Ser Lys Thr Ala Gln Gln Ile Ala Lys Asp Met Glu Arg
100 105 110
Trp Ala Lys Ser Leu Asn Lys Gln Lys Glu Asn Phe Lys Asn Ser Phe
115 120 125
Gln Pro Val Asn Ser Leu Arg Glu Glu Glu Arg Arg Glu Ser Ala Ala
130 135 140
Ala Asp Ala Gly Phe Ala Leu Phe Glu Lys Lys Gly Ala Leu Ala Glu
145 150 155 160
Arg Gln Gln Leu Ile Pro Glu Leu Val Arg Asn Gly Asp Glu Glu Asn
165 170 175
Pro Leu Lys Arg Gly Leu Val Ala Ala Tyr Ser Gly Asp Ser Asp Asn
180 185 190
Glu Glu Glu Leu Val Glu Arg Leu Glu Ser Glu Glu Glu Lys Leu Ala
195 200 205
Asp Trp Lys Lys Met Ala Cys Leu Leu Cys Arg Arg Gln Phe Pro Asn
210 215 220
Lys Asp Ala Leu Val Arg His Gln Gln Leu Ser Asp Leu His Lys Gln
225 230 235 240
Asn Met Asp Ile Tyr Arg Arg Ser Arg Leu Ser Glu Gln Glu Leu Glu
245 250 255
Ala Leu Glu Leu Arg Glu Arg Glu Met Lys Tyr Arg Asp Arg Ala Ala
260 265 270
Glu Arg Arg Glu Lys Tyr Gly Ile Pro Glu Pro Pro Glu Pro Lys Arg
275 280 285
Lys Lys Gln Phe Asp Ala Gly Thr Val Asn Tyr Glu Gln Pro Thr Lys
290 295 300
Asp Gly Ile Asp His Ser Asn Ile Gly Asn Lys Met Leu Gln Ala Met
305 310 315 320
Gly Trp Arg Glu Gly Ser Gly Leu Gly Arg Lys Cys Gln Gly Ile Thr
325 330 335
Ala Pro Ile Glu Ala Gln Val Arg Leu Lys Gly Ala Gly Leu Gly Ala
340 345 350
Lys Gly Ser Ala Tyr Gly Leu Ser Gly Ala Asp Ser Tyr Lys Asp Ala
355 360 365
Val Arg Lys Ala Met Phe Ala Arg Phe Thr Glu Met Glu
370 375 380

<210> 107
<211> 1367
<212> DNA
<213> Homo Sapiens

<400> 107
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tcgaatgcat attcttcagc gagttccacc ccacgctggg acccaagatc acctatcagg 180
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<212> PRT
<213> Homo Sapiens

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        35                  40                  45
His Pro Thr Leu Gly Pro Lys Ile Thr Tyr Gln Val Pro Glu Asp Phe
    50                  55                  60
Ile Ser Arg Glu Leu Phe Asp Thr Val Gln Val Tyr Ile Ile Thr Lys
65                  70                  75                  80
Pro Glu Leu Gln Asn Lys Leu Ile Thr Val Thr Ala Met Glu Lys Lys
                85                  90                  95
Leu Ile Gly Cys Pro Val Cys Ile Glu His Lys Lys Tyr Ser Arg Asn
            100                 105                 110
Ala Leu Leu Phe Asn Leu Gly Phe Val Cys Asp Ala Gln Ala Lys Thr
        115                 120                 125
Cys Ala Leu Glu Pro Ile Val Lys Lys Leu Ala Gly Tyr Leu Thr Thr
    130                 135                 140
Leu Glu Leu Glu Ser Ser Phe Val Ser Met Glu Glu Ser Lys Gln Lys
145                 150                 155                 160
Leu Val Pro Ile Met Thr Ile Leu Leu Glu Glu Leu Asn Ala Ser Gly
                165                 170                 175
Arg Cys Thr Leu Pro Ile Asp Glu Ser Asn Thr Ile His Leu Lys Val
            180                 185                 190
Ile Glu Gln Arg Pro Asp Pro Pro Val Ala Gln Glu Tyr Asp Val Pro
        195                 200                 205
Val Phe Thr Lys Asp Lys Glu Asp Phe Phe Asn Ser Gln Trp Asp Leu
    210                 215                 220
Thr Thr Gln Gln Ile Leu Pro Tyr Ile Asp Gly Phe Arg His Ile Gln
225                 230                 235                 240
Lys Ile Ser Ala Glu Ala Asp Val Glu Leu Asn Leu Val Arg Ile Ala
                245                 250                 255
Ile Gln Asn Leu Leu Tyr Tyr Gly Val Val Thr Leu Val Ser Ile Leu
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Gln Tyr Ser Asn Val Tyr Cys Pro Thr Pro Lys Val Gln Asp Leu Val
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Leu Ser Pro Gly Thr Thr Val Arg Asp Leu Ile Gly Arg His Pro Gln
                325                 330                 335
Gln Leu Gln His Val Asp Glu Arg Lys Leu Ile Gln Phe Gly Leu Met
            340                 345                 350
Lys Asn Leu Ile Arg Arg Leu Gln Lys Tyr Pro Val Arg Val Thr Arg
        355                 360                 365
Glu Glu Gln Ser His Pro Ala Arg Leu Tyr Thr Gly Cys His Ser Tyr
    370                 375                 380
Asp Glu Ile Cys Cys Lys Thr Gly Met Ser Tyr His Glu Leu Asp Glu
385                 390                 395                 400
Arg Leu Glu Asn Asp Pro Asn Ile Ile Ile Cys Trp Lys
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<212> DNA
<213> Homo Sapiens

<400> 109

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tgtacagcaa ccgttctgct gcctatgcca agaaaggaga ctaccagaag gcttatgagg    240
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<211> 543
<212> PRT
<213> Homo Sapiens

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35 40 45
Ala Lys Lys Gly Asp Tyr Gln Lys Ala Tyr Glu Asp Gly Cys Lys Thr
50 55 60
Val Asp Leu Lys Pro Asp Trp Gly Lys Gly Tyr Ser Arg Lys Ala Ala
65 70 75 80
Ala Leu Glu Phe Leu Asn Arg Phe Glu Glu Ala Lys Arg Thr Tyr Glu
85 90 95
Glu Gly Leu Lys His Glu Ala Asn Asn Pro Gln Leu Lys Glu Gly Leu
100 105 110
Gln Asn Met Glu Ala Arg Leu Ala Glu Arg Lys Phe Met Asn Pro Phe
115 120 125
Asn Met Pro Asn Leu Tyr Gln Lys Leu Glu Ser Asp Pro Arg Thr Arg
130 135 140
Thr Leu Leu Ser Asp Pro Thr Tyr Arg Glu Leu Ile Glu Gln Leu Arg
145 150 155 160
Asn Lys Pro Ser Asp Leu Gly Thr Lys Leu Gln Asp Pro Arg Ile Met
165 170 175
Thr Thr Leu Ser Val Leu Leu Gly Val Asp Leu Gly Ser Met Asp Glu
180 185 190
Glu Glu Glu Ile Ala Thr Pro Pro Pro Pro Pro Pro Pro Lys Lys Glu
195 200 205
Thr Lys Pro Glu Pro Met Glu Glu Asp Leu Pro Glu Asn Lys Lys Gln
210 215 220
Ala Leu Lys Glu Lys Glu Leu Gly Asn Asp Ala Tyr Lys Lys Lys Asp
225 230 235 240
Phe Asp Thr Ala Leu Lys His Tyr Asp Lys Ala Lys Glu Leu Asp Pro
245 250 255
Thr Asn Met Thr Tyr Ile Thr Asn Gln Ala Ala Val Tyr Phe Glu Lys
260 265 270
Gly Asp Tyr Asn Lys Cys Arg Glu Leu Cys Glu Lys Ala Ile Glu Val
275 280 285
Gly Arg Glu Asn Arg Glu Asp Tyr Arg Gln Ile Ala Lys Ala Tyr Ala
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Arg Ile Gly Asn Ser Tyr Phe Lys Glu Glu Lys Tyr Lys Asp Ala Ile
305 310 315 320
His Phe Tyr Asn Lys Ser Leu Ala Glu His Arg Thr Pro Asp Val Leu
325 330 335
Lys Lys Cys Gln Gln Ala Glu Lys Ile Leu Lys Glu Gln Glu Arg Leu

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Ala Tyr Ile Asn Pro Asp Leu Ala Leu Glu Glu Lys Asn Lys Gly Asn
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Glu Cys Phe Gln Lys Gly Asp Tyr Pro Gln Ala Met Lys His Tyr Thr
370 375 380
Glu Ala Ile Lys Arg Asn Pro Lys Asp Ala Lys Leu Tyr Ser Asn Arg
385 390 395 400
Ala Ala Cys Tyr Thr Lys Leu Leu Glu Phe Gln Leu Ala Leu Lys Asp
405 410 415
Cys Glu Glu Cys Ile Gln Leu Glu Pro Thr Phe Ile Lys Gly Tyr Thr
420 425 430
Arg Lys Ala Ala Ala Leu Glu Ala Met Lys Asp Tyr Thr Lys Ala Met
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Asp Val Tyr Gln Lys Ala Leu Asp Leu Asp Ser Ser Cys Lys Glu Ala
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Ala Asp Gly Tyr Gln Arg Cys Met Met Ala Gln Tyr Asn Arg His Asp
465 470 475 480
Ser Pro Glu Asp Val Lys Arg Arg Ala Met Ala Asp Pro Glu Val Gln
485 490 495
Gln Ile Met Ser Asp Pro Ala Met Arg Leu Ile Leu Glu Gln Met Gln
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Gln Lys Ile Gln Lys Leu Met Asp Val Gly Leu Ile Ala Ile Arg
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<211> 2765
<212> DNA
<213> Homo Sapiens

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<212> PRT
<213> Homo Sapiens

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35 40 45
His Gly Arg Gln Gly Ile Val Pro Gly Asn Arg Val Lys Leu Leu Ile
50 55 60
Gly Pro Met Gln Glu Thr Ala Ser Ser His Glu Gln Pro Ala Ser Gly
65 70 75 80
Leu Met Gln Gln Thr Phe Gly Gln Gln Lys Leu Tyr Gln Val Pro Asn
85 90 95
Pro Gln Ala Ala Pro Arg Asp Thr Ile Tyr Gln Val Pro Pro Ser Tyr
100 105 110
Gln Asn Gln Gly Ile Tyr Gln Val Pro Thr Gly His Gly Thr Gln Glu
115 120 125
Gln Glu Val Tyr Gln Val Pro Pro Ser Val Gln Arg Ser Ile Gly Gly
130 135 140
Thr Ser Gly Pro His Val Gly Lys Lys Val Ile Thr Pro Val Arg Thr
145 150 155 160
Gly His Gly Tyr Val Tyr Glu Tyr Pro Ser Arg Tyr Gln Lys Asp Val
165 170 175
Tyr Asp Ile Pro Pro Ser His Thr Thr Gln Gly Val Tyr Asp Ile Pro
180 185 190

Pro Ser Ser Ala Lys Gly Pro Val Phe Ser Val Pro Val Gly Glu Ile
195 200 205
Lys Pro Gln Gly Val Tyr Asp Ile Pro Pro Thr Lys Gly Val Tyr Ala
210 215 220
Ile Pro Pro Ser Ala Cys Arg Asp Glu Ala Gly Leu Arg Glu Lys Asp
225 230 235 240
Tyr Asp Phe Pro Pro Pro Met Arg Gln Ala Gly Arg Pro Asp Leu Arg
245 250 255
Pro Glu Gly Val Tyr Asp Ile Pro Pro Thr Cys Thr Lys Pro Ala Gly
260 265 270
Lys Asp Leu His Val Lys Tyr Asn Cys Asp Ile Pro Gly Ala Ala Glu
275 280 285
Pro Val Ala Arg Arg His Gln Ser Leu Ser Pro Asn His Pro Pro Pro
290 295 300
Gln Leu Gly Gln Ser Val Gly Ser Gln Asn Asp Ala Tyr Asp Val Pro
305 310 315 320
Arg Gly Val Gln Phe Leu Glu Pro Pro Ala Glu Thr Ser Glu Lys Ala
325 330 335
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340 345 350
Pro Asp Ala Lys Gly Ser Arg Asp Leu Val Asp Gly Ile Asn Arg Leu
355 360 365
Ser Phe Ser Ser Thr Gly Ser Thr Arg Ser Asn Met Ser Thr Ser Ser
370 375 380
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385 390 395 400
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405 410 415
Gln Gln Ala Leu Glu Met Gly Val Ser Ser Leu Met Ala Leu Val Thr
420 425 430
Thr Asp Trp Arg Cys Tyr Gly Tyr Met Glu Arg His Ile Asn Glu Ile
435 440 445
Arg Thr Ala Val Asp Lys Val Glu Leu Phe Leu Lys Glu Tyr Leu His
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Gln Ile Leu Ser Gln Thr Ser His Asp Leu Asn Glu Cys Ser Trp Ser
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Pro Gly Ser Leu His Leu Lys Asn Gly Pro Glu Ser Ile Met Asn Ser
565 570 575
Thr Glu Tyr Pro His Gly Gly Ser Gln Gly Gln Leu Leu His Pro Gly
580 585 590
Asp His Lys Ala Gln Ala His Asn Lys Ala Leu Pro Pro Gly Leu Ser
595 600 605
Lys Glu Gln Ala Pro Asp Cys Ser Ser Ser Asp Gly Ser Glu Arg Ser
610 615 620
Trp Met Asp Asp Tyr Asp Tyr Val His Leu Gln Gly Lys Glu Glu Phe

625 630 635 640
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645 650 655
Asn Lys Met Gln Leu Glu His His Gln Leu Ser Gln Phe Gln Leu Leu
660 665 670
Glu Gln Glu Ile Thr Lys Pro Val Glu Asn Asp Ile Ser Lys Trp Lys
675 680 685
Pro Ser Gln Ser Leu Pro Thr Thr Asn Ser Gly Val Ser Ala Gln Asp
690 695 700
Arg Gln Leu Leu Cys Phe Tyr Tyr Asp Gln Cys Glu Thr His Phe Ile
705 710 715 720
Ser Leu Leu Asn Ala Ile Asp Ala Leu Phe Ser Cys Val Ser Ser Ala
725 730 735
Gln Pro Pro Arg Ile Phe Val Ala His Ser Lys Phe Val Ile Leu Ser
740 745 750
Ala His Lys Leu Val Phe Ile Gly Asp Thr Leu Thr Arg Gln Val Thr
755 760 765
Ala Gln Asp Ile Arg Asn Lys Val Met Asn Ser Ser Asn Gln Leu Cys
770 775 780
Glu Gln Leu Lys Thr Ile Val Met Ala Thr Lys Met Ala Ala Leu His
785 790 795 800
Tyr Pro Ser Thr Thr Ala Leu Gln Glu Met Val His Gln Val Thr Asp
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<211> 3429
<212> DNA
<213> Homo Sapiens

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gagcaaaaag cgaagattgc ggaacaggtg gccagcttcc aggaagaaaa gagcaagctg 2160
gatgctgaag tgtccaaatg ggacgacagt ggcaatgaca tcattgtgct ggccaagcag 2220
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cgatgccat 3429

<210> 114
<211> 906
<212> PRT
<213> Homo Sapiens

<400> 114
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35 40 45
Asn Lys Lys Arg Gly Arg Ser Lys Lys Ala His Val Leu Ala Ala Ser
50 55 60
Val Glu Gln Ala Thr Glu Asn Phe Leu Glu Lys Gly Asp Lys Ile Ala
65 70 75 80
Lys Glu Ser Gln Phe Leu Lys Glu Glu Leu Val Ala Ala Val Glu Asp

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                 85                  90                  95
Val Arg Lys Gln Gly Asp Leu Met Lys Ala Ala Ala Gly Glu Phe Ala
            100                 105                 110
Asp Asp Pro Cys Ser Ser Val Lys Arg Gly Asn Met Val Arg Ala Ala
        115                 120                 125
Arg Ala Leu Leu Ser Ala Val Thr Arg Leu Leu Ile Leu Ala Asp Met
    130                 135                 140
Ala Asp Val Tyr Lys Leu Leu Val Gln Leu Lys Val Val Glu Asp Gly
145                 150                 155                 160
Ile Leu Lys Leu Arg Asn Ala Gly Asn Glu Gln Asp Leu Gly Ile Gln
                165                 170                 175
Tyr Lys Ala Leu Lys Pro Glu Val Asp Lys Leu Asn Ile Met Ala Ala
            180                 185                 190
Lys Arg Gln Gln Glu Leu Lys Asp Val Gly His Arg Asp Gln Met Ala
        195                 200                 205
Ala Ala Arg Gly Ile Leu Gln Lys Asn Val Pro Ile Leu Tyr Thr Ala
    210                 215                 220
Ser Gln Ala Cys Leu Gln His Pro Asp Val Ala Ala Tyr Lys Ala Asn
225                 230                 235                 240
Arg Asp Leu Ile Tyr Lys Gln Leu Gln Gln Ala Val Thr Gly Ile Ser
                245                 250                 255
Asn Ala Ala Gln Ala Thr Ala Ser Asp Asp Ala Ser Gln His Gln Gly
            260                 265                 270
Gly Gly Gly Gly Glu Leu Ala Tyr Ala Leu Asn Asn Phe Asp Lys Gln
        275                 280                 285
Ile Ile Val Asp Pro Leu Ser Phe Ser Glu Glu Arg Phe Arg Pro Ser
    290                 295                 300
Leu Glu Glu Arg Leu Glu Ser Ile Ile Ser Gly Ala Ala Leu Met Ala
305                 310                 315                 320
Asp Ser Ser Cys Thr Arg Asp Asp Arg Arg Glu Arg Ile Val Ala Glu
                325                 330                 335
Cys Asn Ala Val Arg Gln Ala Leu Gln Asp Leu Leu Ser Glu Tyr Met
            340                 345                 350
Gly Asn Ala Gly Arg Lys Glu Arg Ser Asp Ala Leu Asn Ser Ala Ile
        355                 360                 365
Asp Lys Met Thr Lys Lys Thr Arg Asp Leu Arg Arg Gln Leu Arg Lys
    370                 375                 380
Ala Val Met Asp His Val Ser Asp Ser Phe Leu Glu Thr Asn Val Pro
385                 390                 395                 400
Leu Leu Val Leu Ile Glu Ala Ala Lys Asn Gly Asn Glu Lys Glu Val
                405                 410                 415
Lys Glu Tyr Ala Gln Val Phe Arg Glu His Ala Asn Lys Leu Ile Glu
            420                 425                 430
Val Ala Asn Leu Ala Cys Ser Ile Ser Asn Asn Glu Glu Gly Val Lys
        435                 440                 445
Leu Val Arg Met Ser Ala Ser Gln Leu Glu Ala Leu Cys Pro Gln Val
    450                 455                 460
Ile Asn Ala Ala Leu Ala Leu Ala Ala Lys Pro Gln Ser Lys Leu Ala
465                 470                 475                 480
Gln Glu Asn Met Asp Leu Phe Lys Glu Gln Trp Glu Lys Gln Val Arg
                485                 490                 495
Val Leu Thr Asp Ala Val Asp Asp Ile Thr Ser Ile Asp Asp Phe Leu
            500                 505                 510
Ala Val Ser Glu Asn His Ile Leu Glu Asp Val Asn Lys Cys Val Ile
        515                 520                 525
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Ala Leu Gln Glu Lys Asp Val Asp Gly Leu Asp Arg Thr Ala Gly Ala
530 535 540
Ile Arg Gly Arg Ala Ala Arg Val Ile His Val Val Thr Ser Glu Met
545 550 555 560
Asp Asn Tyr Glu Pro Gly Val Tyr Thr Glu Lys Val Leu Glu Ala Thr
565 570 575
Lys Leu Leu Ser Asn Thr Val Met Pro Arg Phe Thr Glu Gln Val Glu
580 585 590
Ala Ala Val Glu Ala Leu Ser Ser Asp Pro Ala Gln Pro Met Asp Glu
595 600 605
Asn Glu Phe Ile Asp Ala Ser Arg Leu Val Tyr Asp Gly Ile Arg Asp
610 615 620
Ile Arg Lys Ala Val Leu Met Ile Arg Thr Pro Glu Glu Leu Asp Asp
625 630 635 640
Ser Asp Phe Glu Thr Glu Asp Phe Asp Val Arg Ser Arg Thr Ser Val
645 650 655
Gln Thr Glu Asp Asp Gln Leu Ile Ala Gly Gln Ser Ala Arg Ala Ile
660 665 670
Met Ala Gln Leu Pro Gln Glu Gln Lys Ala Lys Ile Ala Glu Gln Val
675 680 685
Ala Ser Phe Gln Glu Glu Lys Ser Lys Leu Asp Ala Glu Val Ser Lys
690 695 700
Trp Asp Asp Ser Gly Asn Asp Ile Ile Val Leu Ala Lys Gln Met Cys
705 710 715 720
Met Ile Met Met Glu Met Thr Asp Phe Thr Arg Gly Lys Gly Pro Leu
725 730 735
Lys Asn Thr Ser Asp Val Ile Ser Ala Ala Lys Lys Ile Ala Glu Ala
740 745 750
Gly Ser Arg Met Asp Lys Leu Gly Arg Thr Ile Ala Asp His Cys Pro
755 760 765
Asp Ser Ala Cys Lys Gln Asp Leu Leu Ala Tyr Leu Gln Arg Ile Ala
770 775 780
Leu Tyr Cys His Gln Leu Asn Ile Cys Ser Lys Val Lys Ala Glu Val
785 790 795 800
Gln Asn Leu Gly Gly Glu Leu Val Val Ser Gly Val Asp Ser Ala Met
805 810 815
Ser Leu Ile Gln Ala Ala Lys Asn Leu Met Asn Ala Val Val Gln Thr
820 825 830
Val Lys Ala Ser Tyr Val Ala Ser Thr Lys Tyr Gln Lys Ser Gln Gly
835 840 845
Met Ala Ser Leu Asn Leu Pro Ala Val Ser Trp Lys Met Lys Ala Pro
850 855 860
Glu Lys Lys Pro Leu Val Lys Arg Glu Lys Gln Asp Glu Thr Gln Thr
865 870 875 880
Lys Ile Lys Arg Ala Ser Gln Lys Lys His Val Asn Pro Val Gln Ala
885 890 895
Leu Ser Glu Phe Lys Ala Met Asp Ser Ile
900 905

<210> 115
<211> 1701
<212> DNA
<213> Homo Sapiens

<400> 115

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gcgggcgcca gcgagaacga gctgaagaag gcatacagaa agttagccaa ggaatatcat     120
cctgataaga atccccaaat gcaggagaca aactttaaag aaataagttt tgcatatgaa     180
gtactatcaa atcctgagaa gcgtgagtta tatgacagat acggagagca aggtcttcgg     240
gaaggcagcg gcggaggtgg gtggcatgga ttgatatttt ctctcaccgt tttttgtggg     300
ggattgttcg gcttcatggg caatcagagt agaagtcgaa atggcagaag aagaggagag     360
gacatgatgc atccactcaa agtatcttta gaagatctgt ataatggcaa gacaaccaaa     420
ctacaactta gcaagaatgt gctctgtagt gcatgcagtg gccaaggcgg aaagtctgga     480
gctgtccaaa agtgtagtgc ttgtcgaggt cgaggtgtgc gcatcatgat cagacagctg     540
gctccaggga tggtacaaca gatgcagtct gtgtgctctg attgtaatgg tgaaggagag     600
gtaattaatg aaaaagaccg ctgtaaaaaa tgtgaaggga agaaggtgat taaagaagtc     660
aagattcttg aagtccacgt agacaaaggc atgaaacatg gacagagaat tacattcact     720
ggggaagcag accaggcccc agagtggaac ccggagacat tgttcttttt gctaccagga     780
gaaaagaaca tggaggtatt tcagagagat gggaatgatt tgcacatgac atataaaata     840
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attgtggtga aatacccccc tggcaaagta attgaaccag ggtgtgttcg tgtagttcga     960
ggtgaaggga tgccgcagta tcgtaatccc tttgaaaaag gtgggcttta cataaagttt    1020
gatgtgcagt ttcctgaaaa caactggatc aacccagaca agctttctga actagaagat    1080
cttctgccat ctagaccgga agttcctaac ataattggag aaacagagga ggtagagctt    1140
caggaatttg atagcactcg aggctcagga ggtggtcaga ggcgtgaagc ctataatgat    1200
agctctgatg aagaaagcag cagccatcat ggacctggag tgcagtgtgc ccatcagtaa    1260
actctgcaaa caaattgcac aggtggattt tctttccaca tttgcctgat ttgttctcag    1320
caatccagct ggagtgtctt atcaatccag atgaactgag ggacatctgt tggtctatgt    1380
ataactttta aaattggtat agtatctaca gagtgtataa tttaaactaa ccacaaagct    1440
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cctttcacac atggattatt ataagtttca atcctggtat ctgtgcttga tttttatcag    1560
ttttgtgtag atttttatgt ttcatatttt aaatttaaat cccacattgt aaagtttgta    1620
caatttgtcc tgaagctttg tgtttggctg cacctgcata agctgctaca aatagaataa    1680
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<210> 116
<211> 415
<212> PRT
<213> Homo Sapiens

<400> 116

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            20                  25                  30
Lys Glu Tyr His Pro Asp Lys Asn Pro Gln Met Gln Glu Thr Asn Phe
        35                  40                  45
Lys Glu Ile Ser Phe Ala Tyr Glu Val Leu Ser Asn Pro Glu Lys Arg
    50                  55                  60
Glu Leu Tyr Asp Arg Tyr Gly Glu Gln Gly Leu Arg Glu Gly Ser Gly
65                  70                  75                  80
Gly Gly Gly Trp His Gly Leu Ile Phe Ser Leu Thr Val Phe Cys Gly
                85                  90                  95
Gly Leu Phe Gly Phe Met Gly Asn Gln Ser Arg Ser Arg Asn Gly Arg
            100                 105                 110
Arg Arg Gly Glu Asp Met Met His Pro Leu Lys Val Ser Leu Glu Asp
        115                 120                 125
Leu Tyr Asn Gly Lys Thr Thr Lys Leu Gln Leu Ser Lys Asn Val Leu
    130                 135                 140
Cys Ser Ala Cys Ser Gly Gln Gly Gly Lys Ser Gly Ala Val Gln Lys
```

145 150 155 160
Cys Ser Ala Cys Arg Gly Arg Gly Val Arg Ile Met Ile Arg Gln Leu
165 170 175
Ala Pro Gly Met Val Gln Gln Met Gln Ser Val Cys Ser Asp Cys Asn
180 185 190
Gly Glu Gly Glu Val Ile Asn Glu Lys Asp Arg Cys Lys Lys Cys Glu
195 200 205
Gly Lys Lys Val Ile Lys Glu Val Lys Ile Leu Glu Val His Val Asp
210 215 220
Lys Gly Met Lys His Gly Gln Arg Ile Thr Phe Thr Gly Glu Ala Asp
225 230 235 240
Gln Ala Pro Glu Trp Asn Pro Glu Thr Leu Phe Phe Leu Leu Pro Gly
245 250 255
Glu Lys Asn Met Glu Val Phe Gln Arg Asp Gly Asn Asp Leu His Met
260 265 270
Thr Tyr Lys Ile Gly Leu Val Glu Ala Leu Cys Gly Phe Gln Phe Thr
275 280 285
Leu Ser His Leu Asp Gly Arg Gln Ile Val Val Lys Tyr Pro Pro Gly
290 295 300
Lys Val Ile Glu Pro Gly Cys Val Arg Val Val Arg Gly Glu Gly Met
305 310 315 320
Pro Gln Tyr Arg Asn Pro Phe Glu Lys Gly Gly Leu Tyr Ile Lys Phe
325 330 335
Asp Val Gln Phe Pro Glu Asn Asn Trp Ile Asn Pro Asp Lys Leu Ser
340 345 350
Glu Leu Glu Asp Leu Leu Pro Ser Arg Pro Glu Val Pro Asn Ile Ile
355 360 365
Gly Glu Thr Glu Glu Val Glu Leu Gln Glu Phe Asp Ser Thr Arg Gly
370 375 380
Ser Gly Gly Gly Gln Arg Arg Glu Ala Tyr Asn Asp Ser Ser Asp Glu
385 390 395 400
Glu Ser Ser Ser His His Gly Pro Gly Val Gln Cys Ala His Gln
405 410 415

<210> 117
<211> 1821
<212> DNA
<213> Homo Sapiens

<400> 117
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aatgaacaaa atggttatca accacttgga gaagttgttt gtgacaaacg atgcagcaac 240
tattttaaga gaactagaag tacagcatcc tgctgcaaaa atgattgtaa tggcttctca 300
tatgcaagag caagaagttg gagatggcac aaactttgtt ctggtatttg ctggagctct 360
cctggaatta gctgaagaac ttctgaggat tggcctgtca gtttcagagg tcatagaagg 420
ttatgaaata gcctgcagaa aagctcatga gattcttcct aatttggtat gttgttctgc 480
aaaaaacctt cgagatattg atgaagtctc atctctactt cgtacctcca taatgagtaa 540
acaatatggt aatgaagtat ttctggccaa gcttattgct caggcatgcg tatctatttt 600
tcctgattcc ggccatttca atgttgataa catcagagtt tgtaaaattc tgggctctgg 660
tatcagttcc tcttcagtat tgcatggcat ggtttttaag aaggaaaccg aaggtgatgt 720
aacatctgtc aaagatgcaa aaatagcagt gtactcttgt ccttttgatg gcatgataac 780
agaaactaag ggaacagtgt tgataaagac tgctgaagaa ttgatgaatt ttagtaaggg 840
agaagaaaac ctcatggatg cacaagtcaa agctattgct gatactggtg caaatgtcgt 900

agtaacaggt ggcaaagtgg cagacatggc tcttcattat gcaaataaat ataatatcat 960
gttagtgagg ctaaactcaa aatgggatct ccgaagactt tgtaaaactg ttggtgctac 1020
agctcttcct agattgacac ctcctgtcct tgaagaaatg ggacactgtg acagtgttta 1080
cctctcagaa gttggagata ctcaggtggt ggtttttaag catgaaaagg aagatggcgc 1140
catttctacc atagtacttc gaggctctac agacaatctg atggatgaca tagaaagggt 1200
agtagacgat ggtgttaata ctttcaaagt tcttacaagg gataaacgtc ttgtacccgg 1260
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gcttaatttt tactgtaggt gaaggctgta tttgtagtag tactcaagaa tcacctgatg 1740
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aataaacata ttgttactgt c 1821

<210> 118
<211> 548
<212> PRT
<213> Homo Sapiens

<400> 118

Met Ala Leu His Val Pro Lys Ala Pro Gly Phe Ala Gln Met Leu Lys
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Glu Gly Ala Lys His Phe Ser Gly Leu Glu Glu Ala Val Tyr Arg Asn
20 25 30
Ile Gln Ala Cys Lys Glu Leu Ala Gln Thr Thr Arg Thr Ala Tyr Gly
35 40 45
Pro Lys Gly Met Asn Lys Met Val Ile Asn His Leu Glu Lys Leu Phe
50 55 60
Val Thr Asn Asp Ala Ala Thr Ile Leu Arg Glu Leu Glu Val Gln His
65 70 75 80
Pro Ala Ala Lys Met Ile Val Met Ala Ser His Met Gln Glu Gln Glu
85 90 95
Val Gly Asp Gly Thr Asn Phe Val Leu Val Phe Ala Gly Ala Leu Leu
100 105 110
Glu Leu Ala Glu Glu Leu Leu Arg Ile Gly Leu Ser Val Ser Glu Val
115 120 125
Ile Glu Gly Tyr Glu Ile Ala Cys Arg Lys Ala His Glu Ile Leu Pro
130 135 140
Asn Leu Val Cys Cys Ser Ala Lys Asn Leu Arg Asp Ile Asp Glu Val
145 150 155 160
Ser Ser Leu Leu Arg Thr Ser Ile Met Ser Lys Gln Tyr Gly Asn Glu
165 170 175
Val Phe Leu Ala Lys Leu Ile Ala Gln Ala Cys Val Ser Ile Phe Pro
180 185 190
Asp Ser Gly His Phe Asn Val Asp Asn Ile Arg Val Cys Lys Ile Leu
195 200 205
Gly Ser Gly Ile Ser Ser Ser Ser Val Leu His Gly Met Val Phe Lys
210 215 220
Lys Glu Thr Glu Gly Asp Val Thr Ser Val Lys Asp Ala Lys Ile Ala
225 230 235 240
Val Tyr Ser Cys Pro Phe Asp Gly Met Ile Thr Glu Thr Lys Gly Thr
245 250 255

Val Leu Ile Lys Thr Ala Glu Glu Leu Met Asn Phe Ser Lys Gly Glu
260 265 270
Glu Asn Leu Met Asp Ala Gln Val Lys Ala Ile Ala Asp Thr Gly Ala
275 280 285
Asn Val Val Val Thr Gly Gly Lys Val Ala Asp Met Ala Leu His Tyr
290 295 300
Ala Asn Lys Tyr Asn Ile Met Leu Val Arg Leu Asn Ser Lys Trp Asp
305 310 315 320
Leu Arg Arg Leu Cys Lys Thr Val Gly Ala Thr Ala Leu Pro Arg Leu
325 330 335
Thr Pro Pro Val Leu Glu Glu Met Gly His Cys Asp Ser Val Tyr Leu
340 345 350
Ser Glu Val Gly Asp Thr Gln Val Val Val Phe Lys His Glu Lys Glu
355 360 365
Asp Gly Ala Ile Ser Thr Ile Val Leu Arg Gly Ser Thr Asp Asn Leu
370 375 380
Met Asp Asp Ile Glu Arg Val Val Asp Asp Gly Val Asn Thr Phe Lys
385 390 395 400
Val Leu Thr Arg Asp Lys Arg Leu Val Pro Gly Gly Gly Ala Thr Glu
405 410 415
Ile Glu Leu Ala Lys Gln Ile Thr Ser Tyr Gly Glu Thr Cys Pro Gly
420 425 430
Leu Glu Gln Tyr Ala Ile Lys Lys Phe Ala Glu Ala Phe Glu Ala Ile
435 440 445
Pro Arg Ala Leu Ala Glu Asn Ser Gly Val Lys Ala Asn Glu Val Ile
450 455 460
Ser Lys Leu Tyr Ala Val His Gln Glu Gly Asn Lys Asn Val Gly Leu
465 470 475 480
Asp Ile Glu Ala Glu Val Pro Ala Val Lys Asp Met Leu Glu Ala Gly
485 490 495
Ile Leu Asp Thr Tyr Leu Gly Lys Tyr Trp Ala Ile Lys Leu Ala Thr
500 505 510
Asn Ala Ala Val Thr Val Leu Arg Val Asp Gln Ile Ile Met Ala Lys
515 520 525
Pro Ala Gly Gly Pro Lys Pro Pro Ser Gly Lys Lys Asp Trp Asp Asp
530 535 540
Asp Gln Asn Asp
545

<210> 119
<211> 1321
<212> DNA
<213> Homo Sapiens

<400> 119
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ctggtagaca gttactggac gaagtagaag tggcgactga acccgccggt tcccggatag 120
tccaggagaa ggtgttcaag ggcttggacc tccttgagaa ggctgccgaa atgttatcgc 180
agctcgactt gttcagccga aatgaagatt tggaagagat tgcttccacc gacctgaagt 240
accttttggt gccagcgttt caaggagccc tcaccatgaa acaagtcaac cccagcaagc 300
gtctagatca tttgcagcgg gctcgagaac actttataaa ctacttaact cagtgccatt 360
gctatcatgt ggcagagttt gagctgccca aaaccatgaa caactctgct gaaaatcaca 420
ctgccaattc ctccatggct tatcctagtc tcgttgctat ggcatctcaa agacaggcta 480
aaatacagag atacaagcag aagaaggagt tggagcatag gttgtctgca atgaaatctg 540
ctgtggaaag tggtcaagca gatgatgagc gtgttcgtga atattatctt cttcaccttc 600

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agaggtggat tgatatcagc ttagaagaga ttgagagcat tgaccaggaa ataaagatcc      660
tgagagaaag agactcttca agagaggcat caacttctaa ctcatctcgc caggagaggc      720
ctccagtgaa acccttcatt ctcactcgga acatggctca agccaaagta tttggagctg      780
gttatccaag tctgccaact atgacggtga gtgactggta tgagcaacat cggaaatatg      840
gagcattacc ggatcaggga atagccaagg cagcaccaga ggaattcaga aaagcagctc      900
agcaacagga agaacaagaa gaaaaggagg aagaggatga tgaacaaaca ctccacagag      960
cccgggagtg ggatgactgg aaggacaccc atcctagggg ctatgggaac cgacagaaca     1020
tgggctgatc ttcccacaac accacaggac tgcagggtgc acaactccct gccaaggaaa     1080
accatgcagt cctcccctcc ctggtctcct gcttcagctc tgtacaacga gggcaaagat     1140
gctaaatctt gctttgcatt cagtaaagtg tcaagtgatt aagtgtgtat ttgtacccta     1200
gatgatatga accagcagtc ttgttttggc atcatcctca tcatgttgta ttccagcttc     1260
ttaagtggaa ggaaaagagt gctgagaaat ggctctgtat aatctatggc tatccgaatt     1320
c                                                                      1321
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<210> 120
<211> 339
<212> PRT
<213> Homo Sapiens

<400> 120

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Met Ala Ala Glu Asp Glu Leu Gln Leu Pro Arg Leu Pro Glu Leu Phe
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Glu Thr Gly Arg Gln Leu Leu Asp Glu Val Glu Val Ala Thr Glu Pro
            20                  25                  30
Ala Gly Ser Arg Ile Val Gln Glu Lys Val Phe Lys Gly Leu Asp Leu
        35                  40                  45
Leu Glu Lys Ala Ala Glu Met Leu Ser Gln Leu Asp Leu Phe Ser Arg
    50                  55                  60
Asn Glu Asp Leu Glu Glu Ile Ala Ser Thr Asp Leu Lys Tyr Leu Leu
65                  70                  75                  80
Val Pro Ala Phe Gln Gly Ala Leu Thr Met Lys Gln Val Asn Pro Ser
                85                  90                  95
Lys Arg Leu Asp His Leu Gln Arg Ala Arg Glu His Phe Ile Asn Tyr
            100                 105                 110
Leu Thr Gln Cys His Cys Tyr His Val Ala Glu Phe Glu Leu Pro Lys
        115                 120                 125
Thr Met Asn Asn Ser Ala Glu Asn His Thr Ala Asn Ser Ser Met Ala
    130                 135                 140
Tyr Pro Ser Leu Val Ala Met Ala Ser Gln Arg Gln Ala Lys Ile Gln
145                 150                 155                 160
Arg Tyr Lys Gln Lys Lys Glu Leu Glu His Arg Leu Ser Ala Met Lys
                165                 170                 175
Ser Ala Val Glu Ser Gly Gln Ala Asp Asp Glu Arg Val Arg Glu Tyr
            180                 185                 190
Tyr Leu Leu His Leu Gln Arg Trp Ile Asp Ile Ser Leu Glu Glu Ile
        195                 200                 205
Glu Ser Ile Asp Gln Glu Ile Lys Ile Leu Arg Glu Arg Asp Ser Ser
    210                 215                 220
Arg Glu Ala Ser Thr Ser Asn Ser Ser Arg Gln Glu Arg Pro Pro Val
225                 230                 235                 240
Lys Pro Phe Ile Leu Thr Arg Asn Met Ala Gln Ala Lys Val Phe Gly
                245                 250                 255
Ala Gly Tyr Pro Ser Leu Pro Thr Met Thr Val Ser Asp Trp Tyr Glu
            260                 265                 270
Gln His Arg Lys Tyr Gly Ala Leu Pro Asp Gln Gly Ile Ala Lys Ala
```

```
        275             280                 285
Ala Pro Glu Glu Phe Arg Lys Ala Ala Gln Gln Gln Glu Glu Gln Glu
    290                 295                 300
Glu Lys Glu Glu Glu Asp Asp Glu Gln Thr Leu His Arg Ala Arg Glu
305                 310                 315                 320
Trp Asp Asp Trp Lys Asp Thr His Pro Arg Gly Tyr Gly Asn Arg Gln
                325                 330                 335
Asn Met Gly
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<210> 121
<211> 2965
<212> DNA
<213> Homo Sapiens

<400> 121

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ccttagcgtt cctctctggg cggcggcggc ggcggctcgg ttgacgcctc ctccgccagc     120
tgagcccgcg ggagcccagg acgccgcttc cccgcccatc cccgctcccc gaggccggcc     180
gcctggtcat ggcgcagccg ggcccggctt cccagcctga cgtttctctt cagcaacggg     240
tagcagaatt ggaaaaaatt aatgcagaat tttacgtgc acaacagcag cttgaacaag      300
aatttaatca aaagagagca aaatttaagg agttatattt ggctaaagag gaggatctga     360
agaggcaaaa tgcagtatta caagctgcac aagatgattt gggacacctt cgaacccagc     420
tgtgggaagc tcaagcagag atggagaata ttaaggcgat tgccacagtc tctgagaaca     480
ccaagcaaga agctatagat gaagtgaaaa gacagtggag agaagaagtt gcttcacttc     540
aggctgttat gaaagaaaca gttcgtgact atgagcacca gttccacctt aggctggagc     600
aggagcgaac acagtgggca cagtatagag aatacgcaga gagggaaata gctgatttaa     660
gaagaaggct gtctgaaggt caagaggagg aaaatttaga aaatgaaatg aaaaaggccc     720
aagaggatgc tgagaaactt cggtccgttg tgatgccaat ggaaaaggaa attgcagctt     780
tgaaggataa actgacagag gctgaagaca aaattaaaga gctggaggcc tcaaaggtta     840
aagaactgaa tcattatctg gaagctgaga aatcttgtag gactgatcta gagatgtatg     900
tagctgtttt gaatactcag aaatctgttc tacaggaaga tgctgagaaa ctgcggaaag     960
aattgcatga agtttgccat ctcttggagc aagagcgaca acaacacaac cagttaaaac    1020
atacgtggca gaaggccaat gaccagtttc tggaatctca gcgtttactg atgagagaca    1080
tgcagcgaat ggagattgtg ctaacttcag aacagctccg acaagttgaa gaactgaaga    1140
agaaagatca ggaggatgat gaacaacaaa gactcaataa gagaaaggat cacaaaaaag    1200
cagatgttga ggaagaaata aaaataccag tagtgtgtgc tttaactcaa gaagaatctt    1260
cagcccagtt atcaaatgaa gaggagcatt tagacagcac ccgtggctca gttcattcct    1320
tagatgcagg cttgctgttg ccatctggag atcctttcag taaatcggac aatgacatgt    1380
ttaaagatgg actcaggaga gcacagtcta cagacagctt gggaacctcg ggctcattgc    1440
aatccaaagc tttaggctat aactacaaag caaaatctgc tggaaacctg gacgagtcag    1500
attttggacc actggtagga gcagattcag tgtctgagaa ctttgatact gcatcccttg    1560
ggtcactcca gatgccaagt gggtttatgt taaccaaaga tcaggaaaga gcaatcaagg    1620
cgatgacacc agaacaagaa gagacagcgt ccctcctctc cagcgttacc cagggcatgg    1680
agagtgccta tgtgtcccct agtggttatc gtttagttag tgaaacagaa tggaatctct    1740
tgcagaaaga ggtacataat gctggaaata aacttggtag acgttgtgat atgtgttcca    1800
attacgaaaa acagttacaa ggaattcaga ttcaggaggc tgaaacgaga gaccaggtga    1860
aaaaactaca gctgatgcta aggcaagcta atgaccagtt agagaagaca atgaaagata    1920
agcaggagct ggaagacttc ataaagcaaa gcagcgaaga ttcgagtcac cagatctctg    1980
cactcgtcct aagagcccag gcctccgaga tcttacttga agagttacag caggggcttt    2040
cccaggcaaa gagggatgtt caggaacaga tggcggtgct gatgcagtca cgggaacagg    2100
tttcagaaga gctggtgagg ttacagaaag ataatgacag tctccaggga aagcacagcc    2160
tgcatgtgtc attacagcaa gcagaagact tcatcctccc agacactaca gaggcactgc    2220
gggagttggt attaaaatac cgtgaggaca tcattaatgt gcggacagca gcagaccacg    2280
tagaagaaaa gctgaaggct gagatacttt tcctaaaaga gcagatccaa gcagaacagt    2340
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gtttaaaaga aaatcttgaa gaaactctgc aactagaaat agaaaactgc aaggaggaaa 2400
tagcttctat ttctagccta aaagctgaat tagaaagaat aaaagtggaa aaaggacagt 2460
tggagtccac attaagagag aagtctcaac agcttgagag tcttcaggaa ataaagatca 2520
gtttggaaga gcagttaaag aaagagactg ctgctaaggc taccgttgaa cagctaatgt 2580
ttgaagagaa gaacaaagct cagagattac agacagaatt agatgtcagt gagcaagtcc 2640
agagagattt tgtaaagctt tcacagaccc ttcaggtgca gttagagcgg atccggcaag 2700
ctgactcctt ggagagaatc cgggcaattc tgaatgatac taaactgaca gacattaacc 2760
agcttcctga gacatgacac cctcatggca ggattctagc ctgcactttg ggtttttaac 2820
tcatctttag agcaacagta attattattt aactcttaac tgaagaaaga gaagtcacaa 2880
caaaaggaag actggagaaa tgcttacttc tagagggaga agactgtgcg gcacaggaaa 2940
cagcaaacag tggggtgatc tgcag 2965

<210> 122
<211> 862
<212> PRT
<213> Homo Sapiens

<400> 122

Met Ala Gln Pro Gly Pro Ala Ser Gln Pro Asp Val Ser Leu Gln Gln
1 5 10 15
Arg Val Ala Glu Leu Glu Lys Ile Asn Ala Glu Phe Leu Arg Ala Gln
20 25 30
Gln Gln Leu Glu Gln Glu Phe Asn Gln Lys Arg Ala Lys Phe Lys Glu
35 40 45
Leu Tyr Leu Ala Lys Glu Glu Asp Leu Lys Arg Gln Asn Ala Val Leu
50 55 60
Gln Ala Ala Gln Asp Asp Leu Gly His Leu Arg Thr Gln Leu Trp Glu
65 70 75 80
Ala Gln Ala Glu Met Glu Asn Ile Lys Ala Ile Ala Thr Val Ser Glu
85 90 95
Asn Thr Lys Gln Glu Ala Ile Asp Glu Val Lys Arg Gln Trp Arg Glu
100 105 110
Glu Val Ala Ser Leu Gln Ala Val Met Lys Glu Thr Val Arg Asp Tyr
115 120 125
Glu His Gln Phe His Leu Arg Leu Glu Gln Glu Arg Thr Gln Trp Ala
130 135 140
Gln Tyr Arg Glu Tyr Ala Glu Arg Glu Ile Ala Asp Leu Arg Arg Arg
145 150 155 160
Leu Ser Glu Gly Gln Glu Glu Glu Asn Leu Glu Asn Glu Met Lys Lys
165 170 175
Ala Gln Glu Asp Ala Glu Lys Leu Arg Ser Val Val Met Pro Met Glu
180 185 190
Lys Glu Ile Ala Ala Leu Lys Asp Lys Leu Thr Glu Ala Glu Asp Lys
195 200 205
Ile Lys Glu Leu Glu Ala Ser Lys Val Lys Glu Leu Asn His Tyr Leu
210 215 220
Glu Ala Glu Lys Ser Cys Arg Thr Asp Leu Glu Met Tyr Val Ala Val
225 230 235 240
Leu Asn Thr Gln Lys Ser Val Leu Gln Glu Asp Ala Glu Lys Leu Arg
245 250 255
Lys Glu Leu His Glu Val Cys His Leu Leu Glu Gln Glu Arg Gln Gln
260 265 270
His Asn Gln Leu Lys His Thr Trp Gln Lys Ala Asn Asp Gln Phe Leu
275 280 285
Glu Ser Gln Arg Leu Leu Met Arg Asp Met Gln Arg Met Glu Ile Val

290 295 300
Leu Thr Ser Glu Gln Leu Arg Gln Val Glu Glu Leu Lys Lys Lys Asp
305 310 315 320
Gln Glu Asp Asp Glu Gln Gln Arg Leu Asn Lys Arg Lys Asp His Lys
325 330 335
Lys Ala Asp Val Glu Glu Glu Ile Lys Ile Pro Val Val Cys Ala Leu
340 345 350
Thr Gln Glu Glu Ser Ser Ala Gln Leu Ser Asn Glu Glu Glu His Leu
355 360 365
Asp Ser Thr Arg Gly Ser Val His Ser Leu Asp Ala Gly Leu Leu Leu
370 375 380
Pro Ser Gly Asp Pro Phe Ser Lys Ser Asp Asn Asp Met Phe Lys Asp
385 390 395 400
Gly Leu Arg Arg Ala Gln Ser Thr Asp Ser Leu Gly Thr Ser Gly Ser
405 410 415
Leu Gln Ser Lys Ala Leu Gly Tyr Asn Tyr Lys Ala Lys Ser Ala Gly
420 425 430
Asn Leu Asp Glu Ser Asp Phe Gly Pro Leu Val Gly Ala Asp Ser Val
435 440 445
Ser Glu Asn Phe Asp Thr Ala Ser Leu Gly Ser Leu Gln Met Pro Ser
450 455 460
Gly Phe Met Leu Thr Lys Asp Gln Glu Arg Ala Ile Lys Ala Met Thr
465 470 475 480
Pro Glu Gln Glu Glu Thr Ala Ser Leu Leu Ser Ser Val Thr Gln Gly
485 490 495
Met Glu Ser Ala Tyr Val Ser Pro Ser Gly Tyr Arg Leu Val Ser Glu
500 505 510
Thr Glu Trp Asn Leu Leu Gln Lys Glu Val His Asn Ala Gly Asn Lys
515 520 525
Leu Gly Arg Arg Cys Asp Met Cys Ser Asn Tyr Glu Lys Gln Leu Gln
530 535 540
Gly Ile Gln Ile Gln Glu Ala Glu Thr Arg Asp Gln Val Lys Lys Leu
545 550 555 560
Gln Leu Met Leu Arg Gln Ala Asn Asp Gln Leu Glu Lys Thr Met Lys
565 570 575
Asp Lys Gln Glu Leu Glu Asp Phe Ile Lys Gln Ser Ser Glu Asp Ser
580 585 590
Ser His Gln Ile Ser Ala Leu Val Leu Arg Ala Gln Ala Ser Glu Ile
595 600 605
Leu Leu Glu Glu Leu Gln Gln Gly Leu Ser Gln Ala Lys Arg Asp Val
610 615 620
Gln Glu Gln Met Ala Val Leu Met Gln Ser Arg Glu Gln Val Ser Glu
625 630 635 640
Glu Leu Val Arg Leu Gln Lys Asp Asn Asp Ser Leu Gln Gly Lys His
645 650 655
Ser Leu His Val Ser Leu Gln Gln Ala Glu Asp Phe Ile Leu Pro Asp
660 665 670
Thr Thr Glu Ala Leu Arg Glu Leu Val Leu Lys Tyr Arg Glu Asp Ile
675 680 685
Ile Asn Val Arg Thr Ala Ala Asp His Val Glu Glu Lys Leu Lys Ala
690 695 700
Glu Ile Leu Phe Leu Lys Glu Gln Ile Gln Ala Glu Gln Cys Leu Lys
705 710 715 720
Glu Asn Leu Glu Glu Thr Leu Gln Leu Glu Ile Glu Asn Cys Lys Glu
725 730 735

Glu Ile Ala Ser Ile Ser Ser Leu Lys Ala Glu Leu Glu Arg Ile Lys
740 745 750
Val Glu Lys Gly Gln Leu Glu Ser Thr Leu Arg Glu Lys Ser Gln Gln
755 760 765
Leu Glu Ser Leu Gln Glu Ile Lys Ile Ser Leu Glu Glu Gln Leu Lys
770 775 780
Lys Glu Thr Ala Ala Lys Ala Thr Val Glu Gln Leu Met Phe Glu Glu
785 790 795 800
Lys Asn Lys Ala Gln Arg Leu Gln Thr Glu Leu Asp Val Ser Glu Gln
805 810 815
Val Gln Arg Asp Phe Val Lys Leu Ser Gln Thr Leu Gln Val Gln Leu
820 825 830
Glu Arg Ile Arg Gln Ala Asp Ser Leu Glu Arg Ile Arg Ala Ile Leu
835 840 845
Asn Asp Thr Lys Leu Thr Asp Ile Asn Gln Leu Pro Glu Thr
850 855 860

<210> 123
<211> 544
<212> DNA
<213> Homo Sapiens

<400> 123
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ttttaaggga agacaggatt caactttgga aacctccata tacagatgaa aataaaaaag 120
ttggtttggc attaaaggac cttgctaagc agtactctga cagactagaa tgctgtgaaa 180
atgaagtaga aaaggtaata gaagaaatac gttgcaaggc aattgagcgt ggaacaggaa 240
atgacaatta tagaacaacg ggaattgcta caatcgaggt gtttttacca ccaagactaa 300
aaaaagatag gaaaaacttg ttggagaccc gattgcacat cactggcaga gaactgaggt 360
ccaaaatagc tgaaaccttt ggacttcaag aanattatat caaaattgtc ataaataaga 420
agcaactacn actagggaaa acccttgaag ancaaggcgt ggctcacaat gtgaaagcga 480
tggtgcttga actaaaacaa tctgaagagg acgcgaggaa aaacttccag ttagaggaag 540
agga 544

<210> 124
<211> 178
<212> PRT
<213> Homo Sapiens

<400> 124
Glu Trp Arg Gly Ala Gly Met Ala Gln Lys Lys Tyr Leu Gln Ala Lys
1 5 10 15
Leu Thr Gln Phe Leu Arg Glu Asp Arg Ile Gln Leu Trp Lys Pro Pro
20 25 30
Tyr Thr Asp Glu Asn Lys Lys Val Gly Leu Ala Leu Lys Asp Leu Ala
35 40 45
Lys Gln Tyr Ser Asp Arg Leu Glu Cys Cys Glu Asn Glu Val Glu Lys
50 55 60
Val Ile Glu Glu Ile Arg Cys Lys Ala Ile Glu Arg Gly Thr Gly Asn
65 70 75 80
Asp Asn Tyr Arg Thr Thr Gly Ile Ala Thr Ile Glu Val Phe Leu Pro
85 90 95
Pro Arg Leu Lys Lys Asp Arg Lys Asn Leu Leu Glu Thr Arg Leu His
100 105 110
Ile Thr Gly Arg Glu Leu Arg Ser Lys Ile Ala Glu Thr Phe Gly Leu

115 120 125
Gln Glu Tyr Ile Lys Ile Val Ile Asn Lys Lys Gln Leu Leu Gly Lys
130 135 140
Thr Leu Glu Gln Gly Val Ala His Asn Val Lys Ala Met Val Leu Glu
145 150 155 160
Leu Lys Gln Ser Glu Glu Asp Ala Arg Lys Asn Phe Gln Leu Glu Glu
165 170 175
Glu Glu

<210> 125
<211> 1302
<212> DNA
<213> Homo Sapiens

<400> 125
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ggtatggaca cgttcatcca ccgcatcgac tccaccgagg tcatctacca gccgcgccgc 120
aagcgggcca agctcatcgg caagtacctg atgggggacc tgctggggga aggctcttac 180
ggcaaggtga aggaggtgct ggactcggag acgctgtgca ggagggccgt caagatcctc 240
aagaagaaga agttgcgaag gatccccaac ggggaggcca acgtgaagaa ggaaattcaa 300
ctactgagga ggttacggca caaaaatgtc atccagctgg tggatgtgtt atacaacgaa 360
gagaagcaga aaatgtatat ggtgatggag tactgcgtgt gtggcatgca ggaaatgctg 420
gacagcgtgc cggagaagcg tttcccagtg tgccaggccc acgggtactt ctgtcagctg 480
attgacggcc tggagtacct gcatagccag ggcattgtgc acaaggacat caagccgggg 540
aacctgctgc tcaccaccgg tggcaccctc aaaatctccg acctgggcgt ggccgaggca 600
ctgcacccgt tcgcggcgga cgacacctgc cggaccagcc agggctcccc ggctttccag 660
ccgcccgaga ttgccaacgg cctggacacc ttctccggct tcaaggtgga catctggtcg 720
gctggggtca ccctctacaa catcaccacg ggtctgtacc ccttcgaagg ggacaacatc 780
tacaagttgt ttgagaacat cgggaagggg agctacgcca tcccgggcga ctgtggcccc 840
ccgctctctg acctgctgaa agggatgctt gagtacgaac cggccaagag gttctccatc 900
cggcagatcc ggcagcacag ctggttccgg aagaaacatc ctccggctga agcaccagtg 960
cccatcccac cgagcccaga caccaaggac cggtggcgca gcatgactgt ggtgccgtac 1020
ttggaggacc tgcacggcgc ggacgaggac gaggacctct tcgacatcga ggatgacatc 1080
atctacactc aggacttcac ggtgcccgga caggtcccag aagaggaggc cagtcacaat 1140
ggacagcgcc ggggcctccc caaggccgtg tgtatgaacg gcacagaggc ggcgcagctg 1200
agcaccaaat ccagggcgga gggccgggcc cccaaccctg cccgcaaggc ctgctccgcc 1260
agcagcaaga tccgccggct gtcggcctgc aagcagcagt ga 1302

<210> 126
<211> 433
<212> PRT
<213> Homo Sapiens

<400> 126
Met Glu Val Val Asp Pro Gln Gln Leu Gly Met Phe Thr Glu Gly Glu
1 5 10 15
Leu Met Ser Val Gly Met Asp Thr Phe Ile His Arg Ile Asp Ser Thr
20 25 30
Glu Val Ile Tyr Gln Pro Arg Arg Lys Arg Ala Lys Leu Ile Gly Lys
35 40 45
Tyr Leu Met Gly Asp Leu Leu Gly Glu Gly Ser Tyr Gly Lys Val Lys
50 55 60
Glu Val Leu Asp Ser Glu Thr Leu Cys Arg Arg Ala Val Lys Ile Leu
65 70 75 80

Lys Lys Lys Lys Leu Arg Arg Ile Pro Asn Gly Glu Ala Asn Val Lys
                85   90   95
Lys Glu Ile Gln Leu Leu Arg Arg Leu Arg His Lys Asn Val Ile Gln
            100   105   110
Leu Val Asp Val Leu Tyr Asn Glu Glu Lys Gln Lys Met Tyr Met Val
        115   120   125
Met Glu Tyr Cys Val Cys Gly Met Gln Glu Met Leu Asp Ser Val Pro
    130   135   140
Glu Lys Arg Phe Pro Val Cys Gln Ala His Gly Tyr Phe Cys Gln Leu
145   150   155   160
Ile Asp Gly Leu Glu Tyr Leu His Ser Gln Gly Ile Val His Lys Asp
                165   170   175
Ile Lys Pro Gly Asn Leu Leu Leu Thr Thr Gly Gly Thr Leu Lys Ile
            180   185   190
Ser Asp Leu Gly Val Ala Glu Ala Leu His Pro Phe Ala Ala Asp Asp
        195   200   205
Thr Cys Arg Thr Ser Gln Gly Ser Pro Ala Phe Gln Pro Pro Glu Ile
    210   215   220
Ala Asn Gly Leu Asp Thr Phe Ser Gly Phe Lys Val Asp Ile Trp Ser
225   230   235   240
Ala Gly Val Thr Leu Tyr Asn Ile Thr Thr Gly Leu Tyr Pro Phe Glu
                245   250   255
Gly Asp Asn Ile Tyr Lys Leu Phe Glu Asn Ile Gly Lys Gly Ser Tyr
            260   265   270
Ala Ile Pro Gly Asp Cys Gly Pro Pro Leu Ser Asp Leu Leu Lys Gly
        275   280   285
Met Leu Glu Tyr Glu Pro Ala Lys Arg Phe Ser Ile Arg Gln Ile Arg
    290   295   300
Gln His Ser Trp Phe Arg Lys Lys His Pro Pro Ala Glu Ala Pro Val
305   310   315   320
Pro Ile Pro Pro Ser Pro Asp Thr Lys Asp Arg Trp Arg Ser Met Thr
                325   330   335
Val Val Pro Tyr Leu Glu Asp Leu His Gly Ala Asp Glu Asp Glu Asp
            340   345   350
Leu Phe Asp Ile Glu Asp Asp Ile Ile Tyr Thr Gln Asp Phe Thr Val
        355   360   365
Pro Gly Gln Val Pro Glu Glu Glu Ala Ser His Asn Gly Gln Arg Arg
    370   375   380
Gly Leu Pro Lys Ala Val Cys Met Asn Gly Thr Glu Ala Ala Gln Leu
385   390   395   400
Ser Thr Lys Ser Arg Ala Glu Gly Arg Ala Pro Asn Pro Ala Arg Lys
                405   410   415
Ala Cys Ser Ala Ser Ser Lys Ile Arg Arg Leu Ser Ala Cys Lys Gln
            420   425   430
Gln

<210> 127
<211> 1488
<212> DNA
<213> Homo Sapiens

<400> 127
gaggggcggg gcggtgccgg caagatggct gcgccgagaga agatgacgtt tcccgagaaa 60
ccaagccaca aaaagtacag ggccgccctg aagaaggaga aacgaaagaa acgtcggcag 120

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gaacttgctc gactgagaga ctcaggactc tcacagaagg aggaagagga ggacactttt    180
attgaagaac aacaactaga agaagagaag ctattggaaa gagagaggca aagattacat    240
gaggagtggt tgctaagaga gcagaaggca caagaagaat tcagaataaa gaaggaaaag    300
gaagaggcgg ctaaaaaacg gcaagaagaa caagagagaa agttaaagga acaatgggaa    360
gaacagcaga ggaaagagag agaagaggag gagcagaaac gacaggagaa gaaagaaaaa    420
gaggaagctt tgcagaagat gctggatcag gctgaaaatg agttggaaaa tggtaccaca    480
tggcaaaacc cagaaccacc cgtggatttc agagtaatgg agaaggatcg agctaattgt    540
cccttctaca gtaaaacagg agcttgcaga tttggagata gatgttcacg taaacataat    600
ttcccaacat ccagtcctac ccttcttatt aagagcatgt ttacgacgtt tggaatggag    660
cagtgcagga gggatgacta tgaccctgac gcaagcctgg agtacagcga ggaagaaacc    720
taccaacagt tcctagactt ctatgaggat gtgttgcccg agttcaagaa cgtggggaaa    780
gtgattcagt tcaaggtcag ctgcaatttg gaacctcacc tgaggggcaa tgtatatgtt    840
cagtaccagt cggaagaaga atgccaagca gccctttctc tgtttaacgg acgatggtat    900
gcaggacgac agctgcagtg tgaattctgc cccgtgaccc ggtggaaaat ggcgatttgt    960
ggtttatttg aaatacaaca atgtccaaga ggaaagcact gcaactttct tcatgtgttc   1020
agaaatccca acaatgaatt ctgggaagct aatagagaca tctacttgtc tccagatcgg   1080
actggctcct cctttgggaa gaactccgaa aggagggaga ggatgggcca ccacgacgac   1140
tactacagca ggctgcgggg aaggagaaac cctagtccag accactccta caaaagaaat   1200
ggggaatccg agaggaaaag tagtcgtcac agggggaaga aatctcacaa acgcacatca   1260
aagagtcggg agaggcacaa ttcacgaagc agaggaagaa atagggaccg cagcagggac   1320
cgcagccggg gccggggcag ccggagccgg agccggagcc ggagccgcag gagccgccgc   1380
agccggagcc aaagttcctc taggtcccga agtcgtggca ggaggaggtc gggtaataga   1440
gacagaactg ttcagagtcc caaatccaaa taaactagtt ttgttctt                1488
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<210> 128
<211> 482
<212> PRT
<213> Homo Sapiens

<400> 128

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Met Ala Ala Pro Glu Lys Met Thr Phe Pro Glu Lys Pro Ser His Lys
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Lys Tyr Arg Ala Ala Leu Lys Lys Glu Lys Arg Lys Lys Arg Arg Gln
            20                  25                  30
Glu Leu Ala Arg Leu Arg Asp Ser Gly Leu Ser Gln Lys Glu Glu Glu
        35                  40                  45
Glu Asp Thr Phe Ile Glu Glu Gln Gln Leu Glu Glu Glu Lys Leu Leu
    50                  55                  60
Glu Arg Glu Arg Gln Arg Leu His Glu Glu Trp Leu Leu Arg Glu Gln
65                  70                  75                  80
Lys Ala Gln Glu Glu Phe Arg Ile Lys Lys Glu Lys Glu Glu Ala Ala
                85                  90                  95
Lys Lys Arg Gln Glu Glu Gln Glu Arg Lys Leu Lys Glu Gln Trp Glu
            100                 105                 110
Glu Gln Gln Arg Lys Glu Arg Glu Glu Glu Glu Gln Lys Arg Gln Glu
        115                 120                 125
Lys Lys Glu Lys Glu Glu Ala Leu Gln Lys Met Leu Asp Gln Ala Glu
    130                 135                 140
Asn Glu Leu Glu Asn Gly Thr Thr Trp Gln Asn Pro Glu Pro Pro Val
145                 150                 155                 160
Asp Phe Arg Val Met Glu Lys Asp Arg Ala Asn Cys Pro Phe Tyr Ser
                165                 170                 175
Lys Thr Gly Ala Cys Arg Phe Gly Asp Arg Cys Ser Arg Lys His Asn
            180                 185                 190
Phe Pro Thr Ser Ser Pro Thr Leu Leu Ile Lys Ser Met Phe Thr Thr
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        195                 200                 205
Phe Gly Met Glu Gln Cys Arg Arg Asp Asp Tyr Asp Pro Asp Ala Ser
    210                 215                 220
Leu Glu Tyr Ser Glu Glu Glu Thr Tyr Gln Gln Phe Leu Asp Phe Tyr
225                 230                 235                 240
Glu Asp Val Leu Pro Glu Phe Lys Asn Val Gly Lys Val Ile Gln Phe
                245                 250                 255
Lys Val Ser Cys Asn Leu Glu Pro His Leu Arg Gly Asn Val Tyr Val
            260                 265                 270
Gln Tyr Gln Ser Glu Glu Glu Cys Gln Ala Ala Leu Ser Leu Phe Asn
        275                 280                 285
Gly Arg Trp Tyr Ala Gly Arg Gln Leu Gln Cys Glu Phe Cys Pro Val
    290                 295                 300
Thr Arg Trp Lys Met Ala Ile Cys Gly Leu Phe Glu Ile Gln Gln Cys
305                 310                 315                 320
Pro Arg Gly Lys His Cys Asn Phe Leu His Val Phe Arg Asn Pro Asn
                325                 330                 335
Asn Glu Phe Trp Glu Ala Asn Arg Asp Ile Tyr Leu Ser Pro Asp Arg
            340                 345                 350
Thr Gly Ser Ser Phe Gly Lys Asn Ser Glu Arg Arg Glu Arg Met Gly
        355                 360                 365
His His Asp Asp Tyr Tyr Ser Arg Leu Arg Gly Arg Arg Asn Pro Ser
    370                 375                 380
Pro Asp His Ser Tyr Lys Arg Asn Gly Glu Ser Glu Arg Lys Ser Ser
385                 390                 395                 400
Arg His Arg Gly Lys Lys Ser His Lys Arg Thr Ser Lys Ser Arg Glu
                405                 410                 415
Arg His Asn Ser Arg Ser Arg Gly Arg Asn Arg Asp Arg Ser Arg Asp
            420                 425                 430
Arg Ser Arg Gly Arg Gly Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg
        435                 440                 445
Arg Ser Arg Arg Ser Arg Ser Gln Ser Ser Ser Arg Ser Arg Ser Arg
    450                 455                 460
Gly Arg Arg Arg Ser Gly Asn Arg Asp Arg Thr Val Gln Ser Pro Lys
465                 470                 475                 480
Ser Lys
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<210> 129
<211> 1663
<212> DNA
<213> Homo Sapiens

<400> 129

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aggccctgag ccaactccgg gtgctctgct gtgagtggct gaggcccgag atccacacca      60
aggagcagat cctggagcta ctggtgctgg agcagttcct gaccatcctg ccccaggagc     120
tccaggcctg ggtgcaggag cattgcccgg agagcgctga agaggctgtc actctcctcg     180
aagatctgga gcgggaactg gatgagccag gacaccaggt ctcaactcct ccaaacgaac     240
agaaaccggt gtgggagaag atatcctcct caggaactgc aaaggaatcc ccgagcagca     300
tgcagccaca gcccttggag accagtcaca aatacgagtc ttgggggccc ctgtacatcc     360
aagagtctgg tgaggagcag gagttcgctc aagatccaag aaaggtccga gattgcagat     420
tgagtaccca gcacgaggaa tcagcagatg agcagaaagg ttctgaagca gaggggctca     480
aaggggatat aatttctgtg attatcgcca ataaacctga ggccagctta gagaggcagt     540
gcgtaaacct tgaaaatgaa aaaggaacaa aacccccctct tcaagaggca ggctccaaga     600
aaggtagaga atcagttcct actaaaccta ccccaggaga gagacgttat atatgtgctg     660
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aatgtggcaa agcctttagt aatagctcaa atctcaccaa acacaggaga acacacactg 720
gggagaaacc ttacgtgtgc accaagtgtg ggaaagcttt cagccacagc tcaaacctca 780
ccctccacta cagaacacac ttggtggacc ggccctatga ctgtaagtgt ggaaaagctt 840
ttgggcagag ctcagacctt cttaaacatc agagaatgca cacagaagag gcgccatatc 900
agtgcaaaga ttgtggcaag gctttcagcg ggaaaggcag cctcattcgt cactatcgga 960
tccacactgg ggagaagcct tatcagtgta acgaatgtgg gaagagcttc agtcagcatg 1020
cgggcctcag ctcccaccag agactccaca ccggagagaa gccatataag tgtaaggagt 1080
gtgggaaagc cttcaaccac agctccaact tcaataaaca ccacagaatc cacaccgggg 1140
aaaagcccta ctggtgtcat cactgtggaa agaccttctg tagcaagtcc aatctttcca 1200
aacatcagcg agtccacact ggagagggag aagcaccgta actttcaagc gctcctgttg 1260
ttgtcgttgt tttaaacttt agaatctgaa aaccagaaag aagtcttgtc attgcagcag 1320
catcgattcc ggtgatagag tttgtatcac tcaacatcag gggatgcctg aggagtgcga 1380
gctccacagc aacatggcag gcaggaggtc ctcagaaggt gtcaggaggt tccacactcg 1440
ccagttcact ggagcagagt cccttcgcca cacttagggt cccagtaagc catgccagca 1500
ttacctttg cgtagttaaa cagacgtgta tccagtctag ttaaggaaga aacattaaga 1560
ttgtttaatt tttaacatat attcaagaat tttaatttgt aaagaattga gccacattga 1620
acacaattga atgagattca gaataaactt ataacatctt aaa 1663

<210> 130
<211> 412
<212> PRT
<213> Homo Sapiens

<400> 130
Ala Leu Ser Gln Leu Arg Val Leu Cys Cys Glu Trp Leu Arg Pro Glu
1 5 10 15
Ile His Thr Lys Glu Gln Ile Leu Glu Leu Leu Val Leu Glu Gln Phe
20 25 30
Leu Thr Ile Leu Pro Gln Glu Leu Gln Ala Trp Val Gln Glu His Cys
35 40 45
Pro Glu Ser Ala Glu Glu Ala Val Thr Leu Leu Glu Asp Leu Glu Arg
50 55 60
Glu Leu Asp Glu Pro Gly His Gln Val Ser Thr Pro Pro Asn Glu Gln
65 70 75 80
Lys Pro Val Trp Glu Lys Ile Ser Ser Ser Gly Thr Ala Lys Glu Ser
85 90 95
Pro Ser Ser Met Gln Pro Gln Pro Leu Glu Thr Ser His Lys Tyr Glu
100 105 110
Ser Trp Gly Pro Leu Tyr Ile Gln Glu Ser Gly Glu Glu Gln Glu Phe
115 120 125
Ala Gln Asp Pro Arg Lys Val Arg Asp Cys Arg Leu Ser Thr Gln His
130 135 140
Glu Glu Ser Ala Asp Glu Gln Lys Gly Ser Glu Ala Glu Gly Leu Lys
145 150 155 160
Gly Asp Ile Ile Ser Val Ile Ile Ala Asn Lys Pro Glu Ala Ser Leu
165 170 175
Glu Arg Gln Cys Val Asn Leu Glu Asn Glu Lys Gly Thr Lys Pro Pro
180 185 190
Leu Gln Glu Ala Gly Ser Lys Lys Gly Arg Glu Ser Val Pro Thr Lys
195 200 205
Pro Thr Pro Gly Glu Arg Arg Tyr Ile Cys Ala Glu Cys Gly Lys Ala
210 215 220
Phe Ser Asn Ser Ser Asn Leu Thr Lys His Arg Arg Thr His Thr Gly
225 230 235 240
Glu Lys Pro Tyr Val Cys Thr Lys Cys Gly Lys Ala Phe Ser His Ser

245 250 255
Ser Asn Leu Thr Leu His Tyr Arg Thr His Leu Val Asp Arg Pro Tyr
260 265 270
Asp Cys Lys Cys Gly Lys Ala Phe Gly Gln Ser Ser Asp Leu Leu Lys
275 280 285
His Gln Arg Met His Thr Glu Glu Ala Pro Tyr Gln Cys Lys Asp Cys
290 295 300
Gly Lys Ala Phe Ser Gly Lys Gly Ser Leu Ile Arg His Tyr Arg Ile
305 310 315 320
His Thr Gly Glu Lys Pro Tyr Gln Cys Asn Glu Cys Gly Lys Ser Phe
325 330 335
Ser Gln His Ala Gly Leu Ser Ser His Gln Arg Leu His Thr Gly Glu
340 345 350
Lys Pro Tyr Lys Cys Lys Glu Cys Gly Lys Ala Phe Asn His Ser Ser
355 360 365
Asn Phe Asn Lys His His Arg Ile His Thr Gly Glu Lys Pro Tyr Trp
370 375 380
Cys His His Cys Gly Lys Thr Phe Cys Ser Lys Ser Asn Leu Ser Lys
385 390 395 400
His Gln Arg Val His Thr Gly Glu Gly Glu Ala Pro
405 410

<210> 131
<211> 724
<212> DNA
<213> Homo Sapiens

<400> 131
ggagaatgaa aagcagaaag tggcagagct gtattctatc cataactctg gagacaaatc 60
tgatattcag gacctcctgg agagtgtcag gctggacaaa gaaaaagcag agactttggc 120
tagtagcttg caggaagatc tggctcatac ccgaaatgat gccaatcgat tacaggatgc 180
cattgctaag gtagaggatg aataccgagc cttccaagaa gaagctaaga aacaaattga 240
agatttgaat atgacgttag aaaaattaag atcagacctg gatgaaaaag aaacagaaag 300
gagtgacatg aaagaaacca tctttgaact tgaagatgaa gtagaacaac atcgtgctgt 360
gaaacttcat gacaacctca ttatttctga tctagagaat acagttaaaa aactccagga 420
ccaaaagcac gacatggaaa gagaaataaa gacactccac agaagacttc gggaagaatc 480
tgcggaatgg cggcagtttc aggctgatct ccagactgca gtagtcattg caaatgacat 540
taaatctgaa gcccaagagg agattggtga tctaaagcgc cgggtacatg aggctcaaga 600
aaaaaatgag aaactcacaa aagaattgga ggaaataagt ccgccaagcc agaagangac 660
gangccggta ttccantaca tgnatgcccg tgagagagaa tttggcaggc cttaaggcag 720
ggaa 724

<210> 132
<211> 218
<212> PRT
<213> Homo Sapiens

<400> 132
Glu Asn Glu Lys Gln Lys Val Ala Glu Leu Tyr Ser Ile His Asn Ser
1 5 10 15
Gly Asp Lys Ser Asp Ile Gln Asp Leu Leu Glu Ser Val Arg Leu Asp
20 25 30
Lys Glu Lys Ala Glu Thr Leu Ala Ser Ser Leu Gln Glu Asp Leu Ala
35 40 45
His Thr Arg Asn Asp Ala Asn Arg Leu Gln Asp Ala Ile Ala Lys Val

```
50                  55                  60
Glu Asp Glu Tyr Arg Ala Phe Gln Glu Glu Ala Lys Lys Gln Ile Glu
65                  70                  75                  80
Asp Leu Asn Met Thr Leu Glu Lys Leu Arg Ser Asp Leu Asp Glu Lys
                85                  90                  95
Glu Thr Glu Arg Ser Asp Met Lys Glu Thr Ile Phe Glu Leu Glu Asp
            100                 105                 110
Glu Val Glu Gln His Arg Ala Val Lys Leu His Asp Asn Leu Ile Ile
        115                 120                 125
Ser Asp Leu Glu Asn Thr Val Lys Lys Leu Gln Asp Gln Lys His Asp
    130                 135                 140
Met Glu Arg Glu Ile Lys Thr Leu His Arg Arg Leu Arg Glu Glu Ser
145                 150                 155                 160
Ala Glu Trp Arg Gln Phe Gln Ala Asp Leu Gln Thr Ala Val Val Ile
                165                 170                 175
Ala Asn Asp Ile Lys Ser Glu Ala Gln Glu Glu Ile Gly Asp Leu Lys
            180                 185                 190
Arg Arg Val His Glu Ala Gln Glu Lys Asn Glu Lys Leu Thr Lys Glu
        195                 200                 205
Leu Glu Glu Ile Ser Pro Pro Ser Gln Lys
    210                 215
```

<210> 133
<211> 719
<212> DNA
<213> Homo Sapiens

<400> 133

```
gagaactaca gagctgggtg cggggccaac ggccagaaag tggcgaggag gcagtgacgc    60
tggtggaggg tttgcagaaa caacccagga gaccaaggcg gtgactgtcc atgttcacgg   120
ccaggaagtc ctgtcagagg agacggtgca tttaggagcg gagcctgagt cacctaatga   180
gctgcaggat cctgtgcaaa gctcgacccc cgagcagtct cctgaggaaa ccacacagag   240
cccagatctg gggcaccgg cagagcagcg tccacaccag gaagaggagc tccagaccct   300
gcaggagagc gaggtcccag tgcccgagga cccagacctt cctgcagaga ggagctctgg   360
agactcagag atggttgctc ttcttactgc tctgtcacag ggactggtaa cgttcaagga   420
tgtggccgta tgcttttccc aggaccagtg gagtgatctg gacccaacac agaaagagtt   480
ctatggagaa tatgtcttgg aagaagactg tggaattgtt gtctctctgt catttccaat   540
ccccagacct gatgagatct cccaggttag agaggaagag cccttgggtc ccagatatcc   600
aagagcctna ggagactcaa gagccagaaa tcctgagttt tacctacaca ggagatagga   660
gtnaagatga aggaaaatgt ctggagccag gaagaatctg agtttggagg atataccca    719
```

<210> 134
<211> 217
<212> PRT
<213> Homo Sapiens

<400> 134

```
Arg Thr Thr Glu Leu Gly Ala Gly Pro Thr Ala Arg Lys Trp Arg Gly
 1               5                  10                  15
Gly Ser Asp Ala Gly Gly Gly Phe Ala Glu Thr Thr Gln Glu Thr Lys
            20                  25                  30
Ala Val Thr Val His Val His Gly Gln Glu Val Leu Ser Glu Glu Thr
        35                  40                  45
Val His Leu Gly Ala Glu Pro Glu Ser Pro Asn Glu Leu Gln Asp Pro
    50                  55                  60
```

Val Gln Ser Ser Thr Pro Glu Gln Ser Pro Glu Glu Thr Thr Gln Ser
65 70 75 80
Pro Asp Leu Gly Ala Pro Ala Glu Gln Arg Pro His Gln Glu Glu Glu
85 90 95
Leu Gln Thr Leu Gln Glu Ser Glu Val Pro Val Pro Glu Asp Pro Asp
100 105 110
Leu Pro Ala Glu Arg Ser Ser Gly Asp Ser Glu Met Val Ala Leu Leu
115 120 125
Thr Ala Leu Ser Gln Gly Leu Val Thr Phe Lys Asp Val Ala Val Cys
130 135 140
Phe Ser Gln Asp Gln Trp Ser Asp Leu Asp Pro Thr Gln Lys Glu Phe
145 150 155 160
Tyr Gly Glu Tyr Val Leu Glu Glu Asp Cys Gly Ile Val Val Ser Leu
165 170 175
Ser Phe Pro Ile Pro Arg Pro Asp Glu Ile Ser Gln Val Arg Glu Glu
180 185 190
Glu Pro Leu Gly Pro Arg Tyr Pro Arg Ala Gly Asp Ser Arg Ala Arg
195 200 205
Asn Pro Glu Phe Tyr Leu His Arg Arg
210 215

<210> 135
<211> 1027
<212> DNA
<213> Homo Sapiens

<400> 135
gcgagggcga gggcgaggcg gtgctcatgg aggaggacct gatccagcag agcctggacg 60
actacgacgc cggcaggtac agcccgcggc tgctcacggc gcacgagctg ccactggacg 120
cgcacgtgct ggaaccggat gaggacctgc agcgcctgca gctctcgcgc cagcagctcc 180
aggtcacggg agacgccagc gagagcgccg aggacatctt cttccggcgg gccaaggagg 240
gcatgggcca ggacgaggcg cagttcagcg tggagatgcc actcaccggc aaggcctacc 300
tgtgggccga caagtaccgg ccacgcaagc cgcgcttctt caaccgcgtg cacacgggct 360
tcgagtggaa caagtacaac cagacgcact acgactttga caacccaccg cccaagatcg 420
tgcagggata caagttcaac atcttctacc ccgacctcat cgacaagcgc tccacgcccg 480
agtacttcct ggaggcctgc gccgacaaca aggatttcgc catcctgcgc ttcacgcggg 540
gccgcctacg aggacatcgc tttcaagatc gtcaaccgcg agtgggaata ctngcaccgc 600
cacggcttcc gctgccagtt tgccaacggc attttccanc tgngctttca cttcaagcgc 660
tnccgctatc ggcggtgacg gccctgggga acggcaggcc aggagggccg agggccacac 720
gggtgccaca gcccaggtcg gagtggccca gccggcaggc ttgtttttca gcatccgacg 780
ggaacatctc caacagaagc aaaacggaaa gtgcctcccg gacccccaga gggccaccca 840
acctcaccag tcaccagccc cagaccaccc acagcccctc ccagacaccc cgcctcatct 900
ggaaatagtt ccgtttgttt ctctaaaaag acttgtaggt gggaaaaaaa atcttttggt 960
ctcatggaat tggcctattg gcaagatcgc atgttttttt aataaacgtt gtattttaga 1020
ataaaaa 1027

<210> 136
<211> 299
<212> PRT
<213> Homo Sapiens

<400> 136
Glu Gly Glu Gly Glu Ala Val Leu Met Glu Glu Asp Leu Ile Gln Gln
1 5 10 15
Ser Leu Asp Asp Tyr Asp Ala Gly Arg Tyr Ser Pro Arg Leu Leu Thr

```
                20                       25                       30
Ala His Glu Leu Pro Leu Asp Ala His Val Leu Glu Pro Asp Glu Asp
            35                      40                      45
Leu Gln Arg Leu Gln Leu Ser Arg Gln Gln Leu Gln Val Thr Gly Asp
        50                      55                      60
Ala Ser Glu Ser Ala Glu Asp Ile Phe Phe Arg Arg Ala Lys Glu Gly
65                      70                      75                      80
Met Gly Gln Asp Glu Ala Gln Phe Ser Val Glu Met Pro Leu Thr Gly
                85                      90                      95
Lys Ala Tyr Leu Trp Ala Asp Lys Tyr Arg Pro Arg Lys Pro Arg Phe
            100                     105                     110
Phe Asn Arg Val His Thr Gly Phe Glu Trp Asn Lys Tyr Asn Gln Thr
        115                     120                     125
His Tyr Asp Phe Asp Asn Pro Pro Pro Lys Ile Val Gln Gly Tyr Lys
    130                     135                     140
Phe Asn Ile Phe Tyr Pro Asp Leu Ile Asp Lys Arg Ser Thr Pro Glu
145                     150                     155                     160
Tyr Phe Leu Glu Ala Cys Ala Asp Asn Lys Asp Phe Ala Ile Leu Arg
                165                     170                     175
Phe Thr Arg Gly Arg Leu Arg Gly His Arg Phe Gln Asp Arg Gln Pro
            180                     185                     190
Arg Val Gly Ile Leu Ala Pro Pro Arg Leu Pro Leu Pro Val Cys Gln
        195                     200                     205
Arg His Phe Pro Leu Ser Leu Gln Ala Leu Pro Leu Ser Ala Val Thr
    210                     215                     220
Ala Leu Gly Asn Gly Arg Pro Gly Gly Pro Arg Ala Thr Arg Val Pro
225                     230                     235                     240
Gln Pro Arg Ser Glu Trp Pro Ser Arg Gln Ala Cys Phe Ser Ala Ser
                245                     250                     255
Asp Gly Asn Ile Ser Asn Arg Ser Lys Thr Glu Ser Ala Ser Arg Thr
            260                     265                     270
Pro Arg Gly Pro Pro Asn Leu Thr Ser His Gln Pro Gln Thr Thr His
        275                     280                     285
Ser Pro Ser Gln Thr Pro Arg Leu Ile Trp Lys
    290                     295
```

<210> 137
<211> 766
<212> DNA
<213> Homo Sapiens

<400> 137

```
caaaggttta cacagtaaac aatgtgaatg tgatcaccaa aatacgcaca gaacatctga     60
ccgaggagga aaaaaagaga tataaagaca ggaacccgct ggaatctttg ctgggaactg    120
tggaacacca atttggtgca caaggggacc tcaccacgga atgtgctact gcaaacaacc    180
ccacagccat cacgcctgat gagtacttca atgaagagtt tgatctgaaa gacagggaca    240
ttggaaggcc gaaagagctg acgattagaa cacagaagtt taaagcaatg ttgtggatgt    300
gtgaagagtt tcccctctct ctggtggagc aggtcattcc catcattgac ctaatggctc    360
gaacgagtgc tcattttgca agactgagag atttcatcaa attggaattc ccacctggat    420
ttcctgtcaa aatagcttcc cacatcacaa actttgaggt tgatcaatct gtgtttgaaa    480
ttcccgaatc ttactatgtt caagacaatg gcagaaatgt gcatttgcaa gatgaagatt    540
acgagataat gcagtttgcc atccagcaaa gtctgctgga gtccagcagg agccaggaac    600
tttcaggacc agcttcgaat ggagggatca gccagacaaa cacctatgac gcccagtatg    660
agagggccat ncaggagagc cttctaccag cacagaaagc ctgtgccccc agcgcccctg    720
agcgagacna gccgttttga taatggactt gcagctaagc catgga                   766
```

<210> 138
<211> 243
<212> PRT
<213> Homo Sapiens

<400> 138

```
Lys Val Tyr Thr Val Asn Asn Val Asn Val Ile Thr Lys Ile Arg Thr
1               5                   10                  15
Glu His Leu Thr Glu Glu Glu Lys Lys Arg Tyr Lys Asp Arg Asn Pro
            20                  25                  30
Leu Glu Ser Leu Leu Gly Thr Val Glu His Gln Phe Gly Ala Gln Gly
        35                  40                  45
Asp Leu Thr Thr Glu Cys Ala Thr Ala Asn Asn Pro Thr Ala Ile Thr
    50                  55                  60
Pro Asp Glu Tyr Phe Asn Glu Glu Phe Asp Leu Lys Asp Arg Asp Ile
65                  70                  75                  80
Gly Arg Pro Lys Glu Leu Thr Ile Arg Thr Gln Lys Phe Lys Ala Met
                85                  90                  95
Leu Trp Met Cys Glu Glu Phe Pro Leu Ser Leu Val Glu Gln Val Ile
            100                 105                 110
Pro Ile Ile Asp Leu Met Ala Arg Thr Ser Ala His Phe Ala Arg Leu
        115                 120                 125
Arg Asp Phe Ile Lys Leu Glu Phe Pro Pro Gly Phe Pro Val Lys Ile
    130                 135                 140
Ala Ser His Ile Thr Asn Phe Glu Val Asp Gln Ser Val Phe Glu Ile
145                 150                 155                 160
Pro Glu Ser Tyr Tyr Val Gln Asp Asn Gly Arg Asn Val His Leu Gln
                165                 170                 175
Asp Glu Asp Tyr Glu Ile Met Gln Phe Ala Ile Gln Gln Ser Leu Leu
            180                 185                 190
Glu Ser Ser Arg Ser Gln Glu Leu Ser Gly Pro Ala Ser Asn Gly Gly
        195                 200                 205
Ile Ser Gln Thr Asn Thr Tyr Asp Ala Gln Tyr Glu Arg Ala Gln Glu
    210                 215                 220
Ser Leu Leu Pro Ala Gln Lys Ala Cys Ala Pro Ser Ala Pro Glu Arg
225                 230                 235                 240
Asp Pro Phe
```

<210> 139
<211> 3060
<212> DNA
<213> Homo Sapiens

<400> 139

```
ccgggcggga gtgcggcgag agccggctgg ctgagcttag cgtccgagga ggcggcggcg      60
gcggcggcgg cagcggcggc ggcggggctg tggggcggtg cggaagcgag aggcgaggag     120
cgcgcgggcc gtggccagag tctggcggcg gcctggcgga gcggagagca gcgcccgcgc     180
ctcgccgtgc ggaggagccc cgcacacaat agcggcgcgc gcagcccgcg cccttccccc     240
cggcgcgccc cgcccccgcgc gccgagcgcc ccgctccgcc tcacctgcca ccagggagtg    300
ggcgggcatt gttcgccgcc gccgccgccg cgcggggcca tgggggccgc ccggcgcccg     360
gggccgggcc tggcgaggcc gccgcgccgc cgctgagacg ggccccgcgc gcagcccggc     420
ggcgcaggta aggccggccg cgccatggtg gacccggtgg gcttcgcgga ggcgtggaag     480
gcgcagttcc cggactcaga gcccccgcgc atggagctgc gctcagtggg cgacatcgag     540
caggagctgg agcgctgcaa ggcctccatt cggcgcctgg agcaggaggt gaaccaggag     600
```

```
cgcttccgca tgatctacct gcagacgttg ctggccaagg aaaagaagag ctatgaccgg    660
cagcgatggg gcttccggcg cgcggcgcag gcccccgacg gcgcctccga gccccgagcg    720
tccgcgtcgc gcccgcagcc agcgcccgcc gacggagccg acccgccgcc cgccgaggag    780
cccgaggccc ggcccgacgg cgagggttct ccgggtaagg ccaggcccgg gaccgcccgc    840
aggcccgggg cagccgcgtc gggggaacgg gacgaccggg gacccccgc cagcgtggcg    900
gcgctcaggt ccaacttcga gcggatccgc aagggccatg gccagcccgg ggcggacgcc    960
gagaagccct tctacgtgaa cgtcgagttt caccacgagc gcggcctggt gaaggtcaac   1020
gacaaagagg tgtcggaccg catcagctcc ctgggcagcc aggccatgca gatggagcgc   1080
aaaaagtccc agcacggcgc gggctcgagc gtgggggatg catccaggcc cccttaccgg   1140
ggacgctcct cggagagcag ctgcggcgtc gacggcgact acgaggacgc cgagttgaac   1200
ccccgcttcc tgaaggacaa cctgatcgac gccaatggcg gtagcaggcc cccttggccg   1260
cccctggagt accagcccta ccagagcatc tacgtcgggg gcatgatgga aggggagggc   1320
aagggcccgc tcctgcgcag ccagagcacc tctgagcagg agaagcgcct tacctggccc   1380
cgcaggtcct actcccccg gagttttgag gattgcggag gcggctatac cccggactgc    1440
agctccaatg agaacctcac ctccagcgag gaggacttct cctctggcca gtccagccgc   1500
gtgtccccaa gccccaccac ctaccgcatg ttccgggaca aaagccgctc tccctcgcag   1560
aactcgcaac agtccttcga cagcagcagt ccccccacgc cgcagtgcca taagcggcac   1620
cggcactgcc cggttgtcgt gtccgaggcc accatcgtgg gcgtccgcaa gaccgggcag   1680
atctggccca acgatggcga gggcgccttc catggagacg cagatggctc gttcggaaca   1740
ccacctggat acggctgcgc tgcagaccgg gcagaggagc agcgccggca ccaagatggg   1800
ctgccctaca ttgatgactc gccctcctca tcgcccccacc tcagcagcaa gggcaggggc   1860
agccgggatg cgctggtctc gggagccctg gagtccacta aagcgagtga gctggacttg   1920
gaaaagggct tggagatgag aaaatgggtc ctgtcgggaa tcctggctag cgaggagact   1980
tacctgagcc acctggaggc actgctgctg cccatgaagc ctttgaaagc cgctgccacc   2040
acctctcagc cggtgctgac gagtcagcag atcgagacca tcttcttcaa agtgcctgag   2100
ctctacgaga tccacaagga gttctatgat gggctcttcc cccgcgtgca gcagtggagc   2160
caccagcagc gggtgggcga cctcttccag aagctggcca gccagctggg tgtgtaccgg   2220
gccttcgtgg acaactacgg agttgccatg gaaatggctg agaagtgctg tcaggccaat   2280
gctcagtttg cagaaatctc cgagaacctg agagccagaa gcaacaaaga tgccaaggat   2340
ccaacgacca agaactctct ggaaactctg ctctacaagc ctgtggaccg tgtgacgagg   2400
agcacgctgg tcctccatga cttgctgaag cacactcctg ccagccaccc tgaccacccc   2460
ttgctgcagg acgccctccg catctcacag aacttcctgt ccagcatcaa tgaggagatc   2520
acaccccgac ggcagtccat gacggtgaag aagggagagc accggcagct gctgaaggac   2580
agcttcatgg tggagctggt ggaggggggcc cgcaagctgc gccacgtctt cctgttcacc   2640
gagctgcttc tctgcaccaa gctcaagaag cagagcggag gcaaaacgca gcagtatgac   2700
tgcaaatggt acattccgct cacggatctc agcttccaga tggtggatga actggaggca   2760
gtgcccaaca tccccctggt gcccgatgag gagctggacg ctttgaagat caagatctcc   2820
cagatcaaga gtgacatcca gagagagaag agggcgaaca agggcagcaa ggctacggag   2880
aggctgaaga agaagctgtc ggagcaggag tcactgctgc tgcttatgtc tcccagcatg   2940
gccttcaggg tgcacagccg caacggcaag agttacacgt tcctgatctc ctctgactat   3000
gagcgtgcag agtggaggga gaacatccgg gagcagcaga agaagtgttt cagaagcttc   3060
```

<210> 140
<211> 872
<212> PRT
<213> Homo Sapiens

<400> 140

```
Met Val Asp Pro Val Gly Phe Ala Glu Ala Trp Lys Ala Gln Phe Pro
 1               5                  10                  15
Asp Ser Glu Pro Pro Arg Met Glu Leu Arg Ser Val Gly Asp Ile Glu
            20                  25                  30
Gln Glu Leu Glu Arg Cys Lys Ala Ser Ile Arg Arg Leu Glu Gln Glu
        35                  40                  45
Val Asn Gln Glu Arg Phe Arg Met Ile Tyr Leu Gln Thr Leu Leu Ala
```

50 55 60
Lys Glu Lys Lys Ser Tyr Asp Arg Gln Arg Trp Gly Phe Arg Arg Ala
65 70 75 80
Ala Gln Ala Pro Asp Gly Ala Ser Glu Pro Arg Ala Ser Ala Ser Arg
85 90 95
Pro Gln Pro Ala Pro Ala Asp Gly Ala Asp Pro Pro Pro Ala Glu Glu
100 105 110
Pro Glu Ala Arg Pro Asp Gly Glu Gly Ser Pro Gly Lys Ala Arg Pro
115 120 125
Gly Thr Ala Arg Arg Pro Gly Ala Ala Ala Ser Gly Glu Arg Asp Asp
130 135 140
Arg Gly Pro Pro Ala Ser Val Ala Ala Leu Arg Ser Asn Phe Glu Arg
145 150 155 160
Ile Arg Lys Gly His Gly Gln Pro Gly Ala Asp Ala Glu Lys Pro Phe
165 170 175
Tyr Val Asn Val Glu Phe His His Glu Arg Gly Leu Val Lys Val Asn
180 185 190
Asp Lys Glu Val Ser Asp Arg Ile Ser Ser Leu Gly Ser Gln Ala Met
195 200 205
Gln Met Glu Arg Lys Lys Ser Gln His Gly Ala Gly Ser Ser Val Gly
210 215 220
Asp Ala Ser Arg Pro Pro Tyr Arg Gly Arg Ser Ser Glu Ser Ser Cys
225 230 235 240
Gly Val Asp Gly Asp Tyr Glu Asp Ala Glu Leu Asn Pro Arg Phe Leu
245 250 255
Lys Asp Asn Leu Ile Asp Ala Asn Gly Gly Ser Arg Pro Pro Trp Pro
260 265 270
Pro Leu Glu Tyr Gln Pro Tyr Gln Ser Ile Tyr Val Gly Gly Met Met
275 280 285
Glu Gly Glu Gly Lys Gly Pro Leu Leu Arg Ser Gln Ser Thr Ser Glu
290 295 300
Gln Glu Lys Arg Leu Thr Trp Pro Arg Arg Ser Tyr Ser Pro Arg Ser
305 310 315 320
Phe Glu Asp Cys Gly Gly Gly Tyr Thr Pro Asp Cys Ser Ser Asn Glu
325 330 335
Asn Leu Thr Ser Ser Glu Glu Asp Phe Ser Ser Gly Gln Ser Ser Arg
340 345 350
Val Ser Pro Ser Pro Thr Thr Tyr Arg Met Phe Arg Asp Lys Ser Arg
355 360 365
Ser Pro Ser Gln Asn Ser Gln Gln Ser Phe Asp Ser Ser Ser Pro Pro
370 375 380
Thr Pro Gln Cys His Lys Arg His Arg His Cys Pro Val Val Val Ser
385 390 395 400
Glu Ala Thr Ile Val Gly Val Arg Lys Thr Gly Gln Ile Trp Pro Asn
405 410 415
Asp Gly Glu Gly Ala Phe His Gly Asp Ala Asp Gly Ser Phe Gly Thr
420 425 430
Pro Pro Gly Tyr Gly Cys Ala Ala Asp Arg Ala Glu Glu Gln Arg Arg
435 440 445
His Gln Asp Gly Leu Pro Tyr Ile Asp Asp Ser Pro Ser Ser Ser Pro
450 455 460
His Leu Ser Ser Lys Gly Arg Gly Ser Arg Asp Ala Leu Val Ser Gly
465 470 475 480
Ala Leu Glu Ser Thr Lys Ala Ser Glu Leu Asp Leu Glu Lys Gly Leu
485 490 495

Glu Met Arg Lys Trp Val Leu Ser Gly Ile Leu Ala Ser Glu Glu Thr
500 505 510
Tyr Leu Ser His Leu Glu Ala Leu Leu Leu Pro Met Lys Pro Leu Lys
515 520 525
Ala Ala Ala Thr Thr Ser Gln Pro Val Leu Thr Ser Gln Gln Ile Glu
530 535 540
Thr Ile Phe Phe Lys Val Pro Glu Leu Tyr Glu Ile His Lys Glu Phe
545 550 555 560
Tyr Asp Gly Leu Phe Pro Arg Val Gln Gln Trp Ser His Gln Gln Arg
565 570 575
Val Gly Asp Leu Phe Gln Lys Leu Ala Ser Gln Leu Gly Val Tyr Arg
580 585 590
Ala Phe Val Asp Asn Tyr Gly Val Ala Met Glu Met Ala Glu Lys Cys
595 600 605
Cys Gln Ala Asn Ala Gln Phe Ala Glu Ile Ser Glu Asn Leu Arg Ala
610 615 620
Arg Ser Asn Lys Asp Ala Lys Asp Pro Thr Thr Lys Asn Ser Leu Glu
625 630 635 640
Thr Leu Leu Tyr Lys Pro Val Asp Arg Val Thr Arg Ser Thr Leu Val
645 650 655
Leu His Asp Leu Leu Lys His Thr Pro Ala Ser His Pro Asp His Pro
660 665 670
Leu Leu Gln Asp Ala Leu Arg Ile Ser Gln Asn Phe Leu Ser Ser Ile
675 680 685
Asn Glu Glu Ile Thr Pro Arg Arg Gln Ser Met Thr Val Lys Lys Gly
690 695 700
Glu His Arg Gln Leu Leu Lys Asp Ser Phe Met Val Glu Leu Val Glu
705 710 715 720
Gly Ala Arg Lys Leu Arg His Val Phe Leu Phe Thr Glu Leu Leu Leu
725 730 735
Cys Thr Lys Leu Lys Lys Gln Ser Gly Gly Lys Thr Gln Gln Tyr Asp
740 745 750
Cys Lys Trp Tyr Ile Pro Leu Thr Asp Leu Ser Phe Gln Met Val Asp
755 760 765
Glu Leu Glu Ala Val Pro Asn Ile Pro Leu Val Pro Asp Glu Glu Leu
770 775 780
Asp Ala Leu Lys Ile Lys Ile Ser Gln Ile Lys Ser Asp Ile Gln Arg
785 790 795 800
Glu Lys Arg Ala Asn Lys Gly Ser Lys Ala Thr Glu Arg Leu Lys Lys
805 810 815
Lys Leu Ser Glu Gln Glu Ser Leu Leu Leu Leu Met Ser Pro Ser Met
820 825 830
Ala Phe Arg Val His Ser Arg Asn Gly Lys Ser Tyr Thr Phe Leu Ile
835 840 845
Ser Ser Asp Tyr Glu Arg Ala Glu Trp Arg Glu Asn Ile Arg Glu Gln
850 855 860
Gln Lys Lys Cys Phe Arg Ser Phe
865 870

<210> 141
<211> 691
<212> DNA
<213> Homo Sapiens

<400> 141

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gttggagtct gatcttttcc cgacgtctac ttccctgagt cccttctacc ttcggccacc 180
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ggacaggttc tctgtcaacc tggatgtgaa gcacttctcc ccagaggaac tcaaagttaa 300
ggtgttggga gatgtgattg aggtgcatgg aaaacatgaa gagcgccagg atgaacatgg 360
tttcatctcc agggagttcc acaggaaata ccggatccca gctgatgtag accctctcac 420
cattacttca tccctgtcat ctgatggggt cctcactgtg aatggaccaa ggaaacaggt 480
ctctggccct gagcgcacca ttcccatcac ccgtgaagag aagcctgctg tcaccgcagc 540
cccaagaaa tagatgccct ttcttgaatt gcattttta aaacaagaaa gtttccccac 600
cagtgaatga aagtcttgtg actagtgctg aagcttatta atgctaaggg caggcccaaa 660
ttatcaagct aataaaatat cattcagcaa c 691

<210> 142
<211> 175
<212> PRT
<213> Homo Sapiens

<400> 142
Met Asp Ile Ala Ile His His Pro Trp Ile Arg Arg Pro Phe Phe Pro
1 5 10 15
Phe His Ser Pro Ser Arg Leu Phe Asp Gln Phe Phe Gly Glu His Leu
20 25 30
Leu Glu Ser Asp Leu Phe Pro Thr Ser Thr Ser Leu Ser Pro Phe Tyr
35 40 45
Leu Arg Pro Pro Ser Phe Leu Arg Ala Pro Ser Trp Phe Asp Thr Gly
50 55 60
Leu Ser Glu Met Arg Leu Glu Lys Asp Arg Phe Ser Val Asn Leu Asp
65 70 75 80
Val Lys His Phe Ser Pro Glu Glu Leu Lys Val Lys Val Leu Gly Asp
85 90 95
Val Ile Glu Val His Gly Lys His Glu Glu Arg Gln Asp Glu His Gly
100 105 110
Phe Ile Ser Arg Glu Phe His Arg Lys Tyr Arg Ile Pro Ala Asp Val
115 120 125
Asp Pro Leu Thr Ile Thr Ser Ser Leu Ser Ser Asp Gly Val Leu Thr
130 135 140
Val Asn Gly Pro Arg Lys Gln Val Ser Gly Pro Glu Arg Thr Ile Pro
145 150 155 160
Ile Thr Arg Glu Glu Lys Pro Ala Val Thr Ala Ala Pro Lys Lys
165 170 175

<210> 143
<211> 1300
<212> DNA
<213> Homo Sapiens

<400> 143
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tcctggatta cttttcagaa agaagtaatc ctttttatga cagaacatgt aataatgaag 120
tggtcaaaat gcagaggcta acattagaac acttgaatca gatggttgga atcgagtaca 180
tccttttgca tgctcaagag cccattcttt tcatcattcg gaagcaacag cggcagtccc 240
ctgcccaagt tatcccacta gctgattact atatcattgc tggagtgatc tatcaggcac 300
cagacttggg atcagttata aactctagag tgcttactgc agtgcatggt attcagtcag 360
cttttgatga agctatgtca tactgtcgat atcatccttc caaagggtat tggtggcact 420

tcaaagatca tgaagagcaa gataaagtca gacctaaagc caaaaggaaa gaagaaccaa 480
gctctatttt tcagagacaa cgtgtggatg ctttactttt agacctcaga caaaaatttc 540
cacccaaatt tgtgcagcta aagcctggag aaaagcctgt tcaagtggat caaacaaaga 600
aagaggcaga acctatacca gaaactgtaa aacctgagga gaaggagacc cccnnagaat 660
gtacaaccag accgggagtg ctaaaggccc ccctgaaaaa cggatgagac ttcagtgagt 720
actggacaaa agagaagcct ggaagactcc tcatgctagt tatcatacct cagtactgtg 780
gctcttgagc tttgaagtac tttattgtaa ccttcttatt tgtatggaat gcgcttattt 840
tttgaaagga tattaggccg gatgtggtgg ctcacgcctg taatcccagc actttgggag 900
gccatggcgg gtggatcact tgaggtcaga agttcaagac cagcctgacc aatatggtga 960
aaccccgtct ctactaaaaa tacaaaaatt agccgggcgt ggtggcgggc gcccgtagtc 1020
ccagctactc gggaggctga gacaggagac ttgcttgaac ccgggaggtg gaggttgccc 1080
tgagctgatt atcatgctgt tgcactccag cttgggcgac agagcgagac tttgtctcaa 1140
aaaagaagaa aagatattac tcccatcatg atttcttgtg aatatttgtt atatgtcttc 1200
tgtaaccttt cctctcccgg acttgagcaa cctacacact cacatgttta ctggtagata 1260
tgtttaaaag caaaataaag gtatttgtat atattgaaaa 1300

<210> 144
<211> 233
<212> PRT
<213> Homo Sapiens

<400> 144
Leu Leu Gly Ile Ser Trp Val Asp Ser Ser Trp Ile Pro Ile Leu Asn
1 5 10 15
Ser Gly Ser Val Leu Asp Tyr Phe Ser Glu Arg Ser Asn Pro Phe Tyr
20 25 30
Asp Arg Thr Cys Asn Asn Glu Val Val Lys Met Gln Arg Leu Thr Leu
35 40 45
Glu His Leu Asn Gln Met Val Gly Ile Glu Tyr Ile Leu Leu His Ala
50 55 60
Gln Glu Pro Ile Leu Phe Ile Ile Arg Lys Gln Gln Arg Gln Ser Pro
65 70 75 80
Ala Gln Val Ile Pro Leu Ala Asp Tyr Tyr Ile Ile Ala Gly Val Ile
85 90 95
Tyr Gln Ala Pro Asp Leu Gly Ser Val Ile Asn Ser Arg Val Leu Thr
100 105 110
Ala Val His Gly Ile Gln Ser Ala Phe Asp Glu Ala Met Ser Tyr Cys
115 120 125
Arg Tyr His Pro Ser Lys Gly Tyr Trp Trp His Phe Lys Asp His Glu
130 135 140
Glu Gln Asp Lys Val Arg Pro Lys Ala Lys Arg Lys Glu Glu Pro Ser
145 150 155 160
Ser Ile Phe Gln Arg Gln Arg Val Asp Ala Leu Leu Leu Asp Leu Arg
165 170 175
Gln Lys Phe Pro Pro Lys Phe Val Gln Leu Lys Pro Gly Glu Lys Pro
180 185 190
Val Gln Val Asp Gln Thr Lys Lys Glu Ala Glu Pro Ile Pro Glu Thr
195 200 205
Val Lys Pro Glu Glu Lys Glu Thr Pro Glu Cys Thr Thr Arg Pro Gly
210 215 220
Val Leu Lys Ala Pro Leu Lys Asn Gly
225 230

<210> 145
<211> 1528

<212> DNA
<213> Homo Sapiens

<400> 145
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gcggccaact ccaatgggcc tttccagccc gtggtccttc tccatattcg agatgttcct     180
cctgctgatc aagagaagct tttatccag aagttacgtc agtgttgcgt cctctttgac      240
tttgtttctg atccactaag tgacctaaag tggaaggaag taaaacgagc tgctttaagt     300
gaaatggtag aatatatcac ccataatcgg aatgtgatca cagagcctat ttacccagaa     360
gtagtccata tgtttgcagt taacatgttt cgaacattac caccttcctc caatcctacg     420
ggagcggaat ttgacccgga ggaagatgaa ccaacgttag aagcagcctg gcctcatcta     480
cagcttgttt atgaattttt cttaagattt ttagagtctc cagatttcca acctaatata     540
gcgaagaaat atattgatca gaagtttgta ttgcagcttt tagagctctt tgacagtgaa     600
gatcctcggg agagagattt tcttaaaacc acccttcaca gaatctatgg gaaattccta     660
ggcttgagag cttacatcag aaaacagata aataatatat tttataggtt tatttatgaa     720
acagagcatc ataatggcat agcagagtta ctggaaatat tgggaagtat aattaatgga     780
tttgccttac cactaaaaga agagcacaag attttcttat tgaaggtgtt actacctttg     840
cacaaagtga aatctctgag tgtctaccat ccccagctgg catactgtgt agtgcagttt     900
ttagaaaagg acagcacccct cacggaacca gtggtgatgg cacttctcaa atactggcca    960
aagactcaca gtccaaaaga agtaatgttc ttaaacgaat tagaagagat tttagatgtc    1020
attgaaccat cagaatttgt gaagatcatg gaacccctct tccggcagtt ggccaaatgt    1080
gtctccagcc cacacttcca ggtggcagag cgagctctct attactggaa taatgaatac    1140
atcatgagtt taatcagtga caacgcagcg aagattctgc ccatcatgtt tccttccttg    1200
taccgcaact caaagaccca ttggaacaag acaatacatg gcttgatata caacgccctg    1260
aagctcttca tggagatgaa ccaaaagcta tttgatgact gtacacaaca gttcaaagca    1320
gagaaactaa aagagaagct aaaaatgaaa gaacgggaag aagcatgggt taaaatagaa    1380
aatctagcca aagccaatcc ccaggtacta aaaaagagaa taacatgaaa aggcccaggg    1440
ttacttgaat gtttttataa gataggaata tatgtcttca ccatgggggg ggtctcgatt    1500
tcactaacgt tgtatatgaa aatgtctg                                       1528
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<210> 146
<211> 449
<212> PRT
<213> Homo Sapiens

<400> 146
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Met Leu Thr Cys Asn Lys Ala Gly Ser Arg Met Val Val Asp Ala Ala
 1               5                  10                  15
Asn Ser Asn Gly Pro Phe Gln Pro Val Val Leu Leu His Ile Arg Asp
            20                  25                  30
Val Pro Pro Ala Asp Gln Glu Lys Leu Phe Ile Gln Lys Leu Arg Gln
        35                  40                  45
Cys Cys Val Leu Phe Asp Phe Val Ser Asp Pro Leu Ser Asp Leu Lys
    50                  55                  60
Trp Lys Glu Val Lys Arg Ala Ala Leu Ser Glu Met Val Glu Tyr Ile
65                  70                  75                  80
Thr His Asn Arg Asn Val Ile Thr Glu Pro Ile Tyr Pro Glu Val Val
                85                  90                  95
His Met Phe Ala Val Asn Met Phe Arg Thr Leu Pro Pro Ser Ser Asn
            100                 105                 110
Pro Thr Gly Ala Glu Phe Asp Pro Glu Glu Asp Glu Pro Thr Leu Glu
        115                 120                 125
Ala Ala Trp Pro His Leu Gln Leu Val Tyr Glu Phe Phe Leu Arg Phe
    130                 135                 140
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Leu Glu Ser Pro Asp Phe Gln Pro Asn Ile Ala Lys Lys Tyr Ile Asp
145 150 155 160
Gln Lys Phe Val Leu Gln Leu Leu Glu Leu Phe Asp Ser Glu Asp Pro
165 170 175
Arg Glu Arg Asp Phe Leu Lys Thr Thr Leu His Arg Ile Tyr Gly Lys
180 185 190
Phe Leu Gly Leu Arg Ala Tyr Ile Arg Lys Gln Ile Asn Asn Ile Phe
195 200 205
Tyr Arg Phe Ile Tyr Glu Thr Glu His His Asn Gly Ile Ala Glu Leu
210 215 220
Leu Glu Ile Leu Gly Ser Ile Ile Asn Gly Phe Ala Leu Pro Leu Lys
225 230 235 240
Glu Glu His Lys Ile Phe Leu Leu Lys Val Leu Leu Pro Leu His Lys
245 250 255
Val Lys Ser Leu Ser Val Tyr His Pro Gln Leu Ala Tyr Cys Val Val
260 265 270
Gln Phe Leu Glu Lys Asp Ser Thr Leu Thr Glu Pro Val Val Met Ala
275 280 285
Leu Leu Lys Tyr Trp Pro Lys Thr His Ser Pro Lys Glu Val Met Phe
290 295 300
Leu Asn Glu Leu Glu Glu Ile Leu Asp Val Ile Glu Pro Ser Glu Phe
305 310 315 320
Val Lys Ile Met Glu Pro Leu Phe Arg Gln Leu Ala Lys Cys Val Ser
325 330 335
Ser Pro His Phe Gln Val Ala Glu Arg Ala Leu Tyr Tyr Trp Asn Asn
340 345 350
Glu Tyr Ile Met Ser Leu Ile Ser Asp Asn Ala Ala Lys Ile Leu Pro
355 360 365
Ile Met Phe Pro Ser Leu Tyr Arg Asn Ser Lys Thr His Trp Asn Lys
370 375 380
Thr Ile His Gly Leu Ile Tyr Asn Ala Leu Lys Leu Phe Met Glu Met
385 390 395 400
Asn Gln Lys Leu Phe Asp Asp Cys Thr Gln Gln Phe Lys Ala Glu Lys
405 410 415
Leu Lys Glu Lys Leu Lys Met Lys Glu Arg Glu Glu Ala Trp Val Lys
420 425 430
Ile Glu Asn Leu Ala Lys Ala Asn Pro Gln Val Leu Lys Lys Arg Ile
435 440 445
Thr

<210> 147
<211> 1580
<212> DNA
<213> Homo Sapiens

<400> 147
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catgctccat cgcctgggaa atttggtgag cggcctccac ctaaacgact tactagggaa 180
gctatgcgaa attatttaaa agagcgaggg gatcaaacag tacttattct tcatgcaaaa 240
gttgcacaga agtcatatgg aaatgaaaaa aggtttttt gcccacctcc ttgtgtatat 300
cttatgggca gcggatggaa gaaaaaaaaa gaacaaatgg aacgcgatgg ttgttctgaa 360
caagagtctc aaccgtgtgc atttattggg ataggaaata gtgaccaaga aatgcagcag 420
ctaaacttgg aaggaaagaa ctattgcaca gccaaaacat tgtatatatc tgactcagac 480

aagcgaaagc acttcatttt ttctgtaaag atgttctatg gcaacagtga tgacattggt 540
gtgttcctca gcaagcggat aaaagtcatc tccaaacctt ccaaaaagaa gcagtcattg 600
aaaaatgctg acttatgcat tgcctcagga acaaaggtgg ctctgtttaa tcgactacga 660
tcccagacag ttagtaccag atacttgcat gtagaaggag gtaattttca tgccagttca 720
cagcagtggg gagccttttt tattcatctc ttggatgatg atgaatcaga aggagaagaa 780
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actggcatgg cactcccaag attgataatt atgaaagttg ataagcatac cgcattattg 900
gatgcagatg atcctgtgtc acaactccat aaatgtgcat ttttacctta ggatacagaa 960
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ggacagaatt tcactccaaa tttacgagtg tggtttgggg atgtagaagc tgaaactatg 1260
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agtgtagcag gagcaatcct tccagccaat tcaagccagg tgccccctaa cgaatcaaac 1500
acaaacagcg agggaagtta cacaaacgcc agcacaaatt caaccagtgt cacatcatct 1560
acagccacag tggtatccta 1580

<210> 148
<211> 500
<212> PRT
<213> Homo Sapiens

<400> 148
Met Asp His Thr Glu Gly Leu Pro Ala Glu Glu Pro Pro Ala His Ala
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Pro Ser Pro Gly Lys Phe Gly Glu Arg Pro Pro Pro Lys Arg Leu Thr
20 25 30
Arg Glu Ala Met Arg Asn Tyr Leu Lys Glu Arg Gly Asp Gln Thr Val
35 40 45
Leu Ile Leu His Ala Lys Val Ala Gln Lys Ser Tyr Gly Asn Glu Lys
50 55 60
Arg Phe Phe Cys Pro Pro Pro Cys Val Tyr Leu Met Gly Ser Gly Trp
65 70 75 80
Lys Lys Lys Lys Glu Gln Met Glu Arg Asp Gly Cys Ser Glu Gln Glu
85 90 95
Ser Gln Pro Cys Ala Phe Ile Gly Ile Gly Asn Ser Asp Gln Glu Met
100 105 110
Gln Gln Leu Asn Leu Glu Gly Lys Asn Tyr Cys Thr Ala Lys Thr Leu
115 120 125
Tyr Ile Ser Asp Ser Asp Lys Arg Lys His Phe Ile Phe Ser Val Lys
130 135 140
Met Phe Tyr Gly Asn Ser Asp Asp Ile Gly Val Phe Leu Ser Lys Arg
145 150 155 160
Ile Lys Val Ile Ser Lys Pro Ser Lys Lys Lys Gln Ser Leu Lys Asn
165 170 175
Ala Asp Leu Cys Ile Ala Ser Gly Thr Lys Val Ala Leu Phe Asn Arg
180 185 190
Leu Arg Ser Gln Thr Val Ser Thr Arg Tyr Leu His Val Glu Gly Gly
195 200 205
Asn Phe His Ala Ser Ser Gln Gln Trp Gly Ala Phe Phe Ile His Leu
210 215 220
Leu Asp Asp Asp Glu Ser Glu Gly Glu Glu Phe Thr Val Arg Asp Val

225 230 235 240
Tyr Ile His Tyr Gly Gln Thr Cys Lys Leu Val Cys Ser Val Thr Gly
245 250 255
Met Ala Leu Pro Arg Leu Ile Ile Met Lys Val Asp Lys His Thr Ala
260 265 270
Leu Leu Asp Ala Asp Asp Pro Val Ser Gln Leu His Lys Cys Ala Phe
275 280 285
Tyr Leu Lys Asp Thr Glu Arg Met Tyr Leu Cys Leu Ser Gln Glu Arg
290 295 300
Ile Ile Gln Phe Gln Ala Thr Pro Cys Pro Lys Glu Pro Asn Lys Glu
305 310 315 320
Met Ile Asn Asp Gly Ala Ser Trp Thr Ile Ile Ser Thr Asp Lys Ala
325 330 335
Glu Tyr Thr Phe Tyr Glu Gly Met Gly Pro Val Leu Ala Pro Val Thr
340 345 350
Pro Val Pro Val Val Glu Ser Leu Gln Leu Asn Gly Gly Gly Asp Val
355 360 365
Ala Met Leu Glu Leu Thr Gly Gln Asn Phe Thr Pro Asn Leu Arg Val
370 375 380
Trp Phe Gly Asp Val Glu Ala Glu Thr Met Tyr Arg Cys Gly Glu Ser
385 390 395 400
Met Leu Cys Val Val Pro Asp Ile Ser Ala Phe Arg Glu Gly Trp Arg
405 410 415
Trp Val Arg Gln Pro Val Gln Val Pro Val Thr Leu Val Arg Asn Asp
420 425 430
Gly Ile Ile Tyr Ser Thr Ser Leu Thr Phe Thr Tyr Thr Pro Glu Pro
435 440 445
Gly Pro Arg Pro His Cys Ser Val Ala Gly Ala Ile Leu Pro Ala Asn
450 455 460
Ser Ser Gln Val Pro Pro Asn Glu Ser Asn Thr Asn Ser Glu Gly Ser
465 470 475 480
Tyr Thr Asn Ala Ser Thr Asn Ser Thr Ser Val Thr Ser Ser Thr Ala
485 490 495
Thr Val Val Ser
500

<210> 149
<211> 1248
<212> DNA
<213> Homo Sapiens

<400> 149
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gccgccatgc gcgacaggac ccacgagctg agacaggggg atgacagctc ggacgaagag 120
gacaaggagc gggtcgcgct ggtggtgcac ccgggcacgg cacggctggg gagcccggac 180
gaggagttct tccacaaggt ccggacaatt cgtcagacta ttgtcaaact ggggaataaa 240
gtccaggagt tggagaaaca gcaggtcacc atcctggcca cgccccttcc cgaggagagc 300
atgaagcagg agctgcagaa cctgcgcgat gagatcaaac agctggggag ggagatccgc 360
ctgcagctga aggccataga gccccagaag gaggaagctg atgagaacta taactccgtc 420
aacacaagaa tgagaaaaac ccagcatggg gtcctgtccc agcaattcgt ggagctcatc 480
aacaagtgca attcaatgca gtccgaatac cgggagaaga acgtggagcg gattcggagg 540
cagctgaaga tcaccaatgc tggcatggtg tctgatgagg agttggatca gatgctggac 600
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gccttaaatg agatctcggc ccggcacagt gagatccagc agcttgaacg cagtattcgt 720
gagctgcacg acatattcac ttttctggct accgaagtgg agatgcaggg ggagatgatc 780

aatcggattg agaagaacat cctgagctca gcggactacg tggaacgtgg gcaggagcac 840
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tgtgtgtcca tcaccgtcgt cctcctagca gtcatcattg gcgtcacagt ggttggataa 960
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agaagggcag acagttcttc tggggttggc agctgctcat tcatgatggc ctcctccttc 1140
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aaaaaattaa aaaacaaaaa aagagcatag aaaaaaaaaa aaccgagt 1248

<210> 150
<211> 297
<212> PRT
<213> Homo Sapiens

<400> 150

Met Arg Asp Arg Thr His Glu Leu Arg Gln Gly Asp Asp Ser Ser Asp
1 5 10 15
Glu Glu Asp Lys Glu Arg Val Ala Leu Val Val His Pro Gly Thr Ala
20 25 30
Arg Leu Gly Ser Pro Asp Glu Glu Phe Phe His Lys Val Arg Thr Ile
35 40 45
Arg Gln Thr Ile Val Lys Leu Gly Asn Lys Val Gln Glu Leu Glu Lys
50 55 60
Gln Gln Val Thr Ile Leu Ala Thr Pro Leu Pro Glu Glu Ser Met Lys
65 70 75 80
Gln Glu Leu Gln Asn Leu Arg Asp Glu Ile Lys Gln Leu Gly Arg Glu
85 90 95
Ile Arg Leu Gln Leu Lys Ala Ile Glu Pro Gln Lys Glu Glu Ala Asp
100 105 110
Glu Asn Tyr Asn Ser Val Asn Thr Arg Met Arg Lys Thr Gln His Gly
115 120 125
Val Leu Ser Gln Gln Phe Val Glu Leu Ile Asn Lys Cys Asn Ser Met
130 135 140
Gln Ser Glu Tyr Arg Glu Lys Asn Val Glu Arg Ile Arg Arg Gln Leu
145 150 155 160
Lys Ile Thr Asn Ala Gly Met Val Ser Asp Glu Glu Leu Asp Gln Met
165 170 175
Leu Asp Ser Gly Gln Ser Glu Val Phe Val Ser Asn Ile Leu Lys Asp
180 185 190
Thr Gln Val Thr Arg Gln Ala Leu Asn Glu Ile Ser Ala Arg His Ser
195 200 205
Glu Ile Gln Gln Leu Glu Arg Ser Ile Arg Glu Leu His Asp Ile Phe
210 215 220
Thr Phe Leu Ala Thr Glu Val Glu Met Gln Gly Glu Met Ile Asn Arg
225 230 235 240
Ile Glu Lys Asn Ile Leu Ser Ser Ala Asp Tyr Val Glu Arg Gly Gln
245 250 255
Glu His Val Lys Thr Ala Leu Glu Asn Gln Lys Lys Val Arg Lys Lys
260 265 270
Lys Val Leu Ile Ala Ile Cys Val Ser Ile Thr Val Val Leu Leu Ala
275 280 285
Val Ile Ile Gly Val Thr Val Val Gly
290 295

<210> 151

<211> 1953
<212> DNA
<213> Homo Sapiens

<400> 151
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ccaacctgcc ggccatggag accccgtccc agcggcgcgc cacccgcagc ggggcgcagg 180
ccagctccac tccgctgtcg cccacccgca tcacccggct gcaggagaag gaggacctgc 240
aggagctcaa tgatcgcttg gcggtctaca tcgaccgtgt gcgctcgctg gaaacggaga 300
acgcagggct gcgccttcgc atcaccgagt ctgaagaggt ggtcagccgc gaggtgtccg 360
gcatcaaggc cgcctacgag gccgagctcg gggatgcccg caagaccctt gactcagtag 420
ccaaggagcg cgcccgcctg cagctggagc tgagcaaagt gcgtgaggag tttaaggagc 480
tgaaagcgcg caataccaag aaggagggtg acctgatagc tgctcaggct cggctgaagg 540
acctggaggc tctgctgaac tccaaggagg ccgcactgag cactgctctc agtgagaagc 600
gcacgctgga gggcgagctg catgatctgc ggggccaggt ggccaagctt gaggcagccc 660
taggtgaggc caagaagcaa cttcaggatg agatgctgcg gcgggtggat gctgagaaca 720
ggctgcagac catgaaggag gaactggact tccagaagaa catctacagt gaggagctgc 780
gtgagaccaa gcgccgtcat gagacccgac tggtggagat tgacaatggg aagcagcgtg 840
agtttgagag ccggctggcg gatgcgctgc aggaactgcg ggcccagcat gaggaccagg 900
tggagcagta taagaaggag ctggagaaga cttattctgc caagctggac aatgccaggc 960
agtctgctga gaggaacagc aacctggtgg gggctgccca cgaggagctg cagcagtcgc 1020
gcatccgcat cgacagcctc tctgcccagc tcagccagct ccagaagcag ctggcagcca 1080
aggaggcgaa gcttcgagac ctggaggact cactggcccg tgagcgggac accagccggc 1140
ggctgctggc ggaaaaggag cgggagatgg ccgagatgcg ggcaaggatg cagcagcagc 1200
tggacgagta ccaggagctt ctggacatca agctggccct ggacatggag atccacgcct 1260
accgcaagct cttggagggc gaggaggaga ggctacgcct gtcccccagc cctacctcgc 1320
agcgcagccg tggccgtgct tcctctcact catcccagac acagggtggg ggcagcgtca 1380
ccaaaaagcg caaactggag tccactgaga gccgcagcag cttctcacag cacgcacgca 1440
ctagcgggcg cgtggccgtg gaggaggtgg atgaggaggg caagtttgtc cggctgcgca 1500
acaagtccaa tgaggaccag tccatgggca attggcagat caagcgccag aatggagatg 1560
atcccttgct gacttaccgg ttcccaccaa agttcaccct gaaggctggg caggtggtga 1620
cgatctgggc tgcaggagct ggggccaccc acagcccccc taccgacctg gtgtggaagg 1680
cacagaacac ctggggctgc gggaacagcc tgcgtacggc tctcatcaac tccactgggg 1740
aagaagtggc catgcgcaag ctggtgcgct cagtgactgt ggttgaggac gacgaggatg 1800
aggatggaga tgacctgctc catcaccacc acgtgagtgg tagccgccgc tgaggccgag 1860
cctgcactgg ggccaccagc caggcctggg ggcagcctct ccccagcctc cccgtgccaa 1920
aaatcttttc attaaagaat gttttggaac ttt 1953

<210> 152
<211> 572
<212> PRT
<213> Homo Sapiens

<400> 152
Met Glu Thr Pro Ser Gln Arg Arg Ala Thr Arg Ser Gly Ala Gln Ala
1 5 10 15
Ser Ser Thr Pro Leu Ser Pro Thr Arg Ile Thr Arg Leu Gln Glu Lys
20 25 30
Glu Asp Leu Gln Glu Leu Asn Asp Arg Leu Ala Val Tyr Ile Asp Arg
35 40 45
Val Arg Ser Leu Glu Thr Glu Asn Ala Gly Leu Arg Leu Arg Ile Thr
50 55 60
Glu Ser Glu Glu Val Val Ser Arg Glu Val Ser Gly Ile Lys Ala Ala
65 70 75 80

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Tyr Glu Ala Glu Leu Gly Asp Ala Arg Lys Thr Leu Asp Ser Val Ala
                85                  90                  95
Lys Glu Arg Ala Arg Leu Gln Leu Glu Leu Ser Lys Val Arg Glu Glu
            100                 105                 110
Phe Lys Glu Leu Lys Ala Arg Asn Thr Lys Lys Glu Gly Asp Leu Ile
        115                 120                 125
Ala Ala Gln Ala Arg Leu Lys Asp Leu Glu Ala Leu Leu Asn Ser Lys
    130                 135                 140
Glu Ala Ala Leu Ser Thr Ala Leu Ser Glu Lys Arg Thr Leu Glu Gly
145                 150                 155                 160
Glu Leu His Asp Leu Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu
                165                 170                 175
Gly Glu Ala Lys Lys Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp
            180                 185                 190
Ala Glu Asn Arg Leu Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys
        195                 200                 205
Asn Ile Tyr Ser Glu Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr
    210                 215                 220
Arg Leu Val Glu Ile Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg
225                 230                 235                 240
Leu Ala Asp Ala Leu Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val
                245                 250                 255
Glu Gln Tyr Lys Lys Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp
            260                 265                 270
Asn Ala Arg Gln Ser Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala
        275                 280                 285
His Glu Glu Leu Gln Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala
    290                 295                 300
Gln Leu Ser Gln Leu Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu
305                 310                 315                 320
Arg Asp Leu Glu Asp Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg
                325                 330                 335
Leu Leu Ala Glu Lys Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met
            340                 345                 350
Gln Gln Gln Leu Asp Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala
        355                 360                 365
Leu Asp Met Glu Ile His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu
    370                 375                 380
Glu Arg Leu Arg Leu Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly
385                 390                 395                 400
Arg Ala Ser Ser His Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr
                405                 410                 415
Lys Lys Arg Lys Leu Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln
            420                 425                 430
His Ala Arg Thr Ser Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu
        435                 440                 445
Gly Lys Phe Val Arg Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met
    450                 455                 460
Gly Asn Trp Gln Ile Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr
465                 470                 475                 480
Tyr Arg Phe Pro Pro Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr
                485                 490                 495
Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu
            500                 505                 510
Val Trp Lys Ala Gln Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr
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515 520 525
Ala Leu Ile Asn Ser Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val
530 535 540
Arg Ser Val Thr Val Val Glu Asp Asp Glu Asp Glu Asp Gly Asp Asp
545 550 555 560
Leu Leu His His His His Val Ser Gly Ser Arg Arg
565 570

<210> 153
<211> 1610
<212> DNA
<213> Homo Sapiens

<400> 153
ctgcaggaat tcggcacgag cggtcacgcc gagccagcgc ctgggcctgg aaccgggccg 60
tagcccccca gtttcgccca ccacctccct accatggacc cccgcaaagt gaacgagctt 120
cgggcctttg tgaaaatgtg taagcaggat ccgagcgttc tgtacaccga ggaaatgcgc 180
ttcctgaggg agtgggtgga gagcataggt ggtaaagtac cacctgctac tcagaaagct 240
atatcagaag aaaataccaa ggaagaaaaa cctgatagta agaaggtgga ggaagactta 300
aaggcagacg aaccatcaag tgaggaaagt gatctagaaa ttgataaaga aggtgtgatt 360
gaaccagaca ctgatgctcc tcaagaaatg ggagatgaaa atgcggagat aacggaggag 420
atgatggatc aggcaaatga taaaaaagtg gctgctattg aagccctaaa tgatggtgaa 480
ctccagaaag ccattgactt attcacagat gccatcaagc tgaatcctcg cttggccatt 540
ttgtatgcca agagggccag tgtcttcgtc aaattacaga agccaaatgc tgccatccga 600
gactgtgaca gagccattga aataaatcct gattcagctc agccttacaa gtggcggggg 660
aaagcacaca gacttctagg ccactgggaa gaagcagccc atgatcttgc ccttgcctgt 720
aaattggatt atgatgaaga tgctagtgca atgctgaaag aagttcaacc tagggcacag 780
aaaattgcag aacatcggag aaagtatgag cgaaaacgtg aagagcgaga gatcaaagaa 840
agaatagaac gagttaagaa ggctcgagaa gagcatgaga gagcccagag ggaggaagaa 900
gccagacgac agtcaggagc tcagtatggc tcttttccag gtggctttcc tgggggaatg 960
cctggtaatt ttcccggagg aatgcctgga atgggagggg gcatgcctgg aatggctgga 1020
atgcctggac tcaatgaaat tcttagtgat ccagaggttc ttgcagccat gcaggatcca 1080
gaagttatgg tggctttcca ggatgtggct cagaacccag caaatatgtc aaaataccag 1140
agcaacccaa aggttatgaa tctcatcagt aaattgtcag ccaaatttgg aggtcaagcg 1200
taatgtcctt ctgataaata aagcccttgc tgaaggaaaa gcaacctaga tcaccttatg 1260
gatgtcgcaa taatacaaac cagtgtacct ctgaccttct catcaagaga gctggggtgc 1320
tttgaagata atccctaccc ctctccccca aatgcagctg aagcatttta cagtggtttg 1380
ccattagggt attcattcag ataatgtttt cctactagga attacaaact ttaaacactt 1440
tttaaatctt caaaatattt aaaacaaatt taaagggcct gttaattctt atatttttct 1500
ttactaatca ttttggattt ttttctttga attattggca gggaatatac ttatgtatgg 1560
aagattactg ctctgagtga aataaaagtt attagtgcga ggcaaacata 1610

<210> 154
<211> 369
<212> PRT
<213> Homo Sapiens

<400> 154
Met Asp Pro Arg Lys Val Asn Glu Leu Arg Ala Phe Val Lys Met Cys
1 5 10 15
Lys Gln Asp Pro Ser Val Leu Tyr Thr Glu Glu Met Arg Phe Leu Arg
20 25 30
Glu Trp Val Glu Ser Ile Gly Gly Lys Val Pro Pro Ala Thr Gln Lys
35 40 45
Ala Ile Ser Glu Glu Asn Thr Lys Glu Glu Lys Pro Asp Ser Lys Lys

50 55 60
Val Glu Glu Asp Leu Lys Ala Asp Glu Pro Ser Ser Glu Glu Ser Asp
65 70 75 80
Leu Glu Ile Asp Lys Glu Gly Val Ile Glu Pro Asp Thr Asp Ala Pro
85 90 95
Gln Glu Met Gly Asp Glu Asn Ala Glu Ile Thr Glu Glu Met Met Asp
100 105 110
Gln Ala Asn Asp Lys Lys Val Ala Ala Ile Glu Ala Leu Asn Asp Gly
115 120 125
Glu Leu Gln Lys Ala Ile Asp Leu Phe Thr Asp Ala Ile Lys Leu Asn
130 135 140
Pro Arg Leu Ala Ile Leu Tyr Ala Lys Arg Ala Ser Val Phe Val Lys
145 150 155 160
Leu Gln Lys Pro Asn Ala Ala Ile Arg Asp Cys Asp Arg Ala Ile Glu
165 170 175
Ile Asn Pro Asp Ser Ala Gln Pro Tyr Lys Trp Arg Gly Lys Ala His
180 185 190
Arg Leu Leu Gly His Trp Glu Glu Ala Ala His Asp Leu Ala Leu Ala
195 200 205
Cys Lys Leu Asp Tyr Asp Glu Asp Ala Ser Ala Met Leu Lys Glu Val
210 215 220
Gln Pro Arg Ala Gln Lys Ile Ala Glu His Arg Arg Lys Tyr Glu Arg
225 230 235 240
Lys Arg Glu Glu Arg Glu Ile Lys Glu Arg Ile Glu Arg Val Lys Lys
245 250 255
Ala Arg Glu Glu His Glu Arg Ala Gln Arg Glu Glu Glu Ala Arg Arg
260 265 270
Gln Ser Gly Ala Gln Tyr Gly Ser Phe Pro Gly Gly Phe Pro Gly Gly
275 280 285
Met Pro Gly Asn Phe Pro Gly Gly Met Pro Gly Met Gly Gly Gly Met
290 295 300
Pro Gly Met Ala Gly Met Pro Gly Leu Asn Glu Ile Leu Ser Asp Pro
305 310 315 320
Glu Val Leu Ala Ala Met Gln Asp Pro Glu Val Met Val Ala Phe Gln
325 330 335
Asp Val Ala Gln Asn Pro Ala Asn Met Ser Lys Tyr Gln Ser Asn Pro
340 345 350
Lys Val Met Asn Leu Ile Ser Lys Leu Ser Ala Lys Phe Gly Gly Gln
355 360 365
Ala

<210> 155
<211> 1323
<212> DNA
<213> Homo Sapiens

<400> 155
cacaaaggca ccaaaccaca aaacgtcaca cgtaaacatc atacgtggca accacaagcc 60
aatcagttgg atatttcatt cattggtata catatggact gtaaggtgtc tttcaggttg 120
cagaaaagat ggaaaaaagg acatgtgcac tctgccccaa agatgtcgaa tataatgtcc 180
tgtactttgc acaatcagag aatatagctg ctcatgagaa ttgtttgctg tattcttcag 240
gacttgtgga atgtgaggat caggatccac ttaatcctga tagaagtttt gatgtggaat 300
cagtaaagaa agaaatccag agaggaagga agttgaaatg caaattttgt cataaaagag 360
gagccaccgt gggatgtgat ttaaaaaact gtaacaagaa ttaccacttt ttctgtgcca 420

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agaaggacga cgcagttcca cagtctgatg gagttcgagg aatttataaa ctgctttgcc     480
agcaacatgc tcaattcccg atcatcgctc aaagtgctaa attttcagga gtgaaaagaa     540
aaagaggaag gaagaaaccc ctctcaggca atcatgtaca gccacccgaa acaatgaaat     600
gtaatacatt cataagacaa gtgaaagaag agcatggcag acacacagat gcaactgtga     660
aagttccttt tcttaagaaa tgcaagggaa gcaggacttc ttaattactt acttgaagaa     720
atattagnca aagttcattc aattccagaa aaactcatgg atgagactta cttcagaatc     780
agactatgaa gaaatcggga gtgcactttt tgactgtaga ttgttcgaag acacatttgt     840
aaattttcaa gcagcaatag agaaaaaaat tcatgcatct caacaaaggt ggcagcagtt     900
gaaggaagag attgagctac ttcaggactt aaaacaaacc ttgtgctctt ttcaagaaaa     960
tagagatctt atgtcaagtt ctacatcaat atcatccctg tcttattagg gattaccatt    1020
tcctaagcca agagtcatgt caaattgcaa tcaggctcaa aaccagagac caggctgtga    1080
aatccacaca tctttagaac tagtcgtctc ctcttggcct cagcagctct tccctgttct    1140
tactggttga cattttgatc actctttgca cactcttgtg tttttgctc actgtcacac     1200
tcccagcacc tagtatgctc agtaaatgtt tgtggaataa gtgcataaaa tgttcttaac    1260
ctttgattct acttacagcc catgatagcc tcttagatat aataaatttg gattatacta    1320
aaa                                                                   1323
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<210> 156
<211> 191
<212> PRT
<213> Homo Sapiens

<400> 156

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Met Glu Lys Arg Thr Cys Ala Leu Cys Pro Lys Asp Val Glu Tyr Asn
 1               5                  10                  15
Val Leu Tyr Phe Ala Gln Ser Glu Asn Ile Ala Ala His Glu Asn Cys
            20                  25                  30
Leu Leu Tyr Ser Ser Gly Leu Val Glu Cys Glu Asp Gln Asp Pro Leu
        35                  40                  45
Asn Pro Asp Arg Ser Phe Asp Val Glu Ser Val Lys Lys Glu Ile Gln
    50                  55                  60
Arg Gly Arg Lys Leu Lys Cys Lys Phe Cys His Lys Arg Gly Ala Thr
65                  70                  75                  80
Val Gly Cys Asp Leu Lys Asn Cys Asn Lys Asn Tyr His Phe Phe Cys
                85                  90                  95
Ala Lys Lys Asp Asp Ala Val Pro Gln Ser Asp Gly Val Arg Gly Ile
            100                 105                 110
Tyr Lys Leu Leu Cys Gln Gln His Ala Gln Phe Pro Ile Ile Ala Gln
        115                 120                 125
Ser Ala Lys Phe Ser Gly Val Lys Arg Lys Arg Gly Arg Lys Lys Pro
    130                 135                 140
Leu Ser Gly Asn His Val Gln Pro Pro Glu Thr Met Lys Cys Asn Thr
145                 150                 155                 160
Phe Ile Arg Gln Val Lys Glu Glu His Gly Arg His Thr Asp Ala Thr
                165                 170                 175
Val Lys Val Pro Phe Leu Lys Lys Cys Lys Gly Ser Arg Thr Ser
            180                 185                 190
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<210> 157
<211> 4065
<212> DNA
<213> Homo Sapiens

<400> 157

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atgtcgactg gggacagttt tgagactcga tttgaaaaaa tggacaacct gctgcgggat      60
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cccaaatcgg aagtgaattc ggattgtttg ctggatggat tggatgcttt ggtatatgat 120
ttggattttc ctgccttaag aaaaaacaaa aatattgaca actttttaag cagatataaa 180
gacacaataa ataaaatcag agatttacga atgaaagctg aagattatga agtagtgaag 240
gtgattggta gaggtgcatt tggagaagtt caattggtaa ggcataaatc caccaggaag 300
gtatatgcta tgaagcttct cagcaaattt gaaatgataa agagatctga ttctgctttt 360
ttctgggaag aaagggacat catggctttt gccaacagtc cttgggttgt tcagcttttt 420
tatgcattcc aagatgatcg ttatctctac atggtgatgg aatacatgcc tggtggagat 480
cttgtaaact taatgagcaa ctatgatgtg cctgaaaaat gggcacgatt ctatactgca 540
gaagtagttc ttgcattgga tgcaatccat tccatgggtt ttattcacag agatgtgaag 600
cctgataaca tgctgctgga taaatctgga catttgaagt tagcagattt tggtacttgt 660
atgaagatga ataaggaagg catggtacga tgtgatacag cggttggaac acctgattat 720
atttcccctg aagtattaaa atcccaaggt ggtgatggtt attatggaag agaatgtgac 780
tggtggtcgg ttggggtatt tttatacgaa atgcttgtag gtgatacacc tttttatgca 840
gattctttgg ttggaactta cagtaaaatt atgaaccata aaaattcact tacctttcct 900
gatgataatg acatatcaaa agaagcaaaa aaccttattt gtgccttcct tactgacagg 960
gaagtgaggt tagggcgaaa tggtgtagaa gaaatcaaac gacatctctt cttcaaaaat 1020
gaccagtggg cttgggaaac gctccgagac actgtagcac cagttgtacc cgatttaagt 1080
agtgacattg atactagtaa ttttgatgac ttggaagaag ataaaggaga ggaagaaaca 1140
ttccctattc ctaaagcttt cgttggcaat caactacctt ttgtaggatt tacatattat 1200
agcaatcgta gatacttatc ttcagcaaat cctaatgata acagaactag ctccaatgca 1260
gataaaagct tgcaggaaag tttgcaaaaa acaatctata agctggaaga acagctgcat 1320
aatgaaatgc agttaaaaga tgaaatggag cagaagtgca gaacctcaaa cataaaacta 1380
gacaagataa tgaaagaatt ggatgaagag ggaaatcaaa gaagaaatct agaatctaca 1440
gtgtctcaga ttgagaagga gaaaatgttg ctacagcata gaattaatga gtaccaaaga 1500
aaagctgaac aggaaaatga gaagagaaga aatgtagaaa atgaagtttc tacattaaag 1560
gatcagttgg aagacttaaa gaaagtcagt cagaattcac agcttgctaa tgagaagctg 1620
tcccagttac aaaagcagct agaagaagcc aatgacttac ttaggacaga atcggacaca 1680
gctgtaagat tgaggaagag tcacacagag atgagcaagt caattagtca gttagagtcc 1740
ctgaacagag agttgcaaga gagaaatcga attttagaga attctaagtc acaaacagac 1800
aaagattatt accagctgca agctatatta gaagctgaac gaagagacag aggtcatgat 1860
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cactcagaaa aggaaaagaa taatttagag atagatttaa actacaaact taaatcatta 2040
caacaacggt tagaacaaga ggtaaatgaa cacaaagtaa ccaaagctcg tttaactgac 2100
aaacatcaat ctattgaaga ggcaaagtct gtggcaatgt gtgagatgga aaaaaagctg 2160
aaagaagaaa gagaagctcg agagaaggct gaaaatcggg ttgttcagat tgagaaacag 2220
tgttccatgc tagacgttga tctgaagcaa tctcagcaga aactagaaca tttgactgga 2280
aataaagaaa ggatggagga tgaagttaag aatctaaccc tgcaactgga gcaggaatca 2340
aataagcggc tgttgttaca aaatgaattg aagactcaag catttgaggc agacaattta 2400
aaaggtttag aaaagcagat gaaacaggaa ataaatactt tattggaagc aaagagatta 2460
ttagaatttg agttagctca gcttacgaaa cagtatagag gaaatgaagg acagatgcgg 2520
gagctacaag atcagcttga agctgagcaa tatttctcga cactttataa aacccaggta 2580
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tctgagcagt tggcgcgagg ccttctggaa gaacagtatt ttgaattgac gcaagaaagc 2760
aagaaagctg cttcaagaaa tagacaagag attacagata aagatcacac tgttagtcgg 2820
cttgaagaag caaacagcat gctaaccaaa gatattgaaa tattaagaag agagaatgaa 2880
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atcagtaatc ttaaggctgc ctttgaaaag aatatcaaca ctgaacgaac ccttaaaaca 3000
caggctgtta acaaattggc agaaataatg aatcgaaaag attttaaaat tgatagaaag 3060
aaagctaata cacaagattt gagaaagaaa gaaaaggaaa atcgaaagct gcaactggaa 3120
ctcaaccaag aaagagagaa attcaaccag atggtagtga aacatcagaa ggaactgaat 3180
gacatgcaag cgcaattggt agaagaatgt gcacatagga atgagcttca gatgcagttg 3240
gccagcaaag agagtgatat tgagcaattg cgtgctaaac ttttggacct ctcggattct 3300
acaagtgttg ctagttttcc tagtgctgat gaaactgatg gtaacctccc agagtcaaga 3360

attgaaggtt ggctttcagt accaaataga ggaaatatca aacgatatgg ctggaagaaa 3420
cagtatgttg tggtaagcag caaaaaaatt ttgttctata atgacgaaca agataaggag 3480
caatccaatc catctatggt attggacata gataaactgt ttcacgttag acctgtaacc 3540
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gcaaatgaag gtgaatgtag aaaagatgta gagatggaac cagtacaaca agctgaaaaa 3660
actaatttcc aaaatcacaa aggccatgag tttattccta cactctacca ctttcctgcc 3720
aattgtgatg cctgtgccaa acctctctgg catgttttta agccaccccc tgccctagag 3780
tgtcgaagat gccatgttaa gtgccacaga gatcacttag ataagaaaga ggacttaatt 3840
tgtccatgta aagtaagtta tgatgtaaca tcagcaagag atatgctgct gttagcatgt 3900
tctcaggatg aacaaaaaaa atgggtaact catttagtaa agaaaatccc taagaatcca 3960
ccatctggtt ttgttcgtgc ttcccctcga acgctttcta caagatccac tgcaaatcag 4020
tctttccgga aagtggtcaa aaatacatct ggaaaaacta gttaa 4065

<210> 158
<211> 1354
<212> PRT
<213> Homo Sapiens

<400> 158
Met Ser Thr Gly Asp Ser Phe Glu Thr Arg Phe Glu Lys Met Asp Asn
1 5 10 15
Leu Leu Arg Asp Pro Lys Ser Glu Val Asn Ser Asp Cys Leu Leu Asp
20 25 30
Gly Leu Asp Ala Leu Val Tyr Asp Leu Asp Phe Pro Ala Leu Arg Lys
35 40 45
Asn Lys Asn Ile Asp Asn Phe Leu Ser Arg Tyr Lys Asp Thr Ile Asn
50 55 60
Lys Ile Arg Asp Leu Arg Met Lys Ala Glu Asp Tyr Glu Val Val Lys
65 70 75 80
Val Ile Gly Arg Gly Ala Phe Gly Glu Val Gln Leu Val Arg His Lys
85 90 95
Ser Thr Arg Lys Val Tyr Ala Met Lys Leu Leu Ser Lys Phe Glu Met
100 105 110
Ile Lys Arg Ser Asp Ser Ala Phe Phe Trp Glu Glu Arg Asp Ile Met
115 120 125
Ala Phe Ala Asn Ser Pro Trp Val Val Gln Leu Phe Tyr Ala Phe Gln
130 135 140
Asp Asp Arg Tyr Leu Tyr Met Val Met Glu Tyr Met Pro Gly Gly Asp
145 150 155 160
Leu Val Asn Leu Met Ser Asn Tyr Asp Val Pro Glu Lys Trp Ala Arg
165 170 175
Phe Tyr Thr Ala Glu Val Val Leu Ala Leu Asp Ala Ile His Ser Met
180 185 190
Gly Phe Ile His Arg Asp Val Lys Pro Asp Asn Met Leu Leu Asp Lys
195 200 205
Ser Gly His Leu Lys Leu Ala Asp Phe Gly Thr Cys Met Lys Met Asn
210 215 220
Lys Glu Gly Met Val Arg Cys Asp Thr Ala Val Gly Thr Pro Asp Tyr
225 230 235 240
Ile Ser Pro Glu Val Leu Lys Ser Gln Gly Gly Asp Gly Tyr Tyr Gly
245 250 255
Arg Glu Cys Asp Trp Trp Ser Val Gly Val Phe Leu Tyr Glu Met Leu
260 265 270
Val Gly Asp Thr Pro Phe Tyr Ala Asp Ser Leu Val Gly Thr Tyr Ser
275 280 285

Lys Ile Met Asn His Lys Asn Ser Leu Thr Phe Pro Asp Asp Asn Asp
290 295 300
Ile Ser Lys Glu Ala Lys Asn Leu Ile Cys Ala Phe Leu Thr Asp Arg
305 310 315 320
Glu Val Arg Leu Gly Arg Asn Gly Val Glu Glu Ile Lys Arg His Leu
325 330 335
Phe Phe Lys Asn Asp Gln Trp Ala Trp Glu Thr Leu Arg Asp Thr Val
340 345 350
Ala Pro Val Val Pro Asp Leu Ser Ser Asp Ile Asp Thr Ser Asn Phe
355 360 365
Asp Asp Leu Glu Glu Asp Lys Gly Glu Glu Glu Thr Phe Pro Ile Pro
370 375 380
Lys Ala Phe Val Gly Asn Gln Leu Pro Phe Val Gly Phe Thr Tyr Tyr
385 390 395 400
Ser Asn Arg Arg Tyr Leu Ser Ser Ala Asn Pro Asn Asp Asn Arg Thr
405 410 415
Ser Ser Asn Ala Asp Lys Ser Leu Gln Glu Ser Leu Gln Lys Thr Ile
420 425 430
Tyr Lys Leu Glu Glu Gln Leu His Asn Glu Met Gln Leu Lys Asp Glu
435 440 445
Met Glu Gln Lys Cys Arg Thr Ser Asn Ile Lys Leu Asp Lys Ile Met
450 455 460
Lys Glu Leu Asp Glu Glu Gly Asn Gln Arg Arg Asn Leu Glu Ser Thr
465 470 475 480
Val Ser Gln Ile Glu Lys Glu Lys Met Leu Leu Gln His Arg Ile Asn
485 490 495
Glu Tyr Gln Arg Lys Ala Glu Gln Glu Asn Glu Lys Arg Arg Asn Val
500 505 510
Glu Asn Glu Val Ser Thr Leu Lys Asp Gln Leu Glu Asp Leu Lys Lys
515 520 525
Val Ser Gln Asn Ser Gln Leu Ala Asn Glu Lys Leu Ser Gln Leu Gln
530 535 540
Lys Gln Leu Glu Glu Ala Asn Asp Leu Leu Arg Thr Glu Ser Asp Thr
545 550 555 560
Ala Val Arg Leu Arg Lys Ser His Thr Glu Met Ser Lys Ser Ile Ser
565 570 575
Gln Leu Glu Ser Leu Asn Arg Glu Leu Gln Glu Arg Asn Arg Ile Leu
580 585 590
Glu Asn Ser Lys Ser Gln Thr Asp Lys Asp Tyr Tyr Gln Leu Gln Ala
595 600 605
Ile Leu Glu Ala Glu Arg Arg Asp Arg Gly His Asp Ser Glu Met Ile
610 615 620
Gly Asp Leu Gln Ala Arg Ile Thr Ser Leu Gln Glu Glu Val Lys His
625 630 635 640
Leu Lys His Asn Leu Glu Lys Val Glu Gly Glu Arg Lys Glu Ala Gln
645 650 655
Asp Met Leu Asn His Ser Glu Lys Glu Lys Asn Asn Leu Glu Ile Asp
660 665 670
Leu Asn Tyr Lys Leu Lys Ser Leu Gln Gln Arg Leu Glu Gln Glu Val
675 680 685
Asn Glu His Lys Val Thr Lys Ala Arg Leu Thr Asp Lys His Gln Ser
690 695 700
Ile Glu Glu Ala Lys Ser Val Ala Met Cys Glu Met Glu Lys Lys Leu
705 710 715 720
Lys Glu Glu Arg Glu Ala Arg Glu Lys Ala Glu Asn Arg Val Val Gln

725 730 735
Ile Glu Lys Gln Cys Ser Met Leu Asp Val Asp Leu Lys Gln Ser Gln
740 745 750
Gln Lys Leu Glu His Leu Thr Gly Asn Lys Glu Arg Met Glu Asp Glu
755 760 765
Val Lys Asn Leu Thr Leu Gln Leu Glu Gln Glu Ser Asn Lys Arg Leu
770 775 780
Leu Leu Gln Asn Glu Leu Lys Thr Gln Ala Phe Glu Ala Asp Asn Leu
785 790 795 800
Lys Gly Leu Glu Lys Gln Met Lys Gln Glu Ile Asn Thr Leu Leu Glu
805 810 815
Ala Lys Arg Leu Leu Glu Phe Glu Leu Ala Gln Leu Thr Lys Gln Tyr
820 825 830
Arg Gly Asn Glu Gly Gln Met Arg Glu Leu Gln Asp Gln Leu Glu Ala
835 840 845
Glu Gln Tyr Phe Ser Thr Leu Tyr Lys Thr Gln Val Lys Glu Leu Lys
850 855 860
Glu Glu Ile Glu Glu Lys Asn Arg Glu Asn Leu Lys Lys Ile Gln Glu
865 870 875 880
Leu Gln Asn Glu Lys Glu Thr Leu Ala Thr Gln Leu Asp Leu Ala Glu
885 890 895
Thr Lys Ala Glu Ser Glu Gln Leu Ala Arg Gly Leu Leu Glu Glu Gln
900 905 910
Tyr Phe Glu Leu Thr Gln Glu Ser Lys Lys Ala Ala Ser Arg Asn Arg
915 920 925
Gln Glu Ile Thr Asp Lys Asp His Thr Val Ser Arg Leu Glu Glu Ala
930 935 940
Asn Ser Met Leu Thr Lys Asp Ile Glu Ile Leu Arg Arg Glu Asn Glu
945 950 955 960
Glu Leu Thr Glu Lys Met Lys Lys Ala Glu Glu Glu Tyr Lys Leu Glu
965 970 975
Lys Glu Glu Glu Ile Ser Asn Leu Lys Ala Ala Phe Glu Lys Asn Ile
980 985 990
Asn Thr Glu Arg Thr Leu Lys Thr Gln Ala Val Asn Lys Leu Ala Glu
995 1000 1005
Ile Met Asn Arg Lys Asp Phe Lys Ile Asp Arg Lys Lys Ala Asn Thr
1010 1015 1020
Gln Asp Leu Arg Lys Lys Glu Lys Glu Asn Arg Lys Leu Gln Leu Glu
1025 1030 1035 104
Leu Asn Gln Glu Arg Glu Lys Phe Asn Gln Met Val Val Lys His Gln
1045 1050 1055
Lys Glu Leu Asn Asp Met Gln Ala Gln Leu Val Glu Glu Cys Ala His
1060 1065 1070
Arg Asn Glu Leu Gln Met Gln Leu Ala Ser Lys Glu Ser Asp Ile Glu
1075 1080 1085
Gln Leu Arg Ala Lys Leu Leu Asp Leu Ser Asp Ser Thr Ser Val Ala
1090 1095 1100
Ser Phe Pro Ser Ala Asp Glu Thr Asp Gly Asn Leu Pro Glu Ser Arg
1105 1110 1115 112
Ile Glu Gly Trp Leu Ser Val Pro Asn Arg Gly Asn Ile Lys Arg Tyr
1125 1130 1135
Gly Trp Lys Lys Gln Tyr Val Val Val Ser Ser Lys Lys Ile Leu Phe
1140 1145 1150
Tyr Asn Asp Glu Gln Asp Lys Glu Gln Ser Asn Pro Ser Met Val Leu
1155 1160 1165

Asp Ile Asp Lys Leu Phe His Val Arg Pro Val Thr Gln Gly Asp Val
1170 1175 1180
Tyr Arg Ala Glu Thr Glu Glu Ile Pro Lys Ile Phe Gln Ile Leu Tyr
1185 1190 1195 120
Ala Asn Glu Gly Glu Cys Arg Lys Asp Val Glu Met Glu Pro Val Gln
1205 1210 1215
Gln Ala Glu Lys Thr Asn Phe Gln Asn His Lys Gly His Glu Phe Ile
1220 1225 1230
Pro Thr Leu Tyr His Phe Pro Ala Asn Cys Asp Ala Cys Ala Lys Pro
1235 1240 1245
Leu Trp His Val Phe Lys Pro Pro Pro Ala Leu Glu Cys Arg Arg Cys
1250 1255 1260
His Val Lys Cys His Arg Asp His Leu Asp Lys Lys Glu Asp Leu Ile
1265 1270 1275 128
Cys Pro Cys Lys Val Ser Tyr Asp Val Thr Ser Ala Arg Asp Met Leu
1285 1290 1295
Leu Leu Ala Cys Ser Gln Asp Glu Gln Lys Lys Trp Val Thr His Leu
1300 1305 1310
Val Lys Lys Ile Pro Lys Asn Pro Pro Ser Gly Phe Val Arg Ala Ser
1315 1320 1325
Pro Arg Thr Leu Ser Thr Arg Ser Thr Ala Asn Gln Ser Phe Arg Lys
1330 1335 1340
Val Val Lys Asn Thr Ser Gly Lys Thr Ser
1345 1350

<210> 159
<211> 683
<212> DNA
<213> Homo Sapiens

<400> 159
acaagctgga gttcgagcct gacagtgagg acaagatctc ggactgtgag gaaggattga 60
gtaatgtggc acttgaatgc agtgagccaa gcacaagtgt atctgcttat gaccagttga 120
aggcaccggc atcccctggt gctggaaacc cacctgggac cccaaaggga aagagagagc 180
tgatgagcaa tggcccaggt tccattattg gtgctaaagc tgggaagaat tctggcaaaa 240
agaagggcct taacaatgaa ctgaacaacc ttccagtaat ctccaacatg acggctgcgt 300
tagacagttg ctcggcagca gacggcagtt tggctgctga gatgcctaaa ctggaagcag 360
aaggattaat tgacaagaaa aatttaggag ataaagaaaa gggcaaaaaa gctaacaact 420
gcaaaacgga caaaaacctc tctaaactga aagtgcccg gcccattgcc cctgccccag 480
cccccactcc cccgcagcta atcgctatac ccactgcaac ctttacaacg accaccactg 540
ggacaatacc cggactgccc tccctcacaa caactgttgt tcaggctaca ccaaagagtc 600
ctccgttaaa acccattcaa ccaaagccca caattatggg agagcccatc accgtgaacc 660
cagctctggt gtcactcaaa gac 683

<210> 160
<211> 227
<212> PRT
<213> Homo Sapiens

<400> 160
Lys Leu Glu Phe Glu Pro Asp Ser Glu Asp Lys Ile Ser Asp Cys Glu
1 5 10 15
Glu Gly Leu Ser Asn Val Ala Leu Glu Cys Ser Glu Pro Ser Thr Ser
20 25 30
Val Ser Ala Tyr Asp Gln Leu Lys Ala Pro Ala Ser Pro Gly Ala Gly

35 40 45
Asn Pro Pro Gly Thr Pro Lys Gly Lys Arg Glu Leu Met Ser Asn Gly
50 55 60
Pro Gly Ser Ile Ile Gly Ala Lys Ala Gly Lys Asn Ser Gly Lys Lys
65 70 75 80
Lys Gly Leu Asn Asn Glu Leu Asn Asn Leu Pro Val Ile Ser Asn Met
85 90 95
Thr Ala Ala Leu Asp Ser Cys Ser Ala Ala Asp Gly Ser Leu Ala Ala
100 105 110
Glu Met Pro Lys Leu Glu Ala Glu Gly Leu Ile Asp Lys Lys Asn Leu
115 120 125
Gly Asp Lys Glu Lys Gly Lys Lys Ala Asn Asn Cys Lys Thr Asp Lys
130 135 140
Asn Leu Ser Lys Leu Lys Ser Ala Arg Pro Ile Ala Pro Ala Pro Ala
145 150 155 160
Pro Thr Pro Pro Gln Leu Ile Ala Ile Pro Thr Ala Thr Phe Thr Thr
165 170 175
Thr Thr Thr Gly Thr Ile Pro Gly Leu Pro Ser Leu Thr Thr Thr Val
180 185 190
Val Gln Ala Thr Pro Lys Ser Pro Pro Leu Lys Pro Ile Gln Pro Lys
195 200 205
Pro Thr Ile Met Gly Glu Pro Ile Thr Val Asn Pro Ala Leu Val Ser
210 215 220
Leu Lys Asp
225

<210> 161
<211> 662
<212> DNA
<213> Homo Sapiens

<400> 161
acccacagca gttgcacttg ctgagcaggc agcttgagga cccaaatggt agcttttcta 60
acgctgagat gagtgaactg agtgtggcac agaaaccaga aaaacttttg gagcgctgca 120
agtactggcc tgcttgtaaa aatggggatg agtgtgccta ccatcacccc atctcaccct 180
gcaaagcctt ccccaattgt aaatttgctg aaaaatgttt gtttgttcac ccaaattgta 240
aatatgatgc aaagtgtact aaaccagatt gtcccttcac tcatgtgagt agaagaattc 300
cagtactgtc tccaaaacca gttgcaccac cagcaccacc ttccagtagt cagctctgcc 360
gttacttccc tgcttgtaag aagatggaat gtcccttcta tcatccaaaa cattgtaggt 420
ttaacactca atgtacaaga ccggactgca cattctacca tcccaccatt aatgtcccac 480
cacgacatgc cttgaaatgg attcgacctc aaaccagcga atagcaccca gtcctgcctg 540
gcagaagatc atgcagtttg gaagttttca tgtctgatga aagatctcta cagaacttgt 600
caaatctttg aaacttggaa tatattgctt tcataatatg aaggtttatt ggctatctaa 660
aa 662

<210> 162
<211> 173
<212> PRT
<213> Homo Sapiens

<400> 162
Pro Gln Gln Leu His Leu Leu Ser Arg Gln Leu Glu Asp Pro Asn Gly
1 5 10 15
Ser Phe Ser Asn Ala Glu Met Ser Glu Leu Ser Val Ala Gln Lys Pro
20 25 30

Glu Lys Leu Leu Glu Arg Cys Lys Tyr Trp Pro Ala Cys Lys Asn Gly
35 40 45
Asp Glu Cys Ala Tyr His His Pro Ile Ser Pro Cys Lys Ala Phe Pro
50 55 60
Asn Cys Lys Phe Ala Glu Lys Cys Leu Phe Val His Pro Asn Cys Lys
65 70 75 80
Tyr Asp Ala Lys Cys Thr Lys Pro Asp Cys Pro Phe Thr His Val Ser
85 90 95
Arg Arg Ile Pro Val Leu Ser Pro Lys Pro Val Ala Pro Pro Ala Pro
100 105 110
Pro Ser Ser Ser Gln Leu Cys Arg Tyr Phe Pro Ala Cys Lys Lys Met
115 120 125
Glu Cys Pro Phe Tyr His Pro Lys His Cys Arg Phe Asn Thr Gln Cys
130 135 140
Thr Arg Pro Asp Cys Thr Phe Tyr His Pro Thr Ile Asn Val Pro Pro
145 150 155 160
Arg His Ala Leu Lys Trp Ile Arg Pro Gln Thr Ser Glu
165 170

<210> 163
<211> 2912
<212> DNA
<213> Homo Sapiens

<400> 163
cagttgcttc agcgtcccgg tgtggctgtg ccgttggtcc tgtgcggtca cttagccaag 60
atgcctgagg aaacccagac ccaagaccaa ccgatggagg aggaggaggt tgagacgttc 120
gcctttcagg cagaaattgc ccagttgatg tcattgatca tcaatacttt ctactcgaac 180
aaagagatct ttctgagaga gctcatttca aattcatcag atgcattgga caaaatccgg 240
tatgaaactt tgacagatcc cagtaaatta gactctggga aagagctgca tattaacctt 300
ataccgaaca aacaagatcg aactctcact attgtggata ctggaattgg aatgaccaag 360
gctgacttga tcaataacct tggtactatc gccaagtctg ggaccaaagc gttcatggaa 420
gctttgcagg ctggtgcaga tatctctatg attggccagt tcggtgttgg tttttattct 480
gcttatttgg ttgctgagaa agtaactgtg atcaccaaac ataacgatga tgagcagtac 540
gcttgggagt cctcagcagg gggatcattc acagtgagga cagacacagg tgaacctatg 600
ggtcgtggaa caaaagttat cctacacctg aaagaagacc aaactgagta cttggaggaa 660
cgaagaataa aggagattgt gaagaaacat tctcagttta ttggatatcc cattactctt 720
tttgtggaga aggaacgtga taaagaagta agcgatgatg aggctgaaga aaaggaagac 780
aaagaagaag aaaaagaaaa agaagagaaa gagtcggaag acaaacctga aattgaagat 840
gttggttctg atgaggaaga agaaaagaag gatggtgaca agaagaagaa gaagaagatt 900
aaggaaaagt acatcgatca agaagagctc aacaaaacaa agcccatctg gaccagaaat 960
cccgacgata ttactaatga ggagtacgga gaattctata agagcttgac caatgactgg 1020
gaagatcact tggcagtgaa gcatttttca gttgaaggac agttggaatt cagagcccttt 1080
ctatttgtcc cacgacgtgc tccttttgat ctgtttgaaa acagaaagaa aaagaacaat 1140
atcaaattgt atgtacgcag agttttcatc atggataact gtgaggagct aatccctgaa 1200
tatctgaact tcattagagg ggtggtagac tcggaggatc tccctctaaa catatcccgt 1260
gagatgttgc aacaaagcaa aattttgaaa gttatcagga agaatttggt caaaaaatgc 1320
ttagaactct ttactgaact ggcggaagat aaagagaact acaagaaatt ctatgagcag 1380
ttctctaaaa acataaagct tggaatacac gaagactctc aaaatcggaa gaagctttca 1440
gagctgttaa ggtactacac atctgcctct ggtgatgaga tggtttctct caaggactac 1500
tgcaccagaa tgaaggagaa ccagaaacat atctattata tcacaggtga gaccaaggac 1560
caggtagcta actcagcctt tgtggaacgt cttcggaaac atggcttaga agtgatctat 1620
atgattgagc ccattgatga gtactgtgtc caacagctga aggaatttga ggggaagact 1680
ttagtgtcag tcaccaaaga aggcctggaa cttccagagg atgaagaaga gaaaaagaag 1740
caggaagaga aaaaaacaaa gtttgagaac ctctgcaaaa tcatgaaaga catattggag 1800

aaaaaagttg aaaaggtggt tgtgtcaaac cgattggtga catctccatg ctgtattgtc 1860
acaagcacat atggctggac agcaaacatg gagagaatca tgaaagctca agccctaaga 1920
gacaactcaa caatgggtta catggcagca aagaaacacc tggagataaa ccctgaccat 1980
tccattattg agaccttaag gcaaaaggca gaggctgata agaacgacaa gtctgtgaag 2040
gatctggtca tcttgcttta tgaaactgcg ctcctgtctt ctggcttcag tctggaagat 2100
ccccagacac atgctaacag gatctacagg atgatcaaac ttggtctggg tattgatgaa 2160
gatgacccta ctgctgatga taccagtgct gctgtaactg aagaaatgcc acccсttgaa 2220
ggagatgacg acacatcacg catggaagaa gtagactaat ctctggctga gggatgactt 2280
acctgttcag tactctacaa ttcctctgat aatatatttt caaggatgtt tttctttatt 2340
tttgttaata ttaaaaagtc tgtatggcat gacaactact ttaaggggaa gataagattt 2400
ctgtctacta agtgatgctg tgatacctta ggcactaaag cagagctagt aatgcttttt 2460
gagtttcatg ttggttcttt cacagatggg gtaacgtgca ctgtaagacg tatgtaacat 2520
gatgttaact ttgtgtggtc taaagtgttt agctgtcaag ccggatgcct aagtagacca 2580
aatcttgtta ttgaagtgtt ctgagctgta tcttgatgtt tagaaaagta ttcgttacat 2640
cttgtaggat ctacttttg aactttcat tccctgtagt tgacaattct gcatgtacta 2700
gtcctctaga aataggttaa actgaagcaa cttgatggaa ggatctctcc acagggcttg 2760
ttttccaaag aaaagtattg tttggaggag caaagttaaa agcctaccta agcatatcgt 2820
aaagctgttc aaatactcga gcccagtctt gtggatggaa atgtagtgct cgagtcacat 2880
tctgcttaaa gttgtaacaa atacagatga gt 2912

<210> 164
<211> 732
<212> PRT
<213> Homo Sapiens

<400> 164
Met Pro Glu Glu Thr Gln Thr Gln Asp Gln Pro Met Glu Glu Glu Glu
1 5 10 15
Val Glu Thr Phe Ala Phe Gln Ala Glu Ile Ala Gln Leu Met Ser Leu
20 25 30
Ile Ile Asn Thr Phe Tyr Ser Asn Lys Glu Ile Phe Leu Arg Glu Leu
35 40 45
Ile Ser Asn Ser Ser Asp Ala Leu Asp Lys Ile Arg Tyr Glu Thr Leu
50 55 60
Thr Asp Pro Ser Lys Leu Asp Ser Gly Lys Glu Leu His Ile Asn Leu
65 70 75 80
Ile Pro Asn Lys Gln Asp Arg Thr Leu Thr Ile Val Asp Thr Gly Ile
85 90 95
Gly Met Thr Lys Ala Asp Leu Ile Asn Asn Leu Gly Thr Ile Ala Lys
100 105 110
Ser Gly Thr Lys Ala Phe Met Glu Ala Leu Gln Ala Gly Ala Asp Ile
115 120 125
Ser Met Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Tyr Leu Val
130 135 140
Ala Glu Lys Val Thr Val Ile Thr Lys His Asn Asp Asp Glu Gln Tyr
145 150 155 160
Ala Trp Glu Ser Ser Ala Gly Gly Ser Phe Thr Val Arg Thr Asp Thr
165 170 175
Gly Glu Pro Met Gly Arg Gly Thr Lys Val Ile Leu His Leu Lys Glu
180 185 190
Asp Gln Thr Glu Tyr Leu Glu Glu Arg Arg Ile Lys Glu Ile Val Lys
195 200 205
Lys His Ser Gln Phe Ile Gly Tyr Pro Ile Thr Leu Phe Val Glu Lys
210 215 220
Glu Arg Asp Lys Glu Val Ser Asp Asp Glu Ala Glu Glu Lys Glu Asp

225 230 235 240

Lys Glu Glu Glu Lys Glu Lys Glu Glu Lys Glu Ser Glu Asp Lys Pro

245 250 255

Glu Ile Glu Asp Val Gly Ser Asp Glu Glu Glu Glu Lys Lys Asp Gly

260 265 270

Asp Lys Lys Lys Lys Lys Lys Ile Lys Glu Lys Tyr Ile Asp Gln Glu

275 280 285

Glu Leu Asn Lys Thr Lys Pro Ile Trp Thr Arg Asn Pro Asp Asp Ile

290 295 300

Thr Asn Glu Glu Tyr Gly Glu Phe Tyr Lys Ser Leu Thr Asn Asp Trp

305 310 315 320

Glu Asp His Leu Ala Val Lys His Phe Ser Val Glu Gly Gln Leu Glu

325 330 335

Phe Arg Ala Leu Leu Phe Val Pro Arg Arg Ala Pro Phe Asp Leu Phe

340 345 350

Glu Asn Arg Lys Lys Lys Asn Asn Ile Lys Leu Tyr Val Arg Arg Val

355 360 365

Phe Ile Met Asp Asn Cys Glu Glu Leu Ile Pro Glu Tyr Leu Asn Phe

370 375 380

Ile Arg Gly Val Val Asp Ser Glu Asp Leu Pro Leu Asn Ile Ser Arg

385 390 395 400

Glu Met Leu Gln Gln Ser Lys Ile Leu Lys Val Ile Arg Lys Asn Leu

405 410 415

Val Lys Lys Cys Leu Glu Leu Phe Thr Glu Leu Ala Glu Asp Lys Glu

420 425 430

Asn Tyr Lys Lys Phe Tyr Glu Gln Phe Ser Lys Asn Ile Lys Leu Gly

435 440 445

Ile His Glu Asp Ser Gln Asn Arg Lys Lys Leu Ser Glu Leu Leu Arg

450 455 460

Tyr Tyr Thr Ser Ala Ser Gly Asp Glu Met Val Ser Leu Lys Asp Tyr

465 470 475 480

Cys Thr Arg Met Lys Glu Asn Gln Lys His Ile Tyr Tyr Ile Thr Gly

485 490 495

Glu Thr Lys Asp Gln Val Ala Asn Ser Ala Phe Val Glu Arg Leu Arg

500 505 510

Lys His Gly Leu Glu Val Ile Tyr Met Ile Glu Pro Ile Asp Glu Tyr

515 520 525

Cys Val Gln Gln Leu Lys Glu Phe Glu Gly Lys Thr Leu Val Ser Val

530 535 540

Thr Lys Glu Gly Leu Glu Leu Pro Glu Asp Glu Glu Glu Lys Lys Lys

545 550 555 560

Gln Glu Glu Lys Lys Thr Lys Phe Glu Asn Leu Cys Lys Ile Met Lys

565 570 575

Asp Ile Leu Glu Lys Lys Val Glu Lys Val Val Val Ser Asn Arg Leu

580 585 590

Val Thr Ser Pro Cys Cys Ile Val Thr Ser Thr Tyr Gly Trp Thr Ala

595 600 605

Asn Met Glu Arg Ile Met Lys Ala Gln Ala Leu Arg Asp Asn Ser Thr

610 615 620

Met Gly Tyr Met Ala Ala Lys Lys His Leu Glu Ile Asn Pro Asp His

625 630 635 640

Ser Ile Ile Glu Thr Leu Arg Gln Lys Ala Glu Ala Asp Lys Asn Asp

645 650 655

Lys Ser Val Lys Asp Leu Val Ile Leu Leu Tyr Glu Thr Ala Leu Leu

660 665 670

Ser Ser Gly Phe Ser Leu Glu Asp Pro Gln Thr His Ala Asn Arg Ile
675 680 685
Tyr Arg Met Ile Lys Leu Gly Leu Gly Ile Asp Glu Asp Asp Pro Thr
690 695 700
Ala Asp Asp Thr Ser Ala Ala Val Thr Glu Glu Met Pro Pro Leu Glu
705 710 715 720
Gly Asp Asp Asp Thr Ser Arg Met Glu Glu Val Asp
725 730

<210> 165
<211> 790
<212> DNA
<213> Homo Sapiens

<400> 165
ccgactcaga aatggcggcc tccatgttct acggcaggct agtggccgtg gccaccccttc 60
ggaaccaccg gcctcggacg gcccagcggg ctgctgctca ggttctggga agttctggat 120
tgtttaataa ccatggactc caagtacagc agcaacagca aaggaatctc tcactacatg 180
aatacatgag tatggaatta ttgcaagaag ctggtgtctc cgttcccaaa ggatatgtgg 240
caaagtcacc agatgaagct tatgcaattg ccaaaaaatt aggttcaaaa gatgtcgtga 300
taaaggcaca ggttttagct ggtggtagag gaaaaggaac atttgaaagt ggcctcaaag 360
gaggagtgaa gatagttttc tctccagaag aagcaaaagc tgtttcttca caaatgattg 420
ggaaaaaatt gtttaccaag caaacgggag aaaagggcag aatatgcaat caagtattgg 480
tctgtgagcg aaaatatccc aggagagaat actactttgc aataacaatg gaaaggtcat 540
ttcaaggtcc tgtattaata ggaagttcac atggtggtgt caacattgaa gatgttgctg 600
ctgagtctcc tgaagcaata attaaagaac ctattgatat tgaagaaggc atcaaaaagg 660
aacaagctct tcagcttgca cagaagaatg ggatttcccc taatattgng ggaatcagca 720
gcaggaaaac atggtcaagc tttacagncn ttttcttgaa atacgatgca acccttgata 780
ggaaattaaa 790

<210> 166
<211> 259
<212> PRT
<213> Homo Sapiens

<400> 166
Asp Ser Glu Met Ala Ala Ser Met Phe Tyr Gly Arg Leu Val Ala Val
1 5 10 15
Ala Thr Leu Arg Asn His Arg Pro Arg Thr Ala Gln Arg Ala Ala Ala
20 25 30
Gln Val Leu Gly Ser Ser Gly Leu Phe Asn Asn His Gly Leu Gln Val
35 40 45
Gln Gln Gln Gln Gln Arg Asn Leu Ser Leu His Glu Tyr Met Ser Met
50 55 60
Glu Leu Leu Gln Glu Ala Gly Val Ser Val Pro Lys Gly Tyr Val Ala
65 70 75 80
Lys Ser Pro Asp Glu Ala Tyr Ala Ile Ala Lys Lys Leu Gly Ser Lys
85 90 95
Asp Val Val Ile Lys Ala Gln Val Leu Ala Gly Gly Arg Gly Lys Gly
100 105 110
Thr Phe Glu Ser Gly Leu Lys Gly Gly Val Lys Ile Val Phe Ser Pro
115 120 125
Glu Glu Ala Lys Ala Val Ser Ser Gln Met Ile Gly Lys Lys Leu Phe
130 135 140
Thr Lys Gln Thr Gly Glu Lys Gly Arg Ile Cys Asn Gln Val Leu Val

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145                 150                 155                 160
Cys Glu Arg Lys Tyr Pro Arg Arg Glu Tyr Tyr Phe Ala Ile Thr Met
                165                 170                 175
Glu Arg Ser Phe Gln Gly Pro Val Leu Ile Gly Ser Ser His Gly Gly
            180                 185                 190
Val Asn Ile Glu Asp Val Ala Ala Glu Ser Pro Glu Ala Ile Ile Lys
        195                 200                 205
Glu Pro Ile Asp Ile Glu Glu Gly Ile Lys Lys Glu Gln Ala Leu Gln
    210                 215                 220
Leu Ala Gln Lys Asn Gly Ile Ser Pro Asn Ile Gly Ile Ser Ser Arg
225                 230                 235                 240
Lys Thr Trp Ser Ser Phe Thr Phe Leu Lys Tyr Asp Ala Thr Leu Asp
                245                 250                 255
Arg Lys Leu
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<210> 167
<211> 5307
<212> DNA
<213> Homo Sapiens

<400> 167
gaataacagt taagttttgg ggagtaaaaa ctgtttcaat ttttgactgt gttgggggtt      60
ggtgctccta atccctgtgt tgttaaaggg tcgactatat tgtatttttg aaaattgcta     120
gagagtggac gtaaagtgtt ctcactaaac aaattataac tatgtgaggt agtgcatata     180
ttaagtagct agatttggtc attccacaat gtatatgtac ttcaaaacat catgttgtac     240
atgagaaaca cagttttatc tgttagtcag ttttaaaaat aaaaaatatt ccaactagaa     300
actctgttgt agtttttgaa attacaactt ggaggctttg aggaactgat tagaagtctc     360
ctttctgttt caggctttca tatccaaacc atagatcttt agaagtaaca tctgttaatt     420
aattattaat aaatagtttg agtctttatt aattcatgga taacttgacc atttctctc      480
tccttttgct tagataatcc cagatcatgg ccgggcacag tagctcacgc ctgtattccc     540
agcagtttgg gaggccgagg caggcagatc acttgaactc aggagtttga gaccagcttg     600
ggcaacatgg caaaaccctg tctctattaa aaatacaaaa attagctggg catggtagtg     660
catgcctgta gtcccagcta cctgggaggc tgaggtggga ggatcgcttg agcctgggag     720
gttgaggctt ctgtgcgcga tgattgctcc agtgatcacg ccattgcact ccagcctggg     780
tgacagagtg agaccctgtc tccaaaaaaa aaaaaaatta agcaagtagc agttacaaga     840
ccaaaagtta ttttcctttt tttttttctc tataaaattg cccatttgga ccaaatctag     900
ttataactta tttcagtgtc attaagaaag ttgatgaata agtcatatta ctcagatgtt     960
agtagctatg catttattaa tagttttatt tataagtatt tagtttcact ctgttgcaga    1020
ctattttatg ctaaaattag ctaaagccaa attactattt cttaaaacat atttttttact    1080
tttttttttt ttttaaatat tattaggtac ttcttgcaag ggatatgcat tagcacatac    1140
tcaagaaggg gaagaaaaga agcaaacttc tggtacatca aataccagag gatcaagacg    1200
aaaacctgca atgacaactc ctacaaggag gtctacacgt aacacaagag ctgaaacagc    1260
cagtcagtct cagagatccc caatatcaga caattctggg tgtgatgccc caggtaacag    1320
taatccatct ttaagtgttc cctcttcagc tgagtcagaa aagcaaacaa gacaggctcc    1380
aaaacggaag tctgtaagaa gaggaagaaa accaccttta ctgaaaaaga aacttcggag    1440
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atctgacaca tcacctgtgt tagaaaaaga gcaccaacca gatgtagaca gtagtaacat    1560
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<211> 1148
<212> PRT
<213> Homo Sapiens

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35 40 45
Ser Glu Lys Gln Thr Arg Gln Ala Pro Lys Arg Lys Ser Val Arg Arg
50 55 60
Gly Arg Lys Pro Pro Leu Leu Lys Lys Lys Leu Arg Ser Ser Val Ala
65 70 75 80
Ala Pro Glu Lys Ser Ser Ser Asn Asp Ser Val Asp Glu Glu Thr Ala
85 90 95
Glu Ser Asp Thr Ser Pro Val Leu Glu Lys Glu His Gln Pro Asp Val
100 105 110
Asp Ser Ser Asn Ile Cys Thr Val Gln Thr His Val Glu Asn Gln Ser
115 120 125
Ala Asn Cys Leu Lys Ser Cys Asn Glu Gln Ile Glu Glu Ser Glu Lys
130 135 140
His Thr Ala Asn Tyr Asp Thr Glu Glu Arg Val Gly Ser Ser Ser Ser
145 150 155 160
Glu Ser Cys Ala Gln Asp Leu Pro Val Leu Val Gly Glu Glu Gly Glu
165 170 175
Val Lys Lys Leu Glu Asn Thr Gly Ile Glu Ala Asn Val Leu Cys Leu
180 185 190
Glu Ser Glu Ile Ser Glu Asn Ile Leu Glu Lys Gly Gly Asp Pro Leu
195 200 205
Glu Lys Gln Asp Gln Ile Ser Gly Leu Ser Gln Ser Glu Val Lys Thr
210 215 220
Asp Val Cys Thr Val His Leu Pro Asn Asp Phe Pro Thr Cys Leu Thr
225 230 235 240
Ser Glu Ser Lys Val Tyr Gln Pro Val Ser Cys Pro Leu Ser Asp Leu
245 250 255
Ser Glu Asn Val Glu Ser Val Val Asn Glu Glu Lys Ile Thr Glu Ser
260 265 270
Ser Leu Val Glu Ile Thr Glu His Lys Asp Phe Thr Leu Lys Thr Glu
275 280 285
Glu Leu Ile Glu Ser Pro Lys Leu Glu Ser Ser Glu Gly Glu Ile Ile
290 295 300
Gln Thr Val Asp Arg Gln Ser Val Lys Ser Pro Glu Val Gln Leu Leu
305 310 315 320
Gly His Val Glu Thr Glu Asp Val Glu Ile Ile Ala Thr Cys Asp Thr
325 330 335
Phe Gly Asn Glu Asp Phe Asn Asn Ile Gln Asp Ser Glu Asn Asn Leu
340 345 350
Leu Lys Asn Asn Leu Leu Asn Thr Lys Leu Glu Lys Ser Leu Glu Glu

355 360 365
Lys Asn Glu Ser Leu Thr Glu His Pro Arg Ser Thr Glu Leu Pro Lys
370 375 380
Thr His Ile Glu Gln Ile Gln Lys His Phe Ser Glu Asp Asn Asn Glu
385 390 395 400
Met Ile Pro Met Glu Cys Asp Ser Phe Cys Ser Asp Gln Asn Glu Ser
405 410 415
Glu Val Glu Pro Ser Val Asn Ala Asp Leu Lys Gln Met Asn Glu Asn
420 425 430
Ser Val Thr His Cys Ser Glu Asn Asn Met Pro Ser Ser Asp Leu Ala
435 440 445
Asp Glu Lys Val Glu Thr Val Ser Gln Pro Ser Glu Ser Pro Lys Asp
450 455 460
Thr Ile Asp Lys Thr Lys Lys Pro Arg Thr Arg Arg Ser Arg Phe His
465 470 475 480
Ser Pro Ser Thr Thr Trp Ser Pro Asn Lys Asp Thr Pro Gln Glu Lys
485 490 495
Lys Arg Pro Gln Ser Pro Ser Pro Arg Arg Glu Thr Gly Lys Glu Ser
500 505 510
Arg Lys Ser Gln Ser Pro Ser Pro Lys Asn Glu Ser Ala Arg Gly Arg
515 520 525
Lys Lys Ser Arg Ser Gln Ser Pro Lys Lys Asp Ile Ala Arg Glu Arg
530 535 540
Arg Gln Ser Gln Ser Arg Ser Pro Lys Arg Asp Thr Thr Arg Glu Ser
545 550 555 560
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565 570 575
Lys Arg Ser Gln Pro Arg Val Lys Asp Ser Ser Pro Gly Glu Lys Ser
580 585 590
Arg Ser Gln Ser Arg Glu Arg Glu Ser Asp Arg Asp Gly Gln Arg Arg
595 600 605
Glu Arg Glu Arg Arg Thr Arg Lys Trp Ser Arg Ser Arg Ser His Ser
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Arg Ser Pro Ser Arg Cys Arg Thr Lys Ser Lys Ser Ser Ser Phe Gly
625 630 635 640
Arg Ile Asp Arg Asp Ser Tyr Ser Pro Arg Trp Lys Gly Arg Trp Ala
645 650 655
Asn Asp Gly Trp Arg Cys Pro Arg Gly Asn Asp Arg Tyr Arg Lys Asn
660 665 670
Asp Pro Glu Lys Gln Asn Glu Asn Thr Arg Lys Glu Lys Asn Asp Ile
675 680 685
His Leu Asp Ala Asp Asp Pro Asn Ser Ala Asp Lys His Arg Asn Asp
690 695 700
Cys Pro Asn Trp Ile Thr Glu Lys Ile Asn Ser Gly Pro Asp Pro Arg
705 710 715 720
Thr Arg Asn Pro Glu Lys Leu Lys Glu Ser His Trp Glu Glu Asn Arg
725 730 735
Asn Glu Asn Ser Gly Asn Ser Trp Asn Lys Asn Phe Gly Ser Gly Trp
740 745 750
Val Ser Asn Arg Gly Arg Gly Arg Gly Asn Arg Gly Arg Gly Thr Tyr
755 760 765
Arg Ser Ser Phe Ala Tyr Lys Asp Gln Asn Glu Asn Arg Trp Gln Asn
770 775 780
Arg Lys Pro Leu Ser Gly Asn Ser Asn Ser Ser Gly Ser Glu Ser Phe
785 790 795 800

Lys Phe Val Glu Gln Gln Ser Tyr Lys Arg Lys Ser Glu Gln Glu Phe
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Ser Phe Asp Thr Pro Ala Asp Arg Ser Gly Trp Thr Ser Ala Ser Ser
            820   825   830
Trp Ala Val Arg Lys Thr Leu Pro Ala Asp Val Gln Asn Tyr Tyr Ser
        835   840   845
Arg Arg Gly Arg Asn Ser Ser Gly Pro Gln Ser Gly Trp Met Lys Gln
    850   855   860
Glu Glu Glu Thr Ser Gly Gln Asp Ser Ser Leu Lys Asp Gln Thr Asn
865   870   875   880
Gln Gln Val Asp Gly Ser Gln Leu Pro Ile Asn Met Met Gln Pro Gln
                885   890   895
Met Asn Val Met Gln Gln Gln Met Asn Ala Gln His Gln Pro Met Asn
            900   905   910
Ile Phe Pro Tyr Pro Val Gly Val His Ala Pro Leu Met Asn Ile Gln
        915   920   925
Arg Asn Pro Phe Asn Ile His Pro Gln Leu Pro Leu His Leu His Thr
    930   935   940
Gly Val Pro Leu Met Gln Val Ala Thr Pro Thr Ser Val Ser Gln Gly
945   950   955   960
Leu Pro Pro Pro Pro Pro Pro Pro Pro Pro Ser Gln Gln Val Asn Tyr
                965   970   975
Ile Ala Ser Gln Pro Asp Gly Lys Gln Leu Gln Gly Ile Pro Ser Ser
            980   985   990
Ser His Val Ser Asn Asn Met Ser Thr Pro Val Leu Pro Ala Pro Thr
        995   1000   1005
Ala Ala Pro Gly Asn Thr Gly Met Val Gln Gly Pro Ser Ser Gly Asn
    1010   1015   1020
Thr Ser Ser Ser Ser His Ser Lys Ala Ser Asn Ala Ala Val Lys Leu
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Ala Glu Ser Lys Val Ser Val Ala Val Glu Ala Ser Ala Asp Ser Ser
                1045   1050   1055
Lys Thr Asp Lys Lys Leu Gln Ile Gln Glu Lys Ala Ala Gln Glu Val
            1060   1065   1070
Lys Leu Ala Ile Lys Pro Phe Tyr Gln Asn Lys Asp Ile Thr Lys Glu
        1075   1080   1085
Glu Tyr Lys Glu Ile Val Arg Lys Ala Val Asp Lys Val Cys His Ser
    1090   1095   1100
Lys Ser Gly Glu Val Asn Ser Thr Lys Val Ala Asn Leu Val Lys Ala
1105   1110   1115   112
Tyr Val Asp Lys Tyr Lys Tyr Ser Arg Lys Gly Ser Gln Lys Lys Thr
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Leu Glu Glu Pro Val Ser Thr Glu Lys Asn Ile Gly
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<211> 597
<212> DNA
<213> Homo Sapiens

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gaagtgctac caaaacacgc aatgactgtc ctaaaagtgc gttctgggat acacctgtaa 180
acttggatca agttccctcc cctctcctca aaatatatcg acttgtgctg aaagaaatca 240

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gcaaacaagg gacaggccct caaagttgtc ggtagggagc caggaccccg ccagtggcgt      420
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aagggctggc taagggaggc cggggcggag gaagccaagc tctgcaggcc ctgacaaagt      540
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<211> 3344
<212> DNA
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cgtatgttca ctcgtctgcc accatcccat tggatgaccc cactttgctc tttgccaatg      240
caggcatgaa ccagtttaaa cccattttcc tgaacacaat tgacccatct caccccatgg      300
caaagctgag cagagctgcc aatacccaga agtgcatccg ggctgggggc aaacaaaatg      360
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<211> 1004
<212> PRT
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35 40 45
Arg Phe Ile Asp Phe Phe Lys Arg Asn Glu His Thr Tyr Val His Ser
50 55 60
Ser Ala Thr Ile Pro Leu Asp Asp Pro Thr Leu Leu Phe Ala Asn Ala
65 70 75 80
Gly Met Asn Gln Phe Lys Pro Ile Phe Leu Asn Thr Ile Asp Pro Ser
85 90 95
His Pro Met Ala Lys Leu Ser Arg Ala Ala Asn Thr Gln Lys Cys Ile
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Arg Ala Gly Gly Lys Gln Asn Asp Leu Asp Asp Val Gly Lys Asp Val
115 120 125
Tyr His His Thr Phe Phe Glu Met Leu Gly Ser Trp Ser Phe Gly Asp
130 135 140
Tyr Phe Lys Glu Leu Ala Cys Lys Met Ala Leu Glu Leu Leu Thr Gln
145 150 155 160
Glu Phe Gly Ile Pro Ile Glu Arg Leu Tyr Val Thr Tyr Phe Gly Gly
165 170 175
Asp Glu Ala Ala Gly Leu Glu Ala Asp Leu Glu Cys Lys Gln Ile Trp
180 185 190
Gln Asn Leu Gly Leu Asp Asp Thr Lys Ile Leu Pro Gly Asn Met Lys
195 200 205
Asp Asn Phe Trp Glu Met Gly Asp Thr Gly Pro Cys Gly Pro Cys Ser
210 215 220
Glu Ile His Tyr Asp Arg Ile Gly Gly Arg Asp Ala Ala His Leu Val
225 230 235 240
Asn Gln Asp Asp Pro Asn Val Leu Glu Ile Trp Asn Leu Val Phe Ile
245 250 255
Gln Tyr Asn Arg Glu Ala Asp Gly Ile Leu Lys Pro Leu Pro Lys Lys
260 265 270

Ser Ile Asp Thr Gly Met Gly Leu Glu Arg Leu Val Ser Val Leu Gln
275 280 285
Asn Lys Met Ser Asn Tyr Asp Thr Asp Leu Phe Val Pro Tyr Phe Glu
290 295 300
Ala Ile Gln Lys Gly Thr Gly Ala Arg Pro Tyr Thr Gly Lys Val Gly
305 310 315 320
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325 330 335
His Ala Arg Thr Ile Thr Val Ala Leu Ala Asp Gly Gly Arg Pro Asp
340 345 350
Asn Thr Gly Arg Gly Tyr Val Leu Arg Arg Ile Leu Arg Arg Ala Val
355 360 365
Arg Tyr Ala His Glu Lys Leu Asn Ala Ser Arg Gly Phe Phe Ala Thr
370 375 380
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Lys Lys Asp Pro Asp Met Val Lys Asp Ile Ile Asn Glu Glu Glu Val
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Gln Phe Leu Lys Thr Leu Ser Arg Gly Arg Arg Ile Leu Asp Arg Lys
420 425 430
Ile Gln Ser Leu Gly Asp Ser Lys Thr Ile Pro Gly Asp Thr Ala Trp
435 440 445
Leu Leu Tyr Asp Thr Tyr Gly Phe Pro Val Asp Leu Thr Gly Leu Ile
450 455 460
Ala Glu Glu Lys Gly Leu Val Val Asp Met Asp Gly Phe Glu Glu Glu
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485 490 495
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500 505 510
Gly Leu Glu Val Thr Asp Asp Ser Pro Lys Tyr Asn Tyr His Leu Asp
515 520 525
Ser Ser Gly Ser Tyr Val Phe Glu Asn Thr Val Ala Thr Val Met Ala
530 535 540
Leu Arg Arg Glu Lys Met Phe Val Glu Glu Val Ser Thr Gly Gln Glu
545 550 555 560
Cys Gly Val Val Leu Asp Lys Thr Cys Phe Tyr Ala Glu Gln Gly Gly
565 570 575
Gln Ile Tyr Asp Glu Gly Tyr Leu Val Lys Val Asp Asp Ser Ser Glu
580 585 590
Asp Lys Thr Glu Phe Thr Val Lys Asn Ala Gln Val Arg Gly Gly Tyr
595 600 605
Val Leu His Ile Gly Thr Ile Tyr Gly Asp Leu Lys Val Gly Asp Gln
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His Thr Ala Thr His Ile Leu Asn Phe Ala Leu Arg Ser Val Leu Gly
645 650 655
Glu Ala Asp Gln Lys Gly Ser Leu Val Ala Pro Asp Arg Leu Arg Phe
660 665 670
Asp Phe Thr Ala Lys Gly Ala Met Ser Thr Gln Gln Ile Lys Lys Ala
675 680 685
Glu Glu Ile Ala Asn Glu Met Ile Glu Ala Ala Lys Ala Val Tyr Thr
690 695 700
Gln Asp Cys Pro Leu Ala Ala Ala Lys Ala Ile Gln Gly Leu Arg Ala

705 710 715 720
Val Phe Asp Glu Thr Tyr Pro Asp Pro Val Arg Val Val Ser Ile Gly
725 730 735
Val Pro Val Ser Glu Leu Leu Asp Asp Pro Ser Gly Pro Ala Gly Ser
740 745 750
Leu Thr Ser Val Glu Phe Cys Gly Gly Thr His Leu Arg Asn Ser Ser
755 760 765
His Ala Gly Ala Phe Val Ile Val Thr Glu Glu Ala Ile Ala Lys Gly
770 775 780
Ile Arg Arg Ile Val Ala Val Thr Gly Ala Glu Ala Gln Lys Ala Leu
785 790 795 800
Arg Lys Ala Glu Ser Leu Lys Lys Cys Leu Ser Val Met Glu Ala Lys
805 810 815
Val Lys Ala Gln Thr Ala Pro Asn Lys Asp Val Gln Arg Glu Ile Ala
820 825 830
Asp Leu Gly Glu Ala Leu Ala Thr Ala Val Ile Pro Gln Trp Gln Lys
835 840 845
Asp Glu Leu Arg Glu Thr Leu Lys Ser Leu Lys Lys Val Met Asp Asp
850 855 860
Leu Asp Arg Ala Ser Lys Ala Asp Val Gln Lys Arg Val Leu Glu Lys
865 870 875 880
Thr Lys Gln Phe Ile Asp Ser Asn Pro Asn Gln Pro Leu Val Ile Leu
885 890 895
Glu Met Glu Ser Gly Ala Ser Ala Lys Ala Leu Asn Glu Ala Leu Lys
900 905 910
Leu Phe Lys Met His Ser Pro Gln Thr Ser Ala Met Leu Phe Thr Val
915 920 925
Asp Asn Glu Ala Gly Lys Ile Thr Cys Leu Cys Gln Val Pro Gln Asn
930 935 940
Ala Ala Asn Arg Gly Leu Lys Ala Ser Glu Trp Val Gln Gln Val Ser
945 950 955 960
Gly Leu Met Asp Gly Lys Gly Gly Gly Lys Asp Val Ser Ala Gln Ala
965 970 975
Thr Gly Lys Asn Val Gly Cys Leu Gln Glu Ala Leu Gln Leu Ala Thr
980 985 990
Ser Phe Ala Gln Leu Arg Leu Gly Asp Val Lys Asn
995 1000

<210> 172
<211> 659
<212> DNA
<213> Homo Sapiens

<400> 172
gcctgagcaa cgtctccgag caggcgctgg gctagaggcg ggtctcaacc agctactcat 60
tggaggcggg cttgagagcg gcggccaggg aggtgcggag cagcctcggc ggcggcggcc 120
gaaccaaccg agtcggatcc tgaccctaaa acctagtatt ttccacttgt tcatcaatat 180
ggaaaactca gattccaatg acaaaggaag tggtgatcag tctgcagcac agcgcagaag 240
tcagatggac cgattggatc gagaagaagc tttctatcaa tttgtaaata acctgagtga 300
agaagattat aggcttatga gagataacaa tttgctaggc accccaggtg aaagtactga 360
ggaagagttg ctgagacgac tacagcaaat taaagaaggc ccaccaccgc aaaactcaga 420
tgaaaataga ggaggagact cttcagatga tgtgtctaat ggtgactcta taatagactg 480
gcttaactct gtcagacaaa ctggaaatac aacaagaagt gggcaaagag gaaaccaatc 540
ttggagagca gtgagtcgga ctaatccaaa cagtgggtga tttcagattc agtttagaga 600
taaatgttaa cccgtaataa tgggagccaa aattcagaga atgaaaatga gccatctgc 659

<210> 173
<211> 192
<212> PRT
<213> Homo Sapiens

<400> 173

Pro Glu Gln Arg Leu Arg Ala Gly Ala Gly Leu Glu Ala Gly Leu Asn
1   5   10   15
Gln Leu Leu Ile Gly Gly Gly Leu Glu Ser Gly Gly Gln Gly Gly Ala
            20   25   30
Glu Gln Pro Arg Arg Arg Arg Pro Asn Gln Pro Ser Arg Ile Leu Thr
        35   40   45
Leu Lys Pro Ser Ile Phe His Leu Phe Ile Asn Met Glu Asn Ser Asp
    50   55   60
Ser Asn Asp Lys Gly Ser Gly Asp Gln Ser Ala Ala Gln Arg Arg Ser
65   70   75   80
Gln Met Asp Arg Leu Asp Arg Glu Glu Ala Phe Tyr Gln Phe Val Asn
                85   90   95
Asn Leu Ser Glu Glu Asp Tyr Arg Leu Met Arg Asp Asn Asn Leu Leu
            100   105   110
Gly Thr Pro Gly Glu Ser Thr Glu Glu Glu Leu Leu Arg Arg Leu Gln
        115   120   125
Gln Ile Lys Glu Gly Pro Pro Pro Gln Asn Ser Asp Glu Asn Arg Gly
    130   135   140
Gly Asp Ser Ser Asp Asp Val Ser Asn Gly Asp Ser Ile Ile Asp Trp
145   150   155   160
Leu Asn Ser Val Arg Gln Thr Gly Asn Thr Thr Arg Ser Gly Gln Arg
                165   170   175
Gly Asn Gln Ser Trp Arg Ala Val Ser Arg Thr Asn Pro Asn Ser Gly
            180   185   190

<210> 174
<211> 610
<212> DNA
<213> Homo Sapiens

<400> 174

gtactggcat cagtcaatgt tctggagtga tttgggcccc gatgttggct atgaagctat 60
tggtcttgtg gacagtagtt tgcccacagt tggtgttttt gcaaaagcaa ctgcacaaga 120
caaccccaaa tctgccacag agcagtcagg aactggtatc cgatcagaga gtgagacaga 180
gtccgaggcc tcagaaatta ctattcctcc cagcaccccg gcagttccac aggctcccgt 240
ccagggggag gactacggca aaggtgtcat cttctacctc agggacaaag tggtcgtggg 300
gattgtgcta tggaacatct ttaaccgaat gccaatagca aggaagatca ttaaggacgg 360
tgagcagcat gaagatctca atgaagtagc caaactattc aacattcatg aagactgaag 420
ccccacagtg gaattggcaa acccactgca gcccctgaga ggaggtcgaa tgggtaaagg 480
agcatttttt tattcagcag actttctctg tgtatgagtg tgaatgatca agtcctttgt 540
gaatattttc aactatgtag gtaaattctt aatgttcnca tagtgaaata aattctgatt 600
cttctaaaaa 610

<210> 175
<211> 138
<212> PRT
<213> Homo Sapiens

<400> 175

Tyr Trp His Gln Ser Met Phe Trp Ser Asp Leu Gly Pro Asp Val Gly
1   5   10   15
Tyr Glu Ala Ile Gly Leu Val Asp Ser Ser Leu Pro Thr Val Gly Val
            20   25   30
Phe Ala Lys Ala Thr Ala Gln Asp Asn Pro Lys Ser Ala Thr Glu Gln
        35   40   45
Ser Gly Thr Gly Ile Arg Ser Glu Ser Glu Thr Glu Ser Glu Ala Ser
    50   55   60
Glu Ile Thr Ile Pro Pro Ser Thr Pro Ala Val Pro Gln Ala Pro Val
65   70   75   80
Gln Gly Glu Asp Tyr Gly Lys Gly Val Ile Phe Tyr Leu Arg Asp Lys
                85   90   95
Val Val Val Gly Ile Val Leu Trp Asn Ile Phe Asn Arg Met Pro Ile
            100   105   110
Ala Arg Lys Ile Ile Lys Asp Gly Glu Gln His Glu Asp Leu Asn Glu
        115   120   125
Val Ala Lys Leu Phe Asn Ile His Glu Asp
    130   135

<210> 176
<211> 805
<212> DNA
<213> Homo Sapiens

<400> 176
gggacagcca agtctgtgac ttgcacgtac tcccctgccc tcaacaagat gttttgccaa 60
ctggccaaga cctgccctgt gcagctgtgg gttgattcca cacccccgcc cggcacccgc 120
gtccgcgcca tggccatcta caagcagtca cagcacatga cggaggttgt gaggcgctgc 180
ccccaccatg agcgctgctc agatagcgat ggtctggccc ctcctcagca tcttatccga 240
gtggaaggaa atttgcgtgt ggagtatttg gatgacagaa acactttcg acatagtgtg 300
gtggtgccct atgagccgcc tgaggttggc tctgactgta ccaccatcca ctacaactac 360
atgtgtaaca gttcctgcat gggcggcatg aaccggaggc ccatcctcac catcatcaca 420
ctggaagact ccagtggtaa tctactggga cggaacagct ttgaggtgcg tgtttgtgcc 480
tgtcctggga gagaccggcg cacagaggaa gagaatctcc gcaagaaagg ggagcctcac 540
cacgaagctg cccccaggga gcactaagcg agcactgccc aacaacacca agctcctctc 600
cccagccaaa gaagaaanca ctggatngag aatatttcac cccttcanat tcgttgggcg 660
tgagcgcttc cganaatgtt ccgaagagct gnaagaaggc cttgggaact caaaggatgc 720
ccaaggcttg ggaaaggagc caangggggg gaancaangg gctcaactnc aagccaacct 780
gaaagttcca aaaaangggt ccagt 805

<210> 177
<211> 626
<212> DNA
<213> Homo Sapiens

<400> 177
ctaatttgtc tgtttattcc cacaaggtag ccaggggtgg gggcgccgag ccaagcccag 60
caggccatgg gaccttcctc cggcggggtg cacgctggat tttcgggtct gccccaccag 120
caggtttgca ggcaggccgt catgagtgcc ggtggaaggc tccgagggcg tgggcagggg 180
ctcgggcggg gccacacact tgtggagcta gaaatantgg ggcaggtcct tctctatcac 240
caggggctcc tccatgggtc cgtagcgctt caccacgcag ccgttcttgt cgatgaggaa 300
ctgtgganan acggtgtcca aactgtgggg ccacccctgc aaggggctga ggctgccctt 360
cctgtccgct gcccatctgg gccacggctg tggccagggg aaactggtcc cctaccccc 420
acagcccccct tacctttggt gaagttccac ttgatggcac tggaaaanaa gcacatggac 480
gtgagcgtcc ccaggcagcc ccccacagtc cccaaagctt gtcctgtctc caaggaggcc 540

anaaaggttg tnagcttccc ccggtncctc cacangccac agtgccccca aancccccc 600
aanagccatc tttaccccaa ggaggg 626

<210> 178
<211> 793
<212> DNA
<213> Homo Sapiens

<400> 178
gcgcgaggct gctgctgctg cccccggccc gcgcggctgg aaacggagag gccgagccaa 60
gcggcggccc ctcttatgct gggaggatgc tggagagtag cggctgcaaa gcgctgaagg 120
agggcgtgct ggagaagcgc agcgacgggt tgttgcagct ctggaagaaa aagtgttgca 180
tcctcaccga ggaagggctg ctgcttatcc cgcccaagca gctgcaacac cagcagcagc 240
agcaacagca gcagcagcag cagcaacaac agcccgggca ggggccggcc gagccgtccc 300
aacccagtgg ccccgctgtc gccagcctcg agccgccggt caagctcaag gaactgcact 360
tctccaacat gaagaccgtg gactgtgtgg agcgcaaggg caagtacatg tacttcactg 420
tggtgatggc agagggcaag gagatcgact ttcggtgccc gcaagaccag ggctggaacg 480
ccgagatcac gctgcagatg gtgcagtaca agaatcgtca ggccatcctg gcggtcaaat 540
ccacgcggca gaagcagcag cacctggtcc agcancagcc cccctcgcag ccgcagccgc 600
agccgcagct ccaagcccca accccagcct tcagcctcaa gccngcaacc ccaagcccca 660
attcacaaac cccaagccct caagccccaa cccaaagccc tcangcccca ngcaagntcc 720
aacccgttat ncggccatcc aacattcaan atccaanact ctcaangcct taactncgcn 780
acccaanaac nct 793

<210> 179
<211> 786
<212> DNA
<213> Homo Sapiens

<400> 179
aatatcagag ttttaatttc aaccagctgg cacaacaatg aaagtgtcag actttctgaa 60
agtactcgag aaataatgaa taaattctta atgttttccc ctccaccgcc ctttttattt 120
ctccaagatt aggaattact acggattagg tttttgaaaa taaagtttcc tttttggaaa 180
atggtctaca ttcagaaatg tcttagaaca agcatttaaa aaaaactaat aaataatcat 240
aaatcaaaat acattaaaat aaaattacag tacatcatcg ctcctagaaa attcaccata 300
caagacgatc ctttcaaagg ttcataaata aaagtcttct tgactcgaaa tcgtttcctg 360
catcgtgatg aaaagtatgc agaaaactaa gaagaatcgc aagttttcag tagggtgatg 420
tccaaactac ttgatctggt gcggggcgga gagactgttt tgcttttgat ccaagtgaag 480
acaatagaaa tgtgctcgtc ccacttcctc aagtcctcaa aaccttgtct tgcccgggag 540
ctgccccttt cangcagagt tgggaggtgc tgcgganaaa ccggtgcccg tgcggctgcc 600
aatgcggctg tgggtgtggg tgcngtattt ggtgccggat gcnggtgccg ggtnaaggtg 660
tggggtgcca antnaaggat gaaaatgtgg atnttngnat nttgattccg gatacggggt 720
gggaacctng cngggggccn naaggcttgg ggttggggct naanggctgg ggttttttaa 780
ttgggg 786

<210> 180
<211> 791
<212> DNA
<213> Homo Sapiens

<400> 180
aggacctcag agacccaggc tctgtgattg tggccttcaa ggaaggggaa cagaaggaga 60
aggagggtat cctgcagctg cgtcgcacca actcagccaa gcccagtcca ctggcaccat 120
ccctcatggc ctcttctccg acttctatct gtgtgtgtgg gcaggtgcca gctggggtgg 180
gagttctgca gtgtgacctg tgtcaggact ggttccatgg gcagtgtgtg tcagtgcccc 240

atctcctcac ctctccaaag cccagtctca cttcatctcc actgctagcc tggtgggaat 300
gggacacaaa attcctgtgt ccactgtgta tgcgctcacg acggccacgc ctagagacaa 360
tcctagcctt gctggttgcc ctgcagaggc tgcccgtgcg gctgcctgag ggtgaggccc 420
ttcagtgtct cacagagagg gccattggct ggcaagaccg tgccagaaag gctctggcct 480
ctgaagatgt gactgctctg ttgcgacagc tggctgagct tcgccaacag ctacaggcca 540
aacccanacc agaggaggcc tcagtctaca cttcagccac tgcctgtgac cctatcagag 600
aaggcagtgg caacaatatt tcnaangtcc aagggctgct ggagaatgga gacantgttg 660
accagtcctg agaacatggc tccaggaaag ggctctgacc tggagctacn gtcctcactg 720
ttgccgcaat ttgactggnc ctgtttttgg ganctgcctg aaggcaatcc cggggctccc 780
cctggaggga g 791

<210> 181
<211> 747
<212> DNA
<213> Homo Sapiens

<400> 181
agtatccaaa catactcatt gttttatttt taacaaaaga aatgaaatta aagatagacc 60
acaggtagag tcatgaaatt cttgtttttc cctattcttt ttggtaatta caacgtacat 120
tgtcttcttt tataataaga cccaagggga gaaaagaaaa ggatgtacaa tgaaggtaca 180
agttttgaag caccaaaata ttttatgaca gggacaaaaa aacaaaaaac aaacaaaaat 240
tgaagtacag aaagagggtg gtgggggcaa aaataaaggt acgcacttgg gcttcctcaa 300
gatttgtttg tccctattca gactagaatg aaactggttt aggaaatcac tcctgtatgc 360
tagcaggaat gttgctggca agacacttct gagcatcggg gtgtggactt tacgaaccaa 420
ccttttaaca gtaactctag gagagaggat atcaaaaatt ggcagtgaaa aattatagat 480
aggcaaaaag ctccttctga ggtccaggcc aggagatagt angatttaag aaacaaacaa 540
acaataacaa ccacaaatgg acctttggtg ccactgtcac aactgttgct catcagagta 600
ggagaattgt ancaaaggca ttaaagaagg gacaagcaag ctgaagagcc tgaatccttg 660
gggttgtaag ccnattttgg gnttcctttc aagaaaaggg ctgttggncg gtggaanggg 720
tcanggaaca ntatttcacg ggtcngc 747

<210> 182
<211> 909
<212> DNA
<213> Homo Sapiens

<400> 182
aaacagagag ccaaatcatg agtgaactcc cattcacaat tgcttccaag ataataaaat 60
acctaggaat ccaacttaca aaggatgtga aggacctctt caaggagaac tacaaaccac 120
tgctcaatga aataaaagag gatacaaaca aatggaagaa cattccatgc tcatgggtag 180
gaagaatcaa tatcgtgaaa atggccatac tgcccaaggt aatgtataga ttcaatgcca 240
tccccatcaa gctaccaatg actttcttca cagaattgga aaaaactact caaaagttca 300
tatggaacca aaaaagagcc cacattgcca agtcaatcct aagccaaaag aacaaagctg 360
gaggcatcac gctacctgac ttcaaactat actacaaggc tacagtaacc aaaacagcgt 420
ggtactggta ccaaaacaga gatataaatc aatgcaacag aacagagccc tcagaaataa 480
tgccacatat ctacaactat ctgatctttg acaaacctga gaaaaacaag caatggggaa 540
aggattccct atttaataaa tggtgctggg aaaactggct agccatatgt agaaagctga 600
aactggatct cttctttata ccttatacaa aaattaattg aagatggntt aaaggactta 660
aacgttagac ctaaaaccat aaaaacccta gaagaaaaac ctaggcatta ccattcangg 720
acataggctt gggcaaggac ttcctgtcta aaacaccaan agcaatggga ncaaaagcca 780
aaattgcaaa tggggattct aattaactaa agggcttttg cacagcnaag aagctccatc 840
agagngaaca ggaacntcaa antgggagaa attttgaacc taccatcnga naaggctaat 900
nccagaatc 909

<210> 183

<211> 708
<212> DNA
<213> Homo Sapiens

<400> 183
attatcatta tactttaagt tttaggttac atgtgcacaa tgtgcaggtt agttacatat 60
gtatacatgt gccatgctgg tgtgctgcac ccattaactc gttatttagc attaggtata 120
tctcctaatg ctatccctcc cgcctccccc caccccacaa cagtccccag agtgtgatgt 180
tccccttcct gtgtccatgt gttctcactg ttcaattccc acctatgagt gagaatatgc 240
ggtgtttggt ttttttgtcc ttgccatagt ttactgagaa tgatgatttc caatttcatc 300
cctgtcccta caaaggacat gaactcatca tttttatgg ctgcatagta ttccatggtg 360
tatatgtgcc acattttctt aatccagtct atcattgttg gccatttggg ttggttccaa 420
gtctttgcta ttgtgaatac tgccgcaata aacatacgtg tgcatgtgtc tttatagcag 480
catgatttat antcctttgg gtatatactc agtaatggga tggctgggtc aaatggnatt 540
ccaantccan atccccttang aattgccaca cggactccac aanggttgaa ctantttaca 600
gtcccancaa cagngtnaaa gggtccnaan tcnccaaaat cctctccaag caccngttgt 660
tcccggactt tttaanggat tgncaattcc aaccgggngt caaaaggg 708

<210> 184
<211> 855
<212> DNA
<213> Homo Sapiens

<400> 184
agactcacag tctgctggtg ggcagagaag acagaaacga catgagcaca gcaggaaaag 60
taatcaaatg caaagcagct gtgctatggg aggtaaagaa acccttttcc attgaggatg 120
tggaggttgc acctcctaag gcttatgaag ttcgcattaa gatggtggct gtaggaatct 180
gtcgcacaga tgaccacgtg gttagtggca acctggtgac ccccttcct gtgattttag 240
gccatgaggc agccggcatc gtggagagtg ttggagaagg ggtgactaca gtcaaaccag 300
gtgataaagt catcccgctc tttactcctc agtgtggaaa atgcagagtt tgtaaaaacc 360
cggagagcaa ctactgcttg aaaaatgatc taggcaatcc tcgggggacc ctgcaggatg 420
gcaccaggag gttcacctgc aggggaagc ccattcacca cttccttggc accagcacct 480
tctcccagta cacggtggtg gatgagaatg cagtggccaa aattgatgca gcctcgcccc 540
tggagaaagt ctgcctcatt ggctgtggat tctcgactgg gttatgggtc tgcagttaac 600
gttgccaagg tcaccccagg ctctacctgt gctgtgtgtg gcctgggaag ggtcggccta 660
tctgctgtta tgggctgtta aagcaactgg aggcanccag aatcaattgc ggtggacatc 720
aacaaggaca aattttgcaa agggcaaaag agttgggtgc cactgaatgc catcaaccct 780
caagnctnca ngnaaaccca tccaggnaag tgctaaaang gaatttaccg attggagggt 840
ttggattttt ccgtt 855

<210> 185
<211> 865
<212> DNA
<213> Homo Sapiens

<400> 185
cacagatgtt caatcaactg atgaagcaag tgtcaggact tactgttgac acagaggagc 60
ggctgaaagg agttattgac ctggtctttg agaaggctat tgatgaaccc agtttctctg 120
tggcttacgc aaacatgtgt cgatgtctag taacgctgaa agtacccatg gcagacaagc 180
ctggtaacac agtgaatttc cggaagctgc tactgaaccg ttgccagaag gagtttgaaa 240
aagataaagc agatgatgat gtctttgaga agaagcagaa agaacttgag gctgccagtg 300
ctccagagga gaggacaagg cttcatgatg aactggaaga agccaaggac aaagcccggc 360
ggagatccat tggcaacatc aagtttattg gagaactctt taaactcaaa atgctgactg 420
aagccatcat gcatgactgt gtggtgaagc tgctaaagaa ccatgatgaa gaatccctgg 480
agtgcctgtg tcgcctgctc accaccattg gcaaagactt ggactttgaa aaagcaaagc 540

cacgtatgga ccagtacttt aatcaagatg gagaaattg tnaaagaaag aaaaacctca 600
tctagggatt cggttcatgc ttcaaagatg ttatanacct aaggctgttg caattggggt 660
atctcgaaag agcagatnaa gggcctnaan ctatcgaaca gattcacaaa ganggctaaa 720
attgaaanaa caagaatagc caaagggaag gnccaacaac tcatggacca anggagaaat 780
agaataccaa ggtgttccaa aaanttggcc aaangnnggt tggaaanacn gttcaaaggg 840
ggccangaaa aantccgggt actgg 865

<210> 186
<211> 736
<212> DNA
<213> Homo Sapiens

<400> 186
aaatatttgt tctatgtatt tacaagcctt aaagttgctc taaagatttc aagagtatta 60
agagtacttt tctcagggta gcactttngt ttttttaaac aattcttgga gttctgtggt 120
ccacagcatt tccttctgtt tcaatgttat gtatgttttg attactattg tgattttttta 180
aattttctga agcaagctga gaggcaggca gaaagatttg atgccaaaaa aaaaaaaatc 240
tttcttacct tgttcacccc aaactttctc aaatctggac taaatgctat accttaaaac 300
aaacatgagg tgcatcttga aggggaggga aatttatttc tctgcttttc tattatacaa 360
gttgtttaca gaaactgcaa attaaaaaat tacactggca tttgcagtcc ttaaaataaa 420
ttaaaagttc tcaacttttt tttttttttg ctaaacattt ttttaagtat gagtccttgt 480
ttaaaaagaa aagattaaaa cagaaaatat tttctataaa taatacatgt attttggttt 540
tagtgctccc gccctaaggt ttgaagttta cttttancca ngtacctttt tcctccatga 600
tcaccttttt ttctctttcc cctctcccaa ntccgtgcac acgtgggggt ttccggcaan 660
aattggcctt gctgnactgt gattgggcga anaacgttga aaaacctttt taaaaaaaaa 720
tacttaaaat tgggtt 736

<210> 187
<211> 946
<212> DNA
<213> Homo Sapiens

<400> 187
tgaaggagct acaggccgag caggaggacc gggctttaag gagttttaag ctgagtgtca 60
ctgtagaccc caaataccat cccaagatta tcgggagaaa gggggcagta attacccaaa 120
tccggttgga gcatgacgtg aacatccagt ttcctgataa ggacgatggg aaccagcccc 180
aggaccaaat taccatcaca gggtacgaaa agaacacaga agctgccagg gatgctatac 240
tgagaattgt gggtgaactt gagcagatgg tttctgagga cgtcccgctg gaccaccgcg 300
ttcacgcccg catcattggt gcccgcggca aagccattcg caaaatcatg gacgaattca 360
aggtggacat tcgcttccca cagagcggag ccccagaccc caactgcgtc actgtgacgg 420
ggctcccaga gaatgtggag gaagccatcg accacatcct caatctggag gaggaatacg 480
tgagtctctg tgggccttgg agccctgagg cgccctggca cgtccaccgg cctgaggccc 540
agccaggagc ttcaggggac aaggtggcac ttgtgtttcc agaggcaagc naagtgcagg 600
ggtgagcaag cnggcgggat gctgggggtg ctggggcaaa ctgaccctgt cttcctgtct 660
tccgcctgca gctagcctga cgttgtggac agtnaangcg cctgcangtt atacatgaaa 720
cccccagcac acgaanaagc caanggnacc tttcaaaagg ctttnttggt gccgggacca 780
acctgggacc gccagcaacc aatnaaaaaa ggcnctgacn ttaaccaagc tcngagggaa 840
tttcccancc tttggggggcc caaggtggct cccaaagaac cctccccntt nggggccccc 900
aaacnaatna ttgttcaaaa anggaacaaa aacccctctc aagccc 946

<210> 188
<211> 802
<212> DNA
<213> Homo Sapiens

<400> 188
aaagtcaagg ncgtttattt ccngaggnca tgacacanga agtggaatcc naaccacggn 60
tgcggnnnaa aagtgatgaa ggccaaagtg ctgactgaca tgccgggtgg accaaganct 120
ggagtcngtt atcntaacac gaatgcccan gaccttggtt taatgttaaa cantggagca 180
ngtcctganc gggcacggcc angcctggag gancggccgc acacacancc angcgcnagg 240
ctccctgcgg gacctcngga aggggaana gcgtcaacaa tttacggngg gtccaaccgc 300
tgggtcaaat tgagacaaac cantgtgtgg ttgggttcgg gtcancangc tgganangggt 360
tcngttcntt ttgatcanta ncntttgggg ccccaaggga nggtcntggg anccacctga 420
nccccaaagc tgggaaattc ctcaaagctg cncatgtcaa gagccttcnc antgctgctg 480
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gccgggggtt tcatgtntac ctgcancgcc tcactgtcca ccaangtcag ctaactgcag 600
gcnnaagaca ggaatnacag ggtcagtctg cccaacaacc ccancatccc ggcccgccct 660
ggctcaaacc ctgcaacctt gcctgccttc cgggaancac aatttcccac ccttgtnccc 720
ctgaaanccn cctggnctgg ggccntcaaa ggccgttgga ncttccanag gncnccccca 780
ggggntccca angggcccac aa 802

<210> 189
<211> 807
<212> DNA
<213> Homo Sapiens

<400> 189
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agcggccttt gagctgtggg gaggttccag cagcagctac agtgacgact aagactccag 120
tgcatttcta tcgtaaccgg gcgcgggga gcgcagatcg gcgcccagca atcacagaag 180
ccgacaaggc gttcaagcga aaacatgacc gctgagccca tgagtgaaag caagttgaat 240
acattggtgc agaagcttca tgacttcctt gcacactcat cagaagaatc tgaagaaaca 300
agttctcctc cacgacttgc aatgaatcaa aacacagata aaatcagtgg ttctggaagt 360
aactctgata tgatggaaaa cagcaaggaa gagggaacta gctcttcaga aaaatccaag 420
tcttcaggat cgtcacgatc aaagaggaaa ccttcaattg taacaaagta tgtagaatca 480
gatgatgaaa aacctttgga tgatgaaact gtaaatgaag atgcgtctaa tgaaaattca 540
gaaaatgata ttactatgca nagcttgcca aaaggtacag tgattgttca gccagagcca 600
gtgctgaatg aagacaaaga tgattttaaa ggggcctgaa tttagaagca gaagttaaaa 660
tgaaaactga naatctcaaa aaacgccgga gaanatgggc ttcatgggga ttgtgangcc 720
tgcactggcn tggtggacaa caaggtcaat caatttcaaa aaggttccat ttatagacaa 780
cccttcaatg caaggtcnta tttgtta 807

<210> 190
<211> 608
<212> DNA
<213> Homo Sapiens

<400> 190
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agattggctt taatttcttc taaaagcatc ttcttggcaa ttctattctc aggatcattg 120
tcgtcatcat catcatccac tgtgacaggc actgatttag ataaggcttc atctcctgaa 180
gattggcaaa atccagtatg tgaagacagc actaaatttt cagtcacagg cttaattttc 240
tgttcatcgc tgcttccctc acctatagaa ttctgatcat catcttctat atcagaagaa 300
gatgaggatg taatgtcagc ttgcttcctt ttagtgcttg ttcttaggga gtttctcttt 360
ttctccttga caatgactgc cttcttttta gatgaagttc tttgcttctt ctttttacta 420
tcttcangaa ctttcctcag catcagatga tgatgangcc actttgtatt tccttagtat 480
ttctctttga acttaaattt cttctttccc tcaattcgag tcttttcagt caccttatca 540
gaagagttac aancatcttc tttcatggga agtatcaaga tgatgaacaa tcttgtcnct 600
tccttgaa 608

<210> 191
<211> 786
<212> DNA
<213> Homo Sapiens

<400> 191
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ggagggacgt ggacaacggc ctctcgctcg tcatcttcag tgactggtac aacacttctg 120
ttatgagaaa agtgaagttt tatgatgaaa acacaaggca gtggtggatg ccggataccg 180
gaggagctaa catcccagct ctgaatgagc tgctgtctgt gtggaacatg gggttcagcg 240
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gcagcatcgc gaagtttcca gaagatggcg tcgtgataac acagactttc aaggaccaag 360
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ggagcaagct cagtcactcc agagaggatg gaaggaaacc atctcatcgg tactccaagg 660
ttctggangg ccatttggga aaaccaaaac ctcgggctcn acaaccctgt ccangcctgt 720
nctgggccaa gccaanagcc tttaaaccan aacggngccc aattaaccct ttggaaaaca 780
tcagaa 786

<210> 192
<211> 819
<212> DNA
<213> Homo Sapiens

<400> 192
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aaattacaaa acatggtggc aggtgatact tacaaaaata aagcgaaggt ctatgtttta 120
cagatttgtg catgtttcct tcaaatctca gtctgtactg tcattaaaaa gatcatggaa 180
tctatgttgt tcctcatgat ggaatagtaa aaaaactgca ttccactgac aaaaaaaata 240
gctttgcttc caaatagcac aagtctttaa agtgactttt cccaacaata aatatagaaa 300
atagccttta acaagcgtct tttagcttgg tcagggttgt atcatttgtt tggaaagtac 360
atccttcccc tgcagtcaga agaccccaga cagcctttcc agttctcccg agtctttggt 420
gcgcacagct gccggcggga agtctcactg gcggcagagc cactaagtcc ctcctgacgg 480
gatccacagg aatcttctcg atgtaccagg agcctctgcc catcacagga gggcaggccc 540
atgtagaaca agactctaac aaacctgcag ctggaaactg gattcctttt aaaccaaccc 600
gccaacacag ctcggntcac ccaccancgc cgtccgtnaa aggggctctc tgggcctcac 660
gggtcagcca ggttgccggt cacaccgaaa ggggtccttg ggcgggtgaa cctgctgcat 720
gaanctggcg gggngcttca accctgggct tcctccggct ttcggcctgg ncctgggcct 780
tgttgaantt gntccacaaa agaaaggcca ggagcaaca 819

<210> 193
<211> 744
<212> DNA
<213> Homo Sapiens

<400> 193
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tgtctgctgt acctactggc agtcagattg caaatattgg tcagcaagca aacataccta 120
ctgcagtgca gcagccctct acccaggttc caccttcagt tattcagcag ggtgctcctc 180
catcttcgca agtggttcca cctgctcaaa ctgggattat tcatcaggga gttcaaacta 240
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ctccccagcc acaaggagta gaatcagtag ctcaaggaat tgtttcacag cagttgcctg 360
cagttagttc tttgccctct gctagtagta tttctgttac aagtcaggtt agttcaactg 420

gtccttctgg aatgccttct gccccaacaa acttggttcc accacaaaat atagcacaaa 480
cccctgctac ccaaaatggt aatttggttc aaagtgttaa gtcaacctcc cttgatagca 540
actaatacaa atttgccttt ggcacaacag ataccactaa gttctaccca agttctccgc 600
acaatcatta gctcaggcaa ttggaagcca aattgaagat gccaggcgtt gcagcggagc 660
cctccttaag ttggcttacc tcaagactaa tcagttggtg acaattgggg ggaatgttca 720
gcaagtttca agattgggaa gtta 744

<210> 194
<211> 567
<212> DNA
<213> Homo Sapiens

<400> 194
atcaacattt atatgcttta ttgaaagttg acaagtgcaa cagttaaata cagtgacacc 60
ttacaattgt gtagagaaca tgcacagaaa catatgcata taactactat acaggtgata 120
tgcagaaacc cctactggga aatccatttc attagttaga actgagcatt tttcaaagta 180
ttcaaccagc tcaattgaaa gacttcagtg aacaaggatt tacttcagcg tattcagcag 240
ctagatttca ggattacaca aagtgagtaa ctgtgccaaa ttcttaaaat ttctttaggt 300
gtggtttttg tcatgtagca gtttttatgt agatcnatat ntaaaagtcc acacctcctc 360
agacangcca atgaaacnac taaatttcaa tctgtacaan ctaaatagta attacagtcc 420
tctangtgnn caangatact tacaccacat anacaaatnt acnntacgca naacaacctt 480
catggggaag gatagcccta ggtccccagc tancctgtca ccatttttgt cactctcata 540
gttttggtgt ccaatccatt ggttttg 567

<210> 195
<211> 771
<212> DNA
<213> Homo Sapiens

<400> 195
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tagttgacaa tgcatacagc tgtgatccaa ggataaaaaa gttcaaggaa gaagaaaaag 120
ccaagaaaga ancanaaaag aaagcaaaag cagaagctaa acggaaggag caagaagcta 180
aagaaaaaca aagacaagct gaattagaag ctgctcggtt agctaaggag aaagaagagg 240
aggaagtcag acagcaagca ttgctggcaa agaaggaaaa agatatccag aaaaaagcca 300
ttaagaagga aaggcaaaaa tttcgaaact catgcaagac ctggaatcat ttttctgata 360
atgaggcaga gcgggttaaa atgatggaag aagtggaaaa actttgtgat cggcttgaac 420
tggcaagctt acagtgcttg aatgaaacac tcacatcatg cacaaaagaa gtnggaaagg 480
ctgctttgga aaaacagata gaagaaataa atgagcaaat cagaaaagag aaagaggaag 540
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aaatggaagt aaaaattggg cacaaagatg ntctacaatt actaatttna aagctgtgaa 660
tcctgttncc tgctggaaca aantcaagat gggaagttat tgccaantac atgaacatac 720
attcctcccn cngggngtcc aaaaagaaac tgccaaaagn atgtttattg g 771

<210> 196
<211> 561
<212> DNA
<213> Homo Sapiens

<400> 196
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tccttgtatc gtttcatgca gtccttcttt gtcctgccag gcaccgcttc tgctattttt 180
tcccatcttt caggtgtatt tactgggtat gttttcaaag cttgttccaa aagcttctgt 240
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gcgttgtctg cttgaggtac cactccatgt tctttttga acttatcaaa tgccttttta 360
tttangtcag cttttgatg agggtcaagt ttttggagac tctttgcttt gccaataaca 420
tctttggnan gttcttttga ctccaagagg aagaangtnt ngttcatgtn antangcaan 480
aacgtcccat ctggaanttt tgttcnacca gggaacanac tcacaagctt taactaagta 540
antgtngnat naccgncngn c 561

<210> 197
<211> 691
<212> DNA
<213> Homo Sapiens

<400> 197
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cgcagcctca gccccagcag cctccacccc caccccctcc ccagcagcag cccccgctgt 120
cacagtgtan tatgaataac agtttcaccc cagctcctat gatcatggag ataccagaat 180
ctggaagcac tgggaacata agtatctatg agaggattcc aggggatttt ggtgccggca 240
gctactctca accatcagcc accttcagcc tagccaagct gcagcagctg accaacacca 300
ttatggaccc tcatgccatg ccttatagcc attctcctgc tgtgacttcc tatgcaacca 360
gtgtttctct gtccaataca ggactggctc agctggctcc atctcatccc ttagctggga 420
ctcctcaagc acangccacc atgacgccac ccccaaactt ggcatccact accatgaacc 480
tcacatctcc tctgcttcag tgcaacatgt ctgccaccaa cattggcatt cctcacacgc 540
aggagattgc aagggcaaat gccagtgaag ggcacatttt ccatccgctc caagtttggc 600
ggcactgccc tctgcngctg ctcaccanna ngcagctggt atgggccgtn tccccaatcg 660
ggcagtttgc caatgcaang gcttgggccc t 691

<210> 198
<211> 646
<212> DNA
<213> Homo Sapiens

<400> 198
acctatccct ggagcaagta ataggaagag aatgggcaaa ctggttgcac gagagaaaag 60
agaatggagt tgggagcaac acatgaactt gcgttataac attctgctgt ccagatctgc 120
cctactgtgc tggtggtcgg tctgtccctc ttctcattag ccactcacag gagaggtgct 180
tgtgcactct gattcacagg ggatgaactc aggatctcaa aagacataca aaaactanag 240
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gcgccatctc ttccaacata aaatanactg tttcaatggt ttgtcagtta tttttcaaat 360
cactaanatg tacagtcatc caccaacaat ttaagaaaga acctaagagg caaatcactg 420
gggactgcta tttgagtttt atcagtcaaa ggctcaagca tcaanaccct cagttancat 480
ttcaaagtac atactangaa acancgaggc tgggtggcgt tgtgtgcgtt anggctgatt 540
caccaggtgg taaancaaca aagnggttaa gnctccnctt tttggattgt taattgncca 600
tcctcnattc ctccaaaagg gctgggattt ggatttggca aagtca 646

<210> 199
<211> 811
<212> DNA
<213> Homo Sapiens

<400> 199
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tatgacaaca tgtccacaat ggtgtacata aaggaagaca agttggagaa gcttacacag 120
gatgaaatta tttctaagac aaagcaagta attcaggggc tggaagcttt gaagaatgag 180
cacaattcca ttttacaaag tttgctggag acactgaagt gtttgaagaa agatgatgaa 240
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ggcctgagtg aggcacaggt tatgatggct ttgtcaaatc acctgaatgc tgtggagtcc 360

gagaagcaga aactgcgtgc gcaggttcgt cgtctgtgcc aggagaatca gtggctacgg 420
gatgaactgg ccaacacgca gcagaaactg cagaagagtg agcagtctgt ggctcaactg 480
gaggaggaga agaagcatct ggagtttatg aatcagctaa aaaaatatga tgacgacatt 540
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aatgatgaag acgacccagg gcaaggaatc cagcagcagc acagcagtgc agccgcggct 660
gcccagcaag gcngctacna agattcccgc gcggctgcgg acgctccaca acctgggtga 720
ttcagttcgc ctcnncangg ggccgctacc aaggtaacct gttgcccccct cctggcaaag 780
caaggncccct gggaagggan cctgggagga a 811

<210> 200
<211> 763
<212> DNA
<213> Homo Sapiens

<400> 200
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acatgtatac agaaatcagg aacccccccca aaaaggacag cagcaccgaa aggaatggcc 120
agttcacaga gaggtgcagc tctgacaaga tcctagaggc tgctagacac agcgggcagc 180
actggagaga gaagggaagc tgcgggaggc gccacccgtc atgcaggaga cagtgtgaga 240
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gtaacagttg gnctatcaac tttgcangct ttgtaccaac cgccatactc tccaaaaaga 600
tgtcccatcc ttttgctttc ctttgcattc ttctctttcc tcaacaatgc atccaaatgg 660
gtttaatttc aacatctaca gaaccaaact ccctttcatg tgcacaagtg agaatcnctt 720
tgtacantgt ttccgccttc cttgaacntt ccctgtttca aaa 763

<210> 201
<211> 717
<212> DNA
<213> Homo Sapiens

<400> 201
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agaatganca caattccatt ttacaaagtt tgctggagac actgaagtgt ttgaagaaag 180
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ttgcagccgc ggctgcccaa gcaaggcggc tacgagattc ccgccgcggc tgccggacgc 660
tccacaacct ggtnatccaa tacgccctcn caaggggcgc taccaagggt aactgtt 717

<210> 202
<211> 647
<212> DNA
<213> Homo Sapiens

<400> 202
cagtcggagt gagtttatta gaagttagaa agacacaaat acacaaatca ctgagcactt 60

caagattagt agagaaaagc agaatgccca aatttcacac acagactaca cagcaaatgc 120
tactggggca tatcctaggg agacccggag tccgagcggg gcccccaggg ctctaagtac 180
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<210> 203
<211> 786
<212> DNA
<213> Homo Sapiens

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acctta 786

<210> 204
<211> 738
<212> DNA
<213> Homo Sapiens

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aaggaaggca anatctgcct caacaacaat tggccttctt cncggccngc tccaattttc 720
nccnggggcc tccttcaa 738

<210> 205
<211> 818
<212> DNA

<213> Homo Sapiens

<400> 205
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tggccctcac aggttgttga gttccagcag ggtctggtcc aaggtctggt gaatctcgac 120
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cctggccacc tcttcatatt tgcggtctga atcctcagcg atgtgcttgg cctccttcag 480
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caacctcggt tcccttnaa cntcntnctg gaagggct 818

<210> 206
<211> 927
<212> DNA
<213> Homo Sapiens

<400> 206
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<210> 207
<211> 910
<212> DNA
<213> Homo Sapiens

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gagataaaac caactttccc aaaaagggag atgttgttca ctgctggtat acaggaacac 420
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ccaagccttt aagttttaag gtcggagtag gcaaagttat cagaggatgg gatgaagctc 540
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<211> 745
<212> DNA
<213> Homo Sapiens

<400> 208
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gggatttatc tctcaaaagc tgggaccaag taaacaaatt ttattaactc cttgaatttt 180
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<210> 209
<211> 965
<212> DNA
<213> Homo Sapiens

<400> 209
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cagaacataa attattagga aacattaaaa atgtggccaa gacagctaac aaggaccact 180
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aaact 965

<210> 210
<211> 867

<212> DNA
<213> Homo Sapiens

<400> 210
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taagggattt atctctcaaa agctgggacc aagtaaacaa attttattaa ctccttgaat 180
tttccagttg actcttcctt tacaatagta acaagttcta actagttgtg taaatttctt 240
caaggccaag ttttatcatt gttgctaata tccttagagc tgaagcactg ctatttcaat 300
caatatccac taattccact tcaaaagtga gttttgcatt tggtggaatt ttggcatcag 360
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aagtttgggt ttaactccct tttttcagaa caagatttag taaaattttg gnnggacccct 660
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acaatttttt acttggctca agaaancntt tacttaaacc tttcaggtac cctttaaaaa 780
nccttangtt ttaaaaaaaa tgggttataa gggctggtaa ccnaaggttg ggcccttggt 840
aaccngttct tggggcaaaa tttttaa 867

<210> 211
<211> 972
<212> DNA
<213> Homo Sapiens

<400> 211
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cagaacataa attattagga aacattaaaa atgtggccaa gacagctaac aaggaccact 180
tggttacagc ctataaccat ctttttgaaa ctaagcgttt taagggtact gaaagtataa 240
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gaaagaaagg acagcctgat gccaaaattc caccaaatgc aaaactcact tttgaagtgg 660
aattagtgga tattgattga aatagcagtg cttcagctct aaggatatta gcaacaatga 720
taaaacttgg ccttgaagaa atttacacaa ctagttagaa cttgttacta ttgtaaagga 780
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gagataaatc ccttatgaat ccctggtcta aaatactttc ctacagctgt gtaaaatact 900
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tgatccactg tc 972

<210> 212
<211> 817
<212> DNA
<213> Homo Sapiens

<400> 212
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tctcgcaaag agcgggaagc tgagcttgga gccaaagcca aggaattcac caatgtttat 180
atcaaaaact ttggggaaga ggtggatgat gagagtctga aagagctatt cagtcagttt 240
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gagttaaaac ggaaatttga acagttgaaa caggagagaa ttagtcgata tcaggggtg 480
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tggacgcatt ttggggctcc aaccactata tgttgccctg gccccanagg aagggaanag 720
agaaaggntc accttgacca accagtttta tgcaacgaan tggctgggaa tngagaacca 780
cttcccngcc aatgccaatc tttaaantca gnttcca 817

<210> 213
<211> 756
<212> DNA
<213> Homo Sapiens

<400> 213
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ggcactttat gatacttttt ctgcttttgg aaacatactg tcctgcaagg tggtgtgtga 180
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agcagagtta aaacggaaat ttgaacagtt gaaacaggag agaattagtc gatatcangg 660
ggtgaatccc cacattaaga acttggatga cactattgat gatgaagaaa attaaggaaa 720
agaattttcn ccntttggga tnaattaaca agttgc 756

<210> 214
<211> 728
<212> DNA
<213> Homo Sapiens

<400> 214
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ttctgggggga aaaaatcaaa ncccacaata aaaaaaaagt taacactgtc tgggccacag 120
cagaacccaa agaacatatt cgtataattg aaaaattcta ggtgcttcat aattgacctt 180
ttgatacaaa atgacctatt aaatttgcaa tttgtaatcc ttggtgttga ggtccatagg 240
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gccctgcaca tggaccgcaa ggctggggtg cctgcaaaan gctgtatggc aaggatgaag 660
ggctgccgac actgggaagg cggtattngt agggggggcaa aaancccggg gaagcancag 720
caacaaca 728

<210> 215
<211> 710
<212> DNA
<213> Homo Sapiens

<400> 215
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atctggggga aaaaatcaaa acccacaata aaaaaaaagt taacactgtc tgggccacag 120
canaacccaa agaacatatt cgtataattg aaaaattcta ggtgcttcan aattgacctt 180
ttgatacaaa atgacctatt aaatttgcaa tttgtaancc ttggtgttga ggtccatagg 240
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atcggttttt ccttgtctaa naggtagcag cagcaacagc gcccaccttc tgggcagctt 360
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gangaagggc ctgcggaana ctgggangcg tatttgttan gggggcaaa 710

<210> 216
<211> 824
<212> DNA
<213> Homo Sapiens

<400> 216
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cacaaaaaga aagtttaaac gggnaggcaa aatttaaaac cggg 824

<210> 217
<211> 749
<212> DNA
<213> Homo Sapiens

<400> 217
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ttctggggga aaaaatcaaa acccacaata aaaaaaaagt taacactgtc tgggccacag 120
cagaacccaa agaacatatt cgtataattg aaaaattcta ggtgcttcat aattgacctt 180
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nccagcagca acancaacng cttggcgcc 749

<210> 218
<211> 600
<212> DNA
<213> Homo Sapiens

<400> 218
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anatttgaat gcattgtttg ggatgangtg gggaanaagc gttctcncag cannengctt 540
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<210> 219
<211> 1077
<212> DNA
<213> Homo Sapiens

<400> 219
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<210> 220
<211> 1007
<212> DNA
<213> Homo Sapiens

<400> 220
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<210> 221
<211> 833
<212> DNA
<213> Homo Sapiens

<400> 221
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aaaggggtga tccagaacgg cagagagaga tggaagaaga ggaggatgag gatgaggatg 480
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tcctgcttcc gtcagaccga gaccggctcc gttcggaggt gaangctggc atggagccgg 600
gaactggnaa acatcatcca ggagacanga gaaaganctg ggacccanat ggggctgaag 660
aanggatcag aatccgggat cggcaatgc tggctctcaa aatcaactct caacaaantc 720
attaaaaaga ctggagggaa aaacaagagt tccaaancct ggtgaannaa gcncataaaa 780
aagaaggttg tcccaaaaaa gnctccccca tcaanccaac cctncaggga aaa 833

<210> 222
<211> 745
<212> DNA
<213> Homo Sapiens

<400> 222
ggattgatgg tccagttgtt tatttagaaa cctgattgtt caagaacatg gtgggtgctt 60
cacacctttt tcactgggat tgtgctggag gtgataggca gcattctacc atttcctcag 120
caacagaggt gaaggctcct caactcagaa gcacaaattg taggggacag ggtgggcagg 180
gaaagggaga aggaaatccc aaggcaattc aatagaagag ggtaaaacga ctccaaacat 240
cactaagggc aggtgggggc ctgcttgctc agtgcctgct aagtgtcctg ccctccttgc 300
tctctctacc cacctccact caaaagatcc tactgaatct ccaggtaggc agcagggaat 360
atcctatcat taggggacaa taacaggaaa agccacagag gagaggaaga ggattgagtg 420
agagttcagg agagcaaata tcacaggccc ggtgaggtct caaggtggct gccagcaggg 480
gcagcaagca ttcacccagg gcccccacac ccacagagtt gcccgagang tccacaagct 540
cagctccact ctgctgtttg gccctcaagg gttccagggt ggggaagtgg ggaagaggca 600
ngccagtcca ggaagatctg gattccgtga angggtcaag tgtagtgttg gtctcagaag 660
tcaaattntc caagtcccct gttgccctcc ccacctggag aagccccana cccggnggta 720
attgctcncc anctccttct gccgc 745

<210> 223
<211> 747
<212> DNA

<213> Homo Sapiens

<400> 223
actacatcga tcgcgtggac gagcccttgt cctgctctta tgtgctgacc attcgcactc 60
ctcggctctg cccccaccct ctcctccggc ccccacccag tgctgcaccg caggccatcc 120
tctgtcaccc ttccctacag cctgaggagt acatggccta cgttcagagg caagccgact 180
caaagcagta tggagataaa atcatagagg agctgcaaga tctaggcccc caagtgtgga 240
gtgagaccaa gtctggggtg gcaccccaaa agatggcagg tgcgagcccg accaaggatg 300
acagtaagga ctcagatttc tggaagatgc ttaatgagcc agaggaccag gccccaggag 360
gggaggaggt gccggctgag gagcaggacc caagccctga ggcagcagat tcagcttctg 420
gtgctcccaa tgattttcag aacaacgtgc aggtcaaagt cattcgaagc cctgcggatt 480
tgattcgatt catagaggag ctgaaaggtg gaacaaaaaa ggggaagcca aatataggcc 540
aagagcagcc tgtggatgat gctgcagaag tccctcagag ggaaccagag aangaaaggg 600
gtgatccaga acggcagaga gagatgggaa ngaagangan gatgaggatg aggatgaggg 660
atgaaagann aaggatgaaa cgggcaagtt actggggaan aattttgana aagggaactg 720
ggaaagggat tcctggcttt ccgttca 747

<210> 224
<211> 618
<212> DNA
<213> Homo Sapiens

<400> 224
gatggtccag ttgtttattt agaaacctga ttgttcaaga acatggtggg tgcttcacac 60
ctttttcgct gggattgtgc tggaggtgat aggcagcatt ctaccatttc ctcagcaaca 120
gaggtgaagg ctcctcaact cagaagcaca aattgtaggg gacagggtgg gcagggaaag 180
ggagaaggaa atcccaaggc aattcaatag aagagggtaa aacgactcca aacatcacta 240
agggcaggtg gggcctgct tgctcagtgc ctgctaagtg tcctgccctc cttgctctct 300
ctacccacct ccactcaaaa gatcctactg aatctccagg tangcancan ggaatatcct 360
atcattaggg gacaatanca ggaaaagcca cagaggagag gaagaggatt gagtganaag 420
ttcangacag caaattatca caggcccggt gaggtctcaa ngtgngctgc caacaagggg 480
caancagcat tcacccangg gccccacacc cacnnnagtt gccccagagg tccacanctc 540
ancctcccan ctgccngttt ggccctcaag gggttccaan gttcgngaaa gtgggggagg 600
aaggcanccc antcccag 618

<210> 225
<211> 765
<212> DNA
<213> Homo Sapiens

<400> 225
caaacatcag agactgcatg ctggagagaa acttgaagaa tgtgagaaaa ccttcagcaa 60
ggatgaggag cttagaaaag agcagagaac tcaccaggaa aagaaagttt attggtgtaa 120
tcagtgtagt aggaccttcc agggcagctc agatctcatc agacatcagg taactcatac 180
aagagagaaa ccatatgaat gtaaagaatg tgggaaaact caatcagagc tcagaccttc 240
tgagacatca tagaattcac agtggagaaa aaccttacgt atgcaataaa tgtggggaat 300
cttttaggag cagctcagat cttattaaac accatcgtgt tcatactgga gagaaacctc 360
atgaatgtag tgaatgtggg aaagtcttta gccagaggtc ccaccttgtc acacaccaga 420
aaatccacac tggagagaag ccctatcagt gcactgaatg tgaaaaagcc ttcaggcggc 480
gttcactcct tattcaacgt cggagaattc atagtggtga gaaaccctat gaatgtaagg 540
aatgtgggaa actcttcatg tggcacacag ctttcctcaa acatcagaga ctgcatgctg 600
gagagaaact tgaagaatgt gagaaaacct tcagcaagga tganggagct taggggagag 660
cagaaaattc accanggaag agaaagcctt attgggngta atcagtgtgg tanggctttc 720
caagggcagc tcangacctc atcgggccat caggtaactc aatac 765

<210> 226
<211> 791
<212> DNA
<213> Homo Sapiens

<400> 226
tggatccaaa gcacccctgg cactgttgtt tatggcccac ctcctgctgg ggcccccatg 60
gtgtatgggc ctccaccccc caacttctcc atccccttca tccctatggg tgtgctgcat 120
tgcaacgtcc ctgaacacca taacttagag aatgaagttt ctagattaga agacataatg 180
cagcatttaa aatcaaagaa gcgggaagaa aggtggatga gagcatccaa gcggcagtcg 240
gagaaagaaa tggaagaact gcatcataat attgatgatc ttttgcaaga gaagaaaagc 300
ttagagtgtg aagtagaaga attacataga actgtccaga aacgtcaaca gcaaaaggac 360
ttcattgatg gaaatgtaga gagtcttatg actgaactag aaatagaaaa atcactcaaa 420
catcatgaag atattgtaga tgaaattgag tgcattgaga agactcttct gaaacgtcgc 480
tcanagctca gggaagctga ccgactcctg gcagaggctg agagtgaact ttcatgcact 540
aaagaaaaga caaaaaatgc tgttgaaaag ttcactgatg ccaagagaag tttattgcaa 600
actgagtcag atgctgaggg aattagaaag gagagctcan gaaactgctg ttaanctcgt 660
caaanctgat cagcagctaa gatcgctcca agctgatgca aaaggatttg gancancaca 720
angatcaagc aagaagaaat cttgaaaaga aattaacnaa aatttntnca gcaaaagact 780
cagacttcaa a 791

<210> 227
<211> 687
<212> DNA
<213> Homo Sapiens

<400> 227
gattgttatc ttttattttc atatgaaaaa tagattttaa gcaaaattca aaaataactc 60
gacactataa aaanagaggg ccttaagtac attctttttg ttaataagat ttaccagttt 120
gtaggttcaa atatgcagtt aaaatcactg tttttttta aacatgttac gaagattaaa 180
aaaaaaaagg ctcagccaca tgttggttta aattcccata tgcaactatt cccatatgta 240
ctatgtacaa gtgatttata aaaacattgg cattaatggt acaggcaaag taaactacag 300
tggagtttca naatctcagt tcactgcatc ttgattaaaa aaaccatgtg acattccaat 360
tatgaagtca gtgaggtagt ggaggtgttt tccttgaata tatttacaca agacagtatt 420
cctcatctgg ctgaggcatt cttttccgga ttttgtccaa gttganagtc ctctgtgagg 480
gaagactcca agctgagaca gactgggtga tgacgctgaa tctgcaaagg tgcctggtga 540
ccaattcccc ctaanagcat cctacttgtc tccncaaact gtgntaaagt gccctctgtc 600
ctgccgcttt cctttaatna aaacttctgg cttngcttgg ggcanacagt gtcggan ttg 660
gggccttgag tcnggcttcc cggggaa 687

<210> 228
<211> 810
<212> DNA
<213> Homo Sapiens

<400> 228
gtctgggcag cgccaggcga tggccctgct gctggtgctc ctcgcctctt ggggcctggg 60
gcagtgaggg ggccggcggg cgtgggccga gtggccgcgg gcgccatgga gggggtgctg 120
tacaantgga ccaactatct gagcggttgg cagcctcgat ggttccttct ctgtggggga 180
atattgtcct attatgattc tcctgaagat gcctggaaag gttgcaaagg gagcatacaa 240
atggcagtct gtgaaattca agttcattct gtagataata cacgcatgga cctgataatc 300
cctggggaac agtatttcta cctgaaggcc agaagtgtgg ctgaaagaca gcggtggctg 360
gtggccctgg gatcagccaa ggcttgcctg actgacagta ggacccagaa ggagaaagag 420
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ctccttgttc ancaagtaga ttaaaacata agaagtgacc acaactggtg tgtccaattc 540

tgaggtaaag gagtcttcca ctctggttgt ttcgtangag ggaattgatg tgggaacttt 600
gctgaaatca anctgntata ctttttctga aagaccttgg taagaattca tgcanatngc 660
aaattgcagc cttnaanctc ctgaagcctn cttctaaccg gcactccaac canggaatna 720
anctnaagct gggccaatgg ctccaaagtt ccaacnaaag gttaaaanat cccagctcaa 780
atttgggcng caaacaaagg gcaatccaac 810

<210> 229
<211> 552
<212> DNA
<213> Homo Sapiens

<400> 229
gtaaatttgt ttgagttcat tgtagattct ggatattagc ccttttgtca gatgagtaga 60
ttgcaaaaat tttctcccat tctgtaggtt gcctgttcac tctgatggta gtttcccttg 120
ctgtgcggaa gctctttagt ttaattagat cccatttgtc aatttcggct tttgttgcca 180
ttgctttcgg tgttttagac atgaagtcct tgcccatgcc tatgtcctga atggttttcc 240
taggttttct tctagggttt ttatggtttt aggtctaaca tttaagtctc gaatccatct 300
tgaattaatt tttgtataag gtgtaaggaa gggatccact ttcagctttc tacgtatggc 360
tagccagttt tcccancacc atttattaaa tagggaatcc tttccccant tcctgttttt 420
gtcangtttg tcaaagatca natggctgta natatgcanc attatttccg agggctctgt 480
tcngttccat tggtctacat ttccgttttg gttccngtac catgctgttt tttgttacng 540
gtanaccttg gt 552

<210> 230
<211> 842
<212> DNA
<213> Homo Sapiens

<400> 230
ctcatcagtt agaagaaaaa gaaaatcaaa ttaagagcat gaaggctgat attgaaagtc 60
ttgtaacaga aaaagaagcc ttacagaagg aaggaggcaa tcagcaacag gctgcttctg 120
aaaaggagtc ttgtataaca cagttgaaga aagagttatc tgaaaacatc aatgctgtca 180
cattgatgaa agaagagctt aaagaaaaaa aagttgagat tagcagtctt agtaaacaac 240
taactgattt gaatgttcag cttcaaaata gcatcagcct atccgaaaaa gaagcagcca 300
tttcatcact aagaaagcag tatgatgaag aaaaatgtga attgctggat caggtgcaag 360
atttatcttt taaagttgac actctgagta aagagaaaat ttctgctctt gagcaggtag 420
atgactggtc caataaattc tcagaatgga agaagaaagc acagtcaaga tttacacagc 480
atcaaaacac tgttaaagaa ttgcagatcc agcttgagtt aaaatcaaag gaagcttatg 540
aaaaggatga gcagataaat ttattgaagg aagagcttga tcagcaaaat aaaagatttg 600
attgtttaaa gggtgaaatg gaagacgaca agagcaagat gggagaaaaa ggagtctaat 660
ttagaaacag agttaaagtc tcaaacagca agaattatgg gattagagga ccatattanc 720
caagaaaact atttggaaat tagagtcctt aaatngaaag ttccttaaaa aattacaatc 780
aacaaaaagg atattggacc acaaagnaat tgggtcaaaa aaccttcaac aantttcaag 840
ga 842

<210> 231
<211> 781
<212> DNA
<213> Homo Sapiens

<400> 231
atatagtaaa taaactttat ttatctgttt ctcagagatg acactgccaa caatcacaga 60
tttgcataca atacagttat gtattggcta ttcacaattt acagtagtgt tttttcctct 120
gaaaatatat agtacaaaag ctaagtaaac aatgaggtac tgccatttgg gattttttac 180
atgtcttagc ttaaagaact ggtctttagc aaatattcaa cagatcaacc tgaataaaat 240

agtcaattaa atgctctaat ttatcagaaa aaatccacta agtttcacct caaaatgtat 300
tgcacaagtc tttttaaaaa atcaccctaa aaataaatag gaaaggtaag ccgttcttta 360
aaaagaatgg atgaaaggaa tattatgtaa gcccataaag caggttaagt tatcaaaata 420
tcttttaaac aacataaaac tcttcccaag agaaaactga agaaaaaact atcaccattt 480
ctccactgat aaaatctatt ttaaaggcag tctgcaactt atctgtgggc cagatttttc 540
ttgggtcttt tggctacatg aggggccctg aatgacaact tcattctcaa agagtagcaa 600
agtgtggaca agttttccaa gcagcangtc acccaatgtc actcttcctc aagatgaagg 660
atcggagcca tgacacatgt ttaactaagc acagaccgga tgggtttacc cagaagatac 720
cactggcaan ggtgaagtaa acatcaggcc gaggcaacct tccccntttc aaaaantttt 780
c 781

<210> 232
<211> 767
<212> DNA
<213> Homo Sapiens

<400> 232
gttatatagt aaataaactt tatttatctg tttctcagag atgacactgc caacaatcac 60
agatttgcat acaatacagt tatgtattgg ctattcacaa tttacagtag tgttttttcc 120
tctgaaaaat ataagtacaa aagctaagta aacaatgagg tactgccatt tgggattttt 180
tacatgtctt agcttaaaga actggtcttt agcaaatatt caacagatca acctgaataa 240
aatagtcaat taaatgctct aatttatcag aaaaaatcca ctaagtttca cctcaaaatg 300
tattgcacaa gtctttttaa aaaatcaccc taaaaataaa taggaaaggt aagccgttct 360
ttaaaaagaa tggatgaaag gaatattatg taagcccata aagcaggtta agttatcaaa 420
atatctttta aacaacataa aactcttccc aagagaaaac tgaagaaaaa actatcacca 480
tttctccact gataaaatct attttanagg cagtctgcaa cttatctgtg ggccagattt 540
ttcttggtct tttggctaca tgaggggccc tgaatgaaaa cttcattctc aaaggagtag 600
caagtgtggg acagttttcc aagcagcagt cacccaatgt cactcttctt caagatgaaa 660
gatcggagnc atgacacatg ttaacctaag nacangactg gagggtttac ncangaagat 720
acactgcgaa ggtgaaagtt aaacatcaag ccgaggaacc tcccctt 767

<210> 233
<211> 879
<212> DNA
<213> Homo Sapiens

<400> 233
gggagtttaa tacacagctg gcacaaaagg aacaagagct ggaaatgacc ataaaagaaa 60
ctatcaataa ggcccaggag gtggaggctg aacttttaga aagccatcaa gaagagacaa 120
atcagttact taaaaaaatt gctgagaaag atgatgatct aaaacgaaca gccaaaagat 180
atgaagaaat ccttgatgct cgtgaagaag aaatgactgc aaaagtaagg gacctgcaga 240
ctcaacttga ggagctgcag aagaaatacc agcaaaagct agagcaggag gagaaccctg 300
gcaatgataa tgtaacaatt atggagctac agacacagct agcacagaag acgactttaa 360
tcagtgattc gaaattgaaa gagcaagagt tcagagaaca gattcacaat ttagaagacc 420
gtttgaagaa atatgaaaag aatgtatatg caacaactgt ggggacacct tacaaaggtg 480
gcaatttgta ccatacggat gtctcactct ttggagaacc taccgaattt gagtatttgc 540
gaaaagtgct tttgagtat atgatgggtc gtgagactaa gaccatggca aaagttataa 600
ccaccgtact gaagttccct gatgatcaga ctcagaaaat tttgggaaaa gagaagatct 660
cggctgatgt ttacttcacc tcgcagtggt atcctcngag taaaccatca gtcgtgccta 720
agtttacatg tgtcatgggt ccgattcttc atcctttgaa gaaagagtgg acattggggt 780
naccggctgc cttgggaaaa ctgtccanac nttgcnaacn ccttggggaa atggaagntt 840
ttccanttca agggccccct caangnttgc ccaaacagg 879

<210> 234
<211> 780

<212> DNA
<213> Homo Sapiens

<400> 234
aaactttatt tatctgtttc tcagagatga cactgccaac aatcacagat ttgcatacaa 60
tacagttatg tattggnnng gcacaattta cagtagtgtt ttttcctctg aaaaatataa 120
gtacaaaagc taagtaaaca atgaggtact gccatttggg attttttaca tgtcttagct 180
taaagaactg gtctttagca aatattcaac agatcaacct gaataaaata gtcaattaaa 240
tgctctaatt tatcagaaaa aatccactaa gtttcacctc aaaatgtatt gcacaagtct 300
ttttaaaaaa tcaccctaaa aataaatagg aaaggtaagc cgttctttaa aaagaatgga 360
tgaaaggaat attatgtaag cccataaagc aggttaagtt atcaaaatat cttttaaaca 420
acataaaact cttcccaaga gaaaactgaa gaaaaaacta tcaccatttc tccactgata 480
aaatctattt taaaggcagt ctgcaactta tctgtgggcc agatttttct tggtcttttg 540
gctacatgag gggccctgaa tgaaaacttc attctcaaag agtagcaagt gtggacaagt 600
tttccaagca gcagtcancc aatgtcactc ttcttcaaga tgaaagatcg gagccatgac 660
acatgttaac taagcacaga cntgatggtt tactncagaa gattaccact gcnaaggtga 720
aagttaaaca tcaagncgag catncntctc tttccaaaaa ttttccggng tccggattca 780

<210> 235
<211> 780
<212> DNA
<213> Homo Sapiens

<400> 235
attctgaggg tatattaagt cagagtcagg ataaatcact tcggagaata gcagaattaa 60
gagaggagct ccaaatggac cagcaggcaa agaaacatct gcaagaggag tttgatgcat 120
ctttagagga gaaagatcag tatatcagtg ttctccaaac tcaggtttct ctactgaaac 180
aacgattacg aaatggcccg atgaatgttg atgtactgaa accacttcct cagctggaac 240
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ctagtgaaaa agaagctctg caagaacaac tggatgaaag acttcaagaa ctagaaaaga 480
taaaggacct tcatatggcc gagaagacta aacttatcac tcagttgcgt gatgcaaaga 540
acttaattga acagcttgaa caaggataag ggaatggtaa tcgcagagac aaaacgtcag 600
atgcatgaaa ccctggaaat gaaagaagaa gaaattgctc aactccgtag tcgcatcaaa 660
cagatgacta cccaagggag aggaattacg ggaacaagan agaaaagtcc gaaagaactg 720
cntttgaggg aacttgaaaa agccttgagt acagnccaaa aanacagngg aagccaccgg 780

<210> 236
<211> 711
<212> DNA
<213> Homo Sapiens

<400> 236
cttggttttt aaatttggtt tcatattcct cattcaaaat atgaatactg tcctccttgg 60
ctgacaattt ctgtgtgagt atctcaattt ctttcttctg tccttctctc atttgtaaaa 120
tcatattttc cttttccacc aagatttgct ttgtctgttc ctgttctttg ttaccatctt 180
caagtttgga ctcatagact tgggttaaag attttacttt ttgctccatt tcactatttt 240
gtttttcaag ttgctgcatt aagtcctgca cctggatttt gtgagcatct aactcagtac 300
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gttccccttc agacctttta atatctgcct ccaaattttc tacatgagcc tgatgctctt 540
tcaaatgctt gtccctttcc ttcaagagaa gctcaagttg nttaanttga tcttttaaag 600
ccttctcaan tcctccggga tanaaaacnt cgtgttcttt naatgagaac ggtcaacntg 660

ccggctgggt gataantttt ccgttcancc anccttgggg ctccaaattc c 711

<210> 237
<211> 658
<212> DNA
<213> Homo Sapiens

<400> 237
atagtaaata aactttattt atctgtttct cagagatgac actgccaaca atcacagatt 60
tgcatacaat acagttatgt attggctatt cacaatttac agtagtgttt tttcctctga 120
aaaatataag tacaaaagct aagtaaacaa tgaggtactg ccatttggga ttttttacat 180
gtcttagctt aaagaactgg tctttagcaa atattcaaca gatcaacctg aataaaatag 240
tcaattaaat gctctaattt atcagaaaaa atccactaag tttcacctca aaatgtattg 300
cacaagtctt tttaaaaaat caccctaaan ataaatagga aaggtaagcc gttctttaaa 360
aagaatggat gaaaggaata ttatgtaagc ccataagagc aggttaagtt atcaaaatat 420
cttttaaaca ncataaaact cttcccanga gaaaactgaa gaaaaaacta tcaccatttc 480
tccactgata aaatctattt taaaggcagt ctgcanctta tctgtgggcc aagatttttc 540
ttggnctttt ggctacatga gggggccctg gaatgaaaaa cttcattccc aanggagttn 600
gcnaggtgtg ggacaggttt tccaaggcaa gcaagtnagc caaatngtca gctcttcc 658

<210> 238
<211> 678
<212> DNA
<213> Homo Sapiens

<400> 238
gttatatagt aaataaactt tatttatctg tttctcagag atgacactgc caacaatcac 60
agatttgcat acaatacagt tatgtattgg ctattcacaa tttacagtag tgtttttttcc 120
tctgaaaaat ataagtacaa aagctaagta aacaatgagg tactgccatt tgggattttt 180
tacatgtctt agcttaaaga actggtcttt agcaaatatt caacagatca acctgaataa 240
aatagtcaat taaatgctct aatttatcag aaaaaatcca ctaagtttca cctcaaaatg 300
tattgcacaa gtctttttaa aaaatcaccc taaaaataaa taggaaaggt aanccgttct 360
ttaaaaagaa tggatgaaag gaatattatg taagcccata aagcaggtta agttatcaaa 420
atatctttta aacaacataa gaactcttcc caaggagaaa actgaannaa aaaactatca 480
ncatttcnnc actgataaaa tctantttaa agggnagtcn gcaacttanc tgtgggccag 540
atttttccgt ggggcttttg ggctacantn agggggccct gaatgaaaaa nttcaattcc 600
ncaaatgnng tagcaaattg tgggncangt tttccaaag cagncaantt canccccnana 660
tgtcactcct tccttcaa 678

<210> 239
<211> 1402
<212> DNA
<213> Homo Sapiens

<400> 239
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ctatcaataa ggcccaggag gtggaggctg aacttttaga aagccatcaa gaagagacaa 120
atcagttact taaaaaaatt gctgagaaag atgatgatct aaaacgaaca gccaaaagat 180
atgaagaaat ccttgatgct cgtgaagaag aaatgactgc aaaagtaagg gacctgcaga 240
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gcaatgataa tgtaacaatt atggagctac agacacagct agcacagaag acgactttaa 360
tcagtgattc gaaattgaaa gagcaagagt tcagagaaca gattcacaat ttagaagacc 420
gtttgaagaa atatgaaaag aatgtatatg caacaactgt ggggacacct tacaaaggtg 480
gcaatttgta ccatacggat gtctcactct ttggagaacc taccgaattt gagtatttgc 540
gaaaagtgct tttgagtat atgatgggtc gtgagactaa gaccatggca aaagttataa 600

ccaccgtact gaagttccct gatgatcaga ctcagaaaat tttggaaaga gaagatgctc 660
ggctgatgtt tacttcacct cgcagtggta tcttctgagt aaaccatcag tctgtgctta 720
gttaacatgt gtcatggctc cgatcttcat cttgaagaag agtgacattg ggtgactgct 780
gcttggaaaa ctgtccacac ttgctactct ttgagaatga agttttcatt cagggcccct 840
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atagatttta tcagtggaga aatggtgata gtttttctt cagttttctc ttgggaagag 960
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ttttaaaaag acttgtgcaa tacattttga ggtgaaactt agtggatttt ttctgataaa 1140
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gttctttaag ctaagacatg taaaaaatcc caaatggcag tacctcattg tttacttagc 1260
ttttgtactt atattttca gaggaaaaa cactactgta aattgtgaat agccaataca 1320
taactgtatt gtatgcaaat ctgtgattgt tggcagtgtc atctctgaga aacagataaa 1380
taaagtttat ttactatata ac 1402

<210> 240
<211> 760
<212> DNA
<213> Homo Sapiens

<400> 240
gtgcagtttc tcttatattc ctcacatatg tgctttcatt catctttcgc aagtggagaa 60
aaaataatgg cttttggtct tttggctttt ttattatctt aatatgtgta tccacaatta 120
tggtatcaac tcaatatgaa aaactcaact taattttgtg catgattttc ataccttcct 180
tcactttgct ggggtatgtc atgttattga tccagctcga ctttatgaga aacttggaca 240
gtctggacaa tagaataaat gaagtcaata aaaccattct tttaacaacc ttaataccat 300
accttcagag tgttattttc ctttttgtca taaggtgtct ggaaatgaag tatggaaatg 360
aaataatgaa taaagaccca gttttcagaa tctctccacg gagtagagaa actcatccca 420
atccggaaga gcccgaagaa gaagatgaag atgttcaagc tgaaagagtc caagcagcaa 480
atgcactcac tgctccaaac ttggaggagg aaccagtcat aactgcaagc tgtttacaca 540
aggaatatta tgagacaaag aaaagttgct tttcaacaag aaagaagaaa atagccatca 600
gaaatgtttc cntttgtgtt aaaaaaggtg aaagttttgg ggattaccta ggacacaatg 660
ggagctggta aaagtacttc cattaaaatg ataacntggg tgcacaaagc caaactgcan 720
ggagtggtgg gtgttacaaa ggnagcagan gcatcnggta 760

<210> 241
<211> 745
<212> DNA
<213> Homo Sapiens

<400> 241
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cncnggtatt acatcaatac agctataaca ttaatgcagc aattatataa cacaaaagtg 120
ctataatgac atgggaaatg ttcatgaact gtgaggtgaa aagatacaga aaatgactat 180
gcctacngat actacctttg aaaaaggatc cataaaaaat acattgaata taagttggct 240
aaagaaaata ttaactgcgg tactttctta cagattangg ctancttctt ccatataact 300
tcaatatgta ctaaaattca catgcattta ttttataatc agaatgtcat tataattaaa 360
tgttangctg tgccatttca tcagtttatc anaccttctt atagtcaatg tcacattaaa 420
ttagaatccg agtaaataan gtttaaaaat anctgataca tttgaagttc aggctaaaaa 480
cctcatattt ttatttgtaa aatgttctca ntgttagctt tattgataat aaccgataac 540
caacctaata ttgtangatt tttaaattat ttttaagcac aaantagacc catgttgggg 600
atgaataaca tgtcngattt tgtnaatttt ggtcnacnac ttttcccaaa aatttccttg 660
tttccttcan ccnaaatttt taaaantgaa aactgtatca attatggaan ggtttattaa 720
aangtttncc tttggtaacc ngaag 745

<210> 242
<211> 818
<212> DNA
<213> Homo Sapiens

<400> 242
gcaacgccgg ggcgcccgag gtctggaagg cgcagaaatg gagcaagagc cacaaaatgg 60
agaacctgct gaaattaaga tcatcagaga agcatataag aaggcctttt tatttgttaa 120
caaaggtctg aatacagatg aattaggtca gaaggaagaa gcaaagaact actataagca 180
aggaatagga cacctgctca gagggatcag catttcatca aaagagtctg aacacacagg 240
tcctgggtgg gaatctgcta gacagatgca acagaaaatg aaagaaactc tacagaatgt 300
acgcaccagg ctggaaattc tagagaaggg tcttgccact tctctgcaga atgatcttca 360
ggaggtgccc aagttatatc cagaatttcc acctaaagac atgtgtgaaa aattaccaga 420
gcctcagtct tttagttcag ctcctcagca tgctgaagta aatggaaaca cctcaactcc 480
aagtgcaggg gcagttgctg cacctgcttc tctgtcttta ccatcacaaa gttgtccagc 540
agaagctcct cctgcttata ctcctcaagc tgctgaaggt cactacactg tatcctatgg 600
aacagattct ggggagtttt catcagttgg agaggagttt tatagggaat cattctcagc 660
caacggcctc ttnagaacct taagggctgg gattcangat gaaattgatt ttgataccaa 720
atgggagtac anntttttt tgtaaatcct gcaangggga ngttatgcan cttcgtancc 780
ccggggtacc ttcnaattgt gaagggtttt gggntaaa 818

<210> 243
<211> 799
<212> DNA
<213> Homo Sapiens

<400> 243
aatttcttga agtacttttt taatccaatt aagctgataa taatcacttc gaattttaat 60
acaatacaat catgttccca aatttccnag gctcataaca atacagtctc aatacaaaag 120
acgtaataat ctatttttat tcattttaaa tcaaagaaac cattccattt cctaacaaac 180
aggtaagtta caaaagtagt ccattttact tttcatcagt ctttccctgt tttgaacaag 240
tctttttgag aattcttagt tttagttttt gtttagctta cacactgaaa attttgagaa 300
gcatctaaaa aaatccacaa ttagtgcaaa aagaggggac aatactttaa gtcattcctt 360
ctataaaaag aattaaggtt actaaatgcc aatttttaag caaatatata gtttcctatt 420
tgccttctga aagacagcag atataaaaat agttcaatat taggtttaac aaggtttgaa 480
caacacatgt actatcagct ttattttacc tgcaaaaata ttttagctac acttggaaaa 540
aaaataaact tgagaatata acttcacatt tctaaggcca gatgcaagaa tacttaatct 600
tttcctttta aatagaagac atgccataaa atttatgaaa agttaatttg taggaatggn 660
atacatttaa aaaatacngg ttaaaccngg tgagggaatt ccacatttgg cctatttaac 720
aaaaatttta aaccaatttt caaaaggggc tttggggtaa aaagtngatt cccaagcaac 780
ntcaancant ttaaccttc 799

<210> 244
<211> 726
<212> DNA
<213> Homo Sapiens

<400> 244
gtgagttgag cgctgctgct ccgcggtgga gtcaccgcac cgctcccggg atcatggtgt 60
tctacttcac cagcagcagc gttaattcat ctgcctacac tatttacatg ggaaaagata 120
aatatgaaaa tgaagatctg atcaagcatg gctggcctga agatatctgg tttcatgtgg 180
acaaactctc ttcggctcat gtataccttc gattacataa gggagagaat atagaagaca 240
tcccaaagga agtgctgatg gactgtgccc accttgtgaa ggccaatagc attcaaggct 300
gcaagatgaa caacgttaat gtggtatata cgccgtggtc taacctgaag aaaacagctg 360
acatggatgt ggggcagata ggctttcaca ggcagaagga tgtaaaaatt gtgacagtgg 420

agaagaaagt aaatgagatc ctgaaccgat tagaaaagac caaagtcgag cggttcccag 480
acctancagc agagaaagaa tgcagagatc gtgaagagag gaatgagaaa aaagcccaaa 540
ttcaggaaat gaaaaagaga gaaanagaag aaatgaagaa gaanagggaa atggatgaac 600
ttangagcta ttcatcacta atgaaagttt gaaaatatgt cttcanatca ggatggcaat 660
ggattcagat gaattcatgt taaaaggaga aaaggngaaa aaggaccttt gaaaaatttg 720
aatgtt 726

<210> 245
<211> 592
<212> DNA
<213> Homo Sapiens

<400> 245
ccagattaaa aaaatggtat tttattataa cttttaaaat tgcggaacat cagactgaat 60
atcatcagac acatacacaa aaccactcat ctctaaagtc attttctata ccctctcaaa 120
atttggccag tgagttttgc ctcagggaat tttccagttc aaccccatac accaacatgg 180
aataaatgga aacactagcc ttttggtttt gcccanagtt ccaaagtgct attacaggtg 240
gaatatctgc tgcaggaagt cattcttgct gctgtgggtg tgagtaaaat gcttagttcc 300
ttctaaaatc ataattgcaa tatggacttc tgcttcacgc tgcatcctaa ggcacaaatc 360
aggtaaccta catctcccaa atgatcaaca ggagcactcc atcctatttt accctcaatg 420
cnganaaatt acncctgggc ccanaagttg tcacataggt ggcttgggtt acttggggct 480
caggcaacaa ctgccacagg ccccagcttg atgaanacca tcnatttctt taaaatatgt 540
tggnnactaa gatggaggcc tccggcncan agggaancan nggacataaa ac 592

<210> 246
<211> 821
<212> DNA
<213> Homo Sapiens

<400> 246
aggatgaaga gctggagagc gccgaggacg acgagcgcag ctgtcggggc cgcgagtcgg 60
acgaagacac tgaggatgct agtgaaactg acctggcaaa gcatgatgaa gaagactatg 120
tagaaatgaa ggaacagatg tatcaggaca aactggcttc tctcaagagg cagttgcaac 180
aactgcaaga aggtacatta caggaatatc agaagagaat gaaaaaacta gatcagcagt 240
acaaagagag gatacggaat gcagaactct tcctccagct ggaaactgaa caagtggaac 300
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tgaaagagaa cctgattgct gagctagaag aaaagaagaa aatgattgaa aatgaaaagc 420
tgacaatgga actgactgga gattctatgg aggtgaaacc tatcatgacc agaaagttgc 480
ggaggcgacc aaatgatccc gtccccatcc cagacaagag gaggaaacct gctccagccc 540
agctaaacta tttgttaaca ggatgaacag atcatggagg atctgagaac attaaataag 600
cttaagtcac ccaagagacc agcatctcca tcctctcctg agcacttgcc tgcaacaccc 660
gccggaatct ccaagcccca gaggttcnaa agccccggat anaagaatgg caaacctgtt 720
actatgacaa aaagatggtt accacaagag ccaaggccat cctatcctgg angtcaaagg 780
gacaaaccan gaaactgaag cctgcctnat taagtttccg t 821

<210> 247
<211> 639
<212> DNA
<213> Homo Sapiens

<400> 247
gttacacaaa gcatttattt ctctgagaag gccgagagcc acgagaattc atcatctcct 60
gctaggacct ctgccccaag cttctgggca aatagtgaat tggacgcgac agggaaagta 120
gctacgtgat ccactaatca gattcaaaac atgaaaatgc actggagagt gtatcccttc 180
ctgctcttct ccatggtaga gagacttaaa gataatcaat aaaaatagct gtcccttcaa 240

actcagagga ggttttcaaa aacaagtata agcaaaaaat aaagaaataa aaggaaagta 300
aatcaaaccc cccaatacgc ctgaaagtaa aacagtctca tggtgactga tgtctggaan 360
aagttgaggc agaaaagact gacaaagttg gaangcatcc cggccacaaa agtgcccnaa 420
aagaattcan tgcagtgctc tccatttcca aggctgagta actattccca gntaagttaa 480
catttttcna nttaaggana nancgaanac anntncatnt ctanatccca ctccagaaat 540
anggtcaatg agaangangc actgtannna aagtcaagna gctgganenc ccgggcggnt 600
tnacccaaga gcccggcgct nnaagcctgg gcccaagct 639

<210> 248
<211> 846
<212> DNA
<213> Homo Sapiens

<400> 248
aacaggatgt caaaaattaa actgcgcttt ccatcacaat agaggacgat atgttgatgg 60
ccttttccta cctccgagca aaactgtgtt gcccactgtg cctgagtcac cagaagagga 120
agtgaaggct agccaacttt cagttcagca gaacaaattg tctgtccagt ccaatccttc 180
ccctcagctg cggagcgtta tgaaagtaga aagttccgaa aatgttccta gccccacgca 240
tccaccagtt gtaattaatg ctgcagatga tgatgaagat gatgatgatc agttttctga 300
ggaaggtgat gaaaccaaaa cacctaccct gcaaccaact cctgaagttc acaatggatt 360
acgagtgact tctgtccgga aacctgcagt caatataaag caaggtgaat gtttgaattt 420
tggaataaaa actcttgagg aaattaagtc aaagaaaatg aaggaaaaat ctaagaagca 480
aggtgagggt tcttcaggag tttccagtct tttactccac cctgagcccg ttccaggtcc 540
tgaaaaagaa aatgtcagga ctgtggtgag gacagtaact ctctccacca aacaaggaga 600
agaacccttg gttagattga gtcttactga gagactgggg aaacgaaaat tttcagcagg 660
cggtgacagt gatcctccat taaagcgtag cctggcacan aggctaaggg aagaaagttg 720
aagctccaga aactaacant gacaaaacac caangaaagc tcaagtttcc aagtcccccct 780
aaaggggcga attaggcatg tcagccngga ttcaagataa tnagggatgc aacaagatta 840
aaggtt 846

<210> 249
<211> 763
<212> DNA
<213> Homo Sapiens

<400> 249
gactttccta catcagtttt atttaaaaca caaacaagta tttctctttc tgtaagggca 60
aatggttcaa ataatgcgga acacgaaaca ttgactaata caagtgcttt aaatatgaaa 120
caaaattatt ttttaaaaaa gcaaaagaat aaagaatata tacaaaaggg acctggaatc 180
tgtaagctga ttccaaaaat gaaataagta gaaaatccat ggtgaaacct gaacattcta 240
cctctgcttt ggagaagggc tatcatacaa cattcagtca gctgaagatg gattggtaga 300
ggtgtgtcta tacataaact tcagtcattt ttgcttgtgc agaatcatcc caatcttccc 360
aagactgaat gggcagtcct gtggctttct tccttttcca tattcccaac aaggctacgt 420
gaagttcaac tcttgatgag ccgcttacaa cagcagttcc ttaggagcca acatgacagg 480
tgggtcagat ttccctatga gaaacaaaac tggccaccta cagcaaaata tcaaaatggg 540
taagtccttc cttcctcttc ctcctgatta tatacaacat atctcctttc aagactatta 600
tttccatcat gccttattcc ttcacaaatc taaaccttga ngtgatatga angaaaccaa 660
catcaagaaa agaaaactca attcagaaat gaanaaaacg ggcaggtata caatacaccc 720
cagagcatct caatatcccc tgggacagnt acaattcagt gtt 763

<210> 250
<211> 899
<212> DNA
<213> Homo Sapiens

<400> 250
attcaagtca agagatgtga gaccatgaga gagaagcaca tgcagaaaca gcaggagagg 60
gaaaaatcag tcttgacacc tcttcgggga gatgtagcct cttgcaatac ccaagtggca 120
gagaaaccag tgctcactgc tgtgccagga atcacacggc acctgaccaa gcggcttccc 180
acaaagtcat cccagaaggt ggaggtagaa acctcaggga ttggagactc attattgaat 240
gtgaaatgtg cagcacagac cttggaaaaa aggggtaaag ctaaacccaa agtgaacgtg 300
aagccatctg tggttaaagt tgtgtcatcc cccaaattgg ccccaaaacg taaggcagtg 360
gagatgcacg ctgctgtcat tgccgctgtg aagccactca gctccagcag tgtcctacag 420
gaacccccag ccaaaaaggc agctgtggct gttgtcccgc ttgtctctga ggacaaatca 480
gtcactgtgc ctgaagcaga aaatcctaga gacagtcttg tgctgcctcc aacccagtcc 540
tcttcagatt cctcaccccc ggaggtgtct ggcccttcct catcccaaat gagcatgaaa 600
actcgccgac tcagctctgc ctcaacaagg aaagccccca ctctctgtgg aggatgattt 660
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tctgggaaaa gatgaagatg acccttccgg cttngngcct atcaannaaa ngattgntan 780
cctgaaaggg tggtaattga nggacncctt naaaaaaaaa atccnccaaa aaaactnggg 840
ccttaanttc naccaaatgg taacaatttn acctgagaat gnttaatttc ctttaggcc 899

<210> 251
<211> 755
<212> DNA
<213> Homo Sapiens

<400> 251
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tcaaataatg cggaacacga aacattgana nagacaagtg ctttaaatat gaaacaaaat 120
tatttttttaa aaaagcaaaa gaataaagaa tatatacaaa agggacctgg aatctgtaag 180
gtgattccaa aaacgaaata agtagaaaat ccatggtgaa acctgaacat tctacctctg 240
ctttggagaa gggctatcat acaacattca gtcagctgaa gatggattgg tagaggtgtg 300
tctatacata aacttcagtc atttttgctt gtgcagaatc atcccaatct tcccaagact 360
gaatgggcag tcctgtggct ttcttccttt tccatattcc caacaaggct acgtgaagtt 420
caactcttga tgagccgctt acaacagcag ttccttagga gccaacatga caggtgggtc 480
agatttccct atgagaaaca aaactggcca cctacagcaa aatatcaaaa tgggtaagtc 540
cttccttcct cttcctcctg attatataca acatatctcc tttcaaagac tattatttcc 600
atcatgctta ntccttcaca aatctaaacc ttgaggtgat atgaaggaaa ccaacatcan 660
gaaaagaaaa ctcaattcag aaatgaagaa aacgggcang tatacaattc ancccccagag 720
caacccaata atccctgggc aaaagttcaa ttcaa 755

<210> 252
<211> 753
<212> DNA
<213> Homo Sapiens

<400> 252
cctacatcag ttttatttaa aacactaaca agtatttctc tttctgtaag ggcaaatggt 60
tcaaataatg cggaacacga aacattgact aatacaagtg ctttaaatat gaaacaaaat 120
tatttttttaa aaaagcaaaa gaataaagaa tatatacaaa agggacctgg aatctgtaag 180
gtgattccaa aaacgaaata agtagaaaat ccatggtgaa acctgaacat tctacctctg 240
ctttggagaa gggctatcat acaacattca gtcagctgaa gatggattgg tagaggtgtg 300
tctatacata aacttcagtc atttttgctt gtgcagaatc atcccaatct tcccaagact 360
gaatgggcag tcctgtggct ttcttccttt tccatattcc caacaaggct acgtgaagtt 420
caactcttga tgagccgctt acaacagcag ttccttagga gccaacatga caggtgggtc 480
agatttccct atgagaaaca aaactggcca cctacagcaa aatatcaaaa tgggtaagtc 540
cttccttcct cttcctcctg gattatatac aacatatctc ctttcaagac tattatttcc 600
atcatgcnta atccttcaca aatctaaaac cttgagggtg atatgaaagg aaaccaacat 660
canagaaaag aaaactcaat tcaagaaaat taagaaaacc tggcaaggta tacaaataca 720

cccccaggag catcccaaat aatccctggg aaa 753

<210> 253
<211> 793
<212> DNA
<213> Homo Sapiens

<400> 253
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aatggttcaa ataatgcgga acacgaaaca ttgactaata caagtgcttt aaatatgaaa 120
caaaattatt ttttaaaaaa gcaaaagaat aaagaatata tacaaaaggg acctggaatc 180
tgtaaggnga ttccaaaaac gaaataagta gaaaatccat ggtgaaacct gaanattcta 240
cctctgcttt gganaagggc tatcatacaa cattcagtca gctgaanatg gattggtaaa 300
ggtgtgtcta tacataaact tcagtcattt ttgcttgtgc anaatcatcc caatcttccc 360
aagactgaat gggcagtcct gtggctttct tccttttcca nattcccaac aaggctacgt 420
gaagttcaac tcttgatgag ccgcttacaa cagcagttcc ttaggagcca acatgacagg 480
tgggtcagat ttccctatga gaaacaaaac tggccaccta cagcaaaata tcaaaatggg 540
taagtccttc cttcctcttc cncctgatta tatacaanat atctcctttc aagactatta 600
tttccatcat gcttattcct tcacanatct aaaccttgan gtgatatgaa nggnaaccaa 660
catcangaaa agaaaactca attcagnaat gaangaaaac tgggaggtat ttaatanacc 720
cccangnnga atccaaatac cctggnaana gttcaattca antgtacngc naaagnccat 780
aantaantat tgg 793

<210> 254
<211> 625
<212> DNA
<213> Homo Sapiens

<400> 254
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tcaaataatg cggaacacga aacattgact aatacaagtg ctttaaatat gaaacaaaat 120
tattttttaa aaaagcaaaa gaataaagaa tatatacaaa agggacctgg aatctgtaag 180
gtgattccaa aaacgaaata agtagaaaat ccatggtgaa acctgaacat tctacctctg 240
ctttggagaa gggctatcat acaacattca gtcagctgaa gatggattgg tanaggtgtg 300
tctatacata aacttcagtc attttttgctt gtgcagaatc atcccaatct tcccaagact 360
gaatgggcag tcctgtggct ttcttccttt tccatattcc caacaaggct acgtgaagtt 420
caactcttga tgagccgctt acaacancaa gttccttang agccaacatg acaggtgggg 480
tcangatttc cctatgagaa acaanactgg ccacctacag caaaaatatn aaaatggggt 540
aagtccttcc ttcctcttcc tcctgaatta tatncaacat ntctcctttt caagacnatt 600
anttccatca gggcttaatc cttca 625

<210> 255
<211> 907
<212> DNA
<213> Homo Sapiens

<400> 255
gccaacagca gcggagaaac gtttctcttt cctctcagtt tgcgcacacc atggcggccc 60
ctgcccagca gactactcag cctggcggcg ggaagcgcaa aggcaaggct cagtatgtgc 120
tggccaagcg cgctcggcgc tgcgacgctg gcgggccccg tcagctagag cccgggctac 180
agggcatcct catcacctgc aatatgaacg agcgcaagtg cgtggaggag gcctacagcc 240
tcctcaacga atacggcgac gacatgtatg ggccagaaaa gtttacagac aaggatcagc 300
agccctctgg aagtgaggga gaggatgatg atgcggaggc tgccttgaag aaagaagttg 360
gtgacattaa ggcatctaca gagatgaggt taagaagatt ccagtcagtg gaaagtggag 420
caaataacgt tgtcttcatc aggacacttg ggatagagcc tgagaaattg gtgcatcata 480

ttctccagga tatgtacaaa accaagaaaa agaagactcg agttattttg cgaatgttac 540
ccatctcagg cacatgcaag gctttttttag aagatatgaa aaaatatgca gaaacatttt 600
tggaaccctg gtttaaagct ccaaacaaag ggacatttca gattgtgtac aaaatctcga 660
nataacagtc atgtnaatag agaagaagtt atcaagagaa tttgcangga atagtgtgca 720
acctcaattc agnaaataaa gtgggtntca acaatccaca agtacacaat ngtaatanaa 780
atcatcaaan ctgtcngttc cctganngtt tgttaaagga ttacaaggtt ggtttannaa 840
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ctcaaag 907

<210> 256
<211> 794
<212> DNA
<213> Homo Sapiens

<400> 256
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ctcctagcaa tagaaaaagt tttctttgaa tttcatcatt tacaaatctt acaaatgcta 180
cagcatgaca aatattagtg aaacctgttg actcatcatc ctggatagag aagctgctac 240
ttttcagtta atgacacaaa acctttttttg catcatatga catatcatca gtaaatcaac 300
ttattgagaa taaagtctct tcaactttgt actgcatctt gccccagcat tttaatgtta 360
ttagattctc accaaccatg catattttcc tttcctgaga taagttctgc tactaaataa 420
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tgttacaatt gctaagtttt gtaagttgca tgtcacagac aatgcacaat gggacaagan 600
aaccttggac ctgagtccac ataaataccc cttgagaagt tancttttcc ttaattaaga 660
caagaatttc ctttggtgtc cccttggttg cactaagtat acttgaaagt ntnctccagn 720
angactggaa gttcttcaat caaccaanct ttttcaagaa aatgtccngt agtttcaang 780
gcctaaaaat gggt 794

<210> 257
<211> 885
<212> DNA
<213> Homo Sapiens

<400> 257
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cccctgccca gcagactact cagcctggcg gcgggaagcg caaaggcaag gctcagtatg 120
tgctggccaa gcgcgctcgg cgctgcgacg ctggcgggcc ccgtcagcta gagcccgggc 180
tacagggcat cctcatcacc tgcaatatga acgagcgcaa gtgcgtggag gaggcctaca 240
gcctcctcaa cgaatacggc gacgacatgt atgggccaga aaagtttaca gacaaggatc 300
agcagccctc tggaagtgag ggagaggatg atgatgcgga ggctgccttg aagaaagaag 360
ttggtgacat taaggcatct acagagatga ggttaagaag attccagtca gtggaaagtg 420
gagcaaataa cgttgtcttc atcaggacac ttgggataga gcctgagaaa ttggtgcatc 480
atattctcca ggatatgtac aaaaccaaga aaaagaagac tcgagttatt ttgcgaatgt 540
tacccatctc aggcacatgc aaggcttttt tagaagatat gaaaaaatat gcagaaacat 600
ttttggaacc ctgggtttaa agctccaaac aaagggacat ttcagattgt gtacaaatct 660
cgaaataaca gtcatgtgaa tngagaaaga agttatcaga gaaattggca aggaatagtt 720
gtgcaccctc aattcagaaa attaaaggtg ggntctcaac caatccacag ttcacagntg 780
gtagttagaa atcaatcaaa acctgtcngt ttgcccgaan ttgnttgtta aaagaattca 840
angttggttt tanaaanaat naaatcccca aagaaggtgg gtgaa 885

<210> 258
<211> 798
<212> DNA

<213> Homo Sapiens

<400> 258
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ccactgatgg ggcaccagga gtgtagatac cagacctctg gttatcagat atgatgtcac 240
aacattatat attggccttt gttctggcag gctcctagca atagaaaaag ttttctttga 300
atttcatcat ttacaaatct tacaaatgct acagcatgac aaatattagt gaaacctgtt 360
gactcatcat cctggataga gaagctgcta cttttcagtt aatgacacaa aacctttttt 420
gcatcatatg acatatcatc aagtaaatca acttattgag aataaagtct cttcaacttt 480
gtactgcatc ttgccccagc attttaatgt tattaagatt ctcaccaacc atgcatattt 540
tcctttcctg agataagttc tgctactaaa taatttgctt cttaaacctt ttgactaaag 600
gtgatttctg aacaaaagcc ttactgtttt tgataagtcc caaaaagcca tttgaaaaat 660
aatgaatatc ctttcntgtc aagtggctgt gaatttaatg ttacaattgc caagttttgt 720
aagttgcatn gtcacangac aatgcacaat ggggacaagg agaaccttgg gcctgagtcc 780
acaataanta ccccttga 798

<210> 259
<211> 831
<212> DNA
<213> Homo Sapiens

<400> 259
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gcgcacacca tggcggcccc tgcccagcag actactcagc ctggcggcgg gaagcgcaaa 120
ggcaaggctc agtatgtgct ggccaagcgc gctcggcgct gcgacgctgg cgggccccgt 180
cagctagagc ccgggctaca gggcatcctc atcacctgca atatgaacga gcgcaagtgc 240
gtggaggagg cctacagcct cctcaacgaa tacggcgacg acatgtatgg gccagaaaag 300
tttacagaca aggatcagca gccctctgga agtgagggag aggatgatga tgcggaggct 360
gccttgaaga aagaagttgg tgacattaag gcatctacag agatgaggtt aagaagattc 420
cagtcagtgg aaagtggagc aaataacgtt gtcttcatca ggacacttgg gatanagcct 480
gagaaattgg tgcatcatat tctccaggat atgtacaaaa ccaagaaaaa gaagactcga 540
gttattttgc gaatgttacc catctcaggc acatgcaang ctttttttaga agatatgaaa 600
aaatatgcan aaacattttt ggaancctgg tttaaagctc caaacaaagg gacatttcag 660
attgtgttca aatctcgaaa ataacagtca tgttgaatag aagaagaagt tatcagagaa 720
nttggcaagg aataatgntg caacctcaat tcagaaaata aaagtggatt tcaccaattc 780
cacagtncac aantggtagt agaaatcatc aaaagctntc tgtttgcccg a 831

<210> 260
<211> 772
<212> DNA
<213> Homo Sapiens

<400> 260
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gacctctggt tatcagatat gatgtcacaa cattatatat tggcctttgt tctggcaggc 120
tcctagcaat agaaaaagtt ttctttgaat ttcatcattt acaaatctta caaatgctac 180
agcatgacaa atattagtga aacctgttga ctcatcatcc tggatagaga agctgctact 240
tttcagttaa tgacacaaaa ccttttttgc atcatatgac atatcatcag taaatcaact 300
tattgagaat aaagtctctt caactttgta ctgcatcttg ccccagcatt ttaatgttat 360
tagattctca ccaaccatgc atattttcct ttcctgagat aagttctgct actaaataat 420
ttgcttctta aaccttttga ctaaaggtga tttctgaaca aaagccttac tgtttttgat 480
agtccaaaag ccatttgaaa ataatgaata tcctttcttg tcaagtggcn gtgatttatt 540
gttacaattg ctagttttgt nagttgcatg tcacagacaa tgcacaatgg gacangagag 600

cctgggactg agtccacata ataccentga gaagtannct ttctttatta agacagaant 660
tctttgtgtc ccttgttgca caagtntact gaagtntcnc aagaaggact ggangtcntc 720
ataancaacc ttttagaaat gtccgtattc ctaaggccca aaaangggtc cc 772

<210> 261
<211> 753
<212> DNA
<213> Homo Sapiens

<400> 261
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atggcggccc ctgcccagca gactactcag cctggcggcg ggaagcgcaa aggcaaggct 120
cagtatgtgc tggccaagcg cgctcggcgc tgcgacgctg gcgggccccg tcagctagag 180
cccgggctac agggcatcct catcacctgc aatatgaacg agcgcaagtg cgtggaggag 240
gcctacagcc tcctcaacga atacggcgac gacatgtatg ggccagaaaa gtttacagac 300
aaggatcagc agccctctgg aagtgaggga gaggatgatg atgcggaggc tgccttgaag 360
aaagaagttg gtgacattaa ggcatctaca gagatgaggt taagaagatt ccagtcagtg 420
gaaagtggag caaataacgt tgtcttcatc aggacacttg ggatagagcc tgagaaattg 480
gtgcatcata ttctccagga tatgtacaaa accaagaaaa agaagactcg agttattttg 540
cgaatgttac ccatctcagg cacatgcaag gctttttttag aaagatatga anaaatatgc 600
anaaaacatt tttggaaccc tgggtttaaa gctccaaaca aagggacatt tcagaattgt 660
ggtacaaatc tcgaaatanc agtcatgtta antagagaan naagtttttc agaagaattt 720
ggcaaggaat nagtnntgca accctcaatt tca 753

<210> 262
<211> 659
<212> DNA
<213> Homo Sapiens

<400> 262
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gacctctggt tatcagatat gatgtcacaa cattatatat tggcctttgt tctggcaggc 120
tcctagcaat agaaaaagtt ttctttgaat ttcatcattt acaaatctta caaatgctac 180
agcatgacaa atattagtga aacctgttga ctcatcatcc tggatagaga agctgctact 240
tttcagttaa tgacacaaaa cctttttgc atcatatgac atatcatcag taaatcaact 300
tattgagaat aaagtctctt caactttgta ctgcatcttg ccccagcatt ttaatgttat 360
tagattctca ccangccatg catattttcc tttcctgaga taagttctgc tactaaagaa 420
tttgcttctt aaacctttg actaaaggtg atttctgaac aaaagcctta ctgtttttga 480
nnagtccana agccatttga aaaataatga atatcctttc cttgtcaagt ggcngtgatt 540
tantgttaca atttgcnagg ttttgtaagt tgcatggtca cagnanaatg cacantnggg 600
acanngagan cntgggncng aagtccacat tatanccctt tgagnaangt agctttccc 659

<210> 263
<211> 673
<212> DNA
<213> Homo Sapiens

<400> 263
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tttaaggggt ctgtcatgga aggtgctctt ccaggaacct ctgtgatgga ggtcacagcc 120
acagacgcgg acgatgatgt gaacacctac aatgccgcca tcgcttacac catcctcagc 180
caagatcctg agctccctga caaaaatatg ttcaccatta acaggaacac aggagtcatc 240
agtgtggtca ccactgggct ggaccgagag agtttcccta cgtataccct ggtggttcaa 300
gctgctgacc ttcaaggtga ggggttaagc acaacagcaa cagctgtgat cacagtcact 360
gacaccaacg ataatcctcc gatcttcaat cccaccacgt acaaggtca ggtgcctgaa 420

aacgaggcta acgtcgtaat caccacactg aaagtgactg atgctgatgc ccccaatacc 480
ccagcgttgg gaggctgtat acaccatatt gaatgatgat ggtgggacaa tttgtcgtca 540
ccacaaatcc agtgaacaac gatggcattt tgaaaaacag caaagttgaa gtcaagtgat 600
tttgctggtt cngaatcaat tgttgcctcn gttgggagaa aggtntccaa cacatacccc 660
gggattngtt att 673

<210> 264
<211> 661
<212> DNA
<213> Homo Sapiens

<400> 264
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acctccaact gcatctccta ctctgaaatn cctcttgagc agccaagggt ggccagttct 120
gctcctcatt ttcctgaaga anaatctcag cctgaaagaa tatagagcta ggtgacatat 180
gggtggccaa ccgcttctcc tcaagttcca anagagtggg caattagtga aattccatca 240
gtcatgttaa aatatacttt caccaggtan acatccttct ttcaatgcta gaggacagtg 300
aaaaatgtag attaatgaga tctgtaactg tcttctctta actgtacacc cctcaggctg 360
aacgcgggag tgctgaacac atgccctcgg aagggaccct gaagacccaa gtgacctgca 420
ccataaaacc accccgaggg tcagccatgc tgccagcact caagaagcag cagggccacc 480
tgctggaaaa ctgggcacgg ctctgggtgc ctggccctgc ctgcctcctc cacgtccttg 540
gagccaggtc tacggcaggg aacatgatct tcttctccag cttctgtgga aggaacanga 600
aatttttcat gatgtcntcc agctcttcta nggccaactg ggcatgganc ttggccacgt 660
c 661

<210> 265
<211> 659
<212> DNA
<213> Homo Sapiens

<400> 265
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acctccaact gcatctccta ctctgaaatg cctcttgagc agccaagggt ggccagttct 120
gctcctcatt ttcctgaana anaatctcag cctgaaagaa tatanagcta ggtgacatat 180
gggtggccaa ccgcttctcc tcaagttcca ananagtggg caattagtga aattccatca 240
gtcatgttaa aatatacttt caccaggtan acatccttct ttcaatgcta gaggacagtg 300
aaaaatgtag attaatgaga tctgtaactg tcttctctta actgtacacc cctcaggctg 360
aacgcgggag tgctgaacac atgccctcgg aagggaccct gaagacccaa gtgacctgca 420
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tgctggaana actgggcacg gctctgggtg cctggccctg cctgcctcct ccacgtcctt 540
gganccaggt ctacggnagg accatgatct tcttctccan cttctgtgga aggaacanga 600
antttttcat gatgtcntcc actcttctag ggccaactgg gcatggactt ggccacgtc 659

<210> 266
<211> 620
<212> DNA
<213> Homo Sapiens

<400> 266
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acctccaact gcatctccta ttntnaaatg cctcttgagc agccaagggt ggccagttct 120
gctcctcatt ttcctgaana anaatctcag cctgaaagaa tatagagcta ggtgacatat 180
gggtggccaa ccgcttctcc tcaagttcca ananagtggg caattagtga aattccatca 240
gtcatgttaa aatatacttt caccaggtan acatccttct ttcaatgcta gaggacagtg 300
aaaaatgtag attaatgaga tctgtaactg tcttctctta actgtacacc cctcaggctg 360

aacgcgggag tgctgaacac atgccctcgg aagggaccct gaagacccaa gtgacctgca 420
ccataaaacc accccgaggg tcagccatgc tgccagcact caagaagcag cagggccacc 480
tgctggaaga cctgggcacg gctctgggtg cctggccctg cctgcctcct ccacgtcctt 540
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ntttttcatg atgtcatcca 620

<210> 267
<211> 745
<212> DNA
<213> Homo Sapiens

<400> 267
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tgtcagctta tgaccctcaa attccaacac gggctgctgc cctgcgtact ctttcccact 180
ggatagagca gagagaagca aaagcccttg agatgcaaga gaagcttctc aagatattct 240
tggaaaactt ggaacatgaa gacacttttg tatatctatc tgcaattcag gggggttgccc 300
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attgctgtgg ccaaaaacat tntntgaaag ttcaagttcg cannagctgg ccaanacaat 660
gtggggttgt gcctgcnngc tttcgggggga actcaaccca agaaaaagct tantgtaagg 720
gtggnttaan ccnccggtcc ttcaa 745

<210> 268
<211> 676
<212> DNA
<213> Homo Sapiens

<400> 268
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acctccaact gcatctccta ctctgaaatg cctcttgagc agccaagggt ggccagttct 120
gctcctcatt ttcctgaana anaatctcag cctgaaagaa tatagagcta ggtgacatat 180
gggtggccaa ccgcttctcc tcaagttcca ananagtggg caattagtga aattccatca 240
gtcatgttaa aatatacttt caccaggtag acatccttct ttcaatgcta gaggacagtg 300
aaaaatgtag attaatgaga tctgtaactg tcttctctta actgtacacc cctcaggctg 360
aacgcgggag tgctgaacac atgccctcgg aagggaccct gaagacccaa gtgacctgca 420
ccataaaacc accccgaggg tcagccatgc tgccagcact caagaagcag cagggccacc 480
tgctggaana cctgggcacg gctctgggtg cctggccctg cctgcctcct ccacgtcctt 540
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gaagtttttc atgatgtcat ccanctcttc taaggccaac tgggcatgga acttggccac 660
gtcatcgggc tccaaa 676

<210> 269
<211> 737
<212> DNA
<213> Homo Sapiens

<400> 269
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gtgtcatcca acgggaatgc agttgaggat ccaatggaga ttttgatcac ggtaaccgat 180
cagaatgaca acaagcccga attcacccag gaggtcttta aggggtctgt catggaaggt 240

gctcttccag gaacctctgt gatggaggtc acagccacag acgcggacga tgatgtgaac 300
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cgagagagtt tccctacgta taccctggtg gttcaagctg ctgaccttca aggtgagggg 480
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caacactgaa aagtgactga tgcctgatgc cccccaatta ncccanccgt gggaagctgt 660
ntacaccata tngaaatgat gatgggtggg cnaatttgtn cgttcaccaa caaatnccan 720
gtggaacaac caatggg 737

<210> 270
<211> 726
<212> DNA
<213> Homo Sapiens

<400> 270
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acctccaact gcatctccta ctctgaaatg cctcttgagc agccaagggt ggccagttct 120
gctcctcatt ttcctgaana anaatctcag cctgaaagaa tatanagcta ggtgacatat 180
gggtggccaa ccgcttctcc tcaagttcca ananagtggg caattagtga aattccatca 240
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aaaaatgtag attaatgaga tctgtaactg tcttctctta actgtacacc cctcaggctg 360
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<210> 271
<211> 814
<212> DNA
<213> Homo Sapiens

<400> 271
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gctcctcatt ttcctgaaga agaatctcag cctgaaagaa tatagagcta ggtgacatat 180
gggtggccaa ccgcttctcc tcaagttcca agagagtggg caattagtga aattccatca 240
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aaaaatgtag attaatgaga tctgtaactg tcttctctta actgtacacc cctcaggctg 360
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gaagtttttc aatgatgtca tccagctctt cctanggcca actgggcaag ggagcttggg 660
caacgtcatc ggggctccag acaaaactac gtgcttcanc aanggtggta aaanatcctt 720
gaaggacggg ggctcaacaa cccaagtanc ctttccnggg ctgaatcccc ngaagcaagc 780
aagnacaaac cacatgtttt gggaagctcc ggcg 814

<210> 272
<211> 862
<212> DNA
<213> Homo Sapiens

<400> 272
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aaagacccac tgatgtagct catagccacc ttgaacaaca gcagagccat gagacagccc 120
cccagacagg cctgcagtca aatgctccaa tcattcctca aggagtcaat gagcccagca 180
ctactacaag tcagaaatct ggaagcgtaa ccacagaaca gctccaagag gttcttttgt 240
cagcttatga ccctcaaatt ccaacacggg ctgctgccct gcgtactctt tcccactgga 300
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gccctgaatt gctgtgggcc aaaaacaaga tnggtgaaag tttaaagtta cgcaaaactg 780
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<210> 273
<211> 677
<212> DNA
<213> Homo Sapiens

<400> 273
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antggaacct tgggcaa 677

<210> 274
<211> 863
<212> DNA
<213> Homo Sapiens

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<211> 821
<212> DNA
<213> Homo Sapiens

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<211> 722
<212> DNA
<213> Homo Sapiens

<400> 276
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tgatgctgat gcccccaata ccccagcgtg ggaggctgta tacaccatat tgaatgatga 180
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gtcagaaatc tggaagcgtt accacagaac agctccaaga ggttcntttg tcagctttat 660
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<210> 277
<211> 805
<212> DNA
<213> Homo Sapiens

<400> 277
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<210> 278
<211> 1358
<212> DNA
<213> Homo Sapiens

<400> 278
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<210> 279
<211> 702
<212> DNA
<213> Homo Sapiens

<400> 279
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gtngaggttt tttccangna accgggggaa gaccttaaaa gg 702

<210> 280
<211> 874
<212> DNA
<213> Homo Sapiens

<400> 280
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<210> 281
<211> 730
<212> DNA
<213> Homo Sapiens

<400> 281
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ttaaaggttg 730

<210> 282
<211> 699
<212> DNA
<213> Homo Sapiens

<400> 282
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<210> 283
<211> 759
<212> DNA
<213> Homo Sapiens

<400> 283
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<210> 284
<211> 764
<212> DNA
<213> Homo Sapiens

<400> 284
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<210> 285
<211> 586
<212> DNA
<213> Homo Sapiens

<400> 285
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<210> 286
<211> 666
<212> DNA
<213> Homo Sapiens

<400> 286
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atttct 666

<210> 287
<211> 782
<212> DNA
<213> Homo Sapiens

<400> 287
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aa 782

<210> 288
<211> 707
<212> DNA

<213> Homo Sapiens

<400> 288

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<210> 289
<211> 673
<212> DNA
<213> Homo Sapiens

<400> 289

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aaaaaaacnc gagagtactt ctaaagcggc cgcgggccna tcgattttcc acccgggtgg    540
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gtcgttttta aaacgtcntg acgggggaaa accctggngt taccaactta atccccccttg   660
caacaaatnc ccc                                                       673
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<210> 290
<211> 573
<212> DNA
<213> Homo Sapiens

<400> 290

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ccatcaatat ctgcttcnct gatcatttca tctacttctt catctgttag tttttcnccn    180
aagtttgtca tgacgtgacg tagttctgct gcactgatat aaccattgcc atccttgtca    240
aagactcgga atgcctcacg gatttcttct tcactatctg tatctttcan ttttcnagcc    300
atcatagtca aaaattcggg gaantcaatg gngccattac catcagcatc cacttcattg    360
atcatatcct gnaattcaan cttctgttgg gttntgaccc antgaccnca nggacaagtt    420
ccaagttccc tttggttgtg aagggtgcca nctcgtgccc gaattccttt gggntccnac    480
ganggtcna accctgcana ggngccgcga ancctccaan cttttggttc ccctttanat    540
ngagggttaa atttcgaact ttggnttttt tcc                                 573
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<210> 291
<211> 819
<212> DNA

<213> Homo Sapiens

<400> 291
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cacgtgtcga ggcagcaagt ctaggcggca gtggcaaagc ctactctgtt gttgcccaag 180
tcgtagacgg aatagtagga cctgaggaag acatccccga ggatccacag gggctggccg 240
ttctgggagg acaggtaggt gggctcgact cccacggtgc agtagccgtt gttactgagg 300
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gtggcctgca gaagagcact catgtactgc tggggcacag tgagcagaga ggtgcctgtg 480
tccacgatgg cctggcaacc ctcagaacac cagccggagg cctggccgcc gatgaggaac 540
tcttcaatgc caatctgcca gtagagttcc tgggtgacan gcgcccagta gatctgcccc 600
gtgtacangc tgctatccac acccccaaag gacaaccgct cccccgctgg gagccctgct 660
ggttgctgan gtaaaccctg aanacggggc tggttnaggg cgccctcctg cacatgccct 720
gcatactgtg gtggcctcat ccacggncna aaccanggta aggcaaggcc catgatgcca 780
tcaaactgcc ataacaaatt tgtacaaggc tcaatccca 819

<210> 292
<211> 664
<212> DNA
<213> Homo Sapiens

<400> 292
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tccaagatct gtgccaatgt gttttgtgga gccggccggg aatgtgcagt cacagagaaa 120
ggggaaccca cctgtctctg cattgagcaa tgcaaacctc acaagaggcc tgtgtgtggc 180
agtaatggca agacctacct caaccactgt gaactgcatc gagatgcctg cctcactgga 240
tccaaaatcc aggttgatta cgatggacac tgcaaagaga agaaatccgt aagtccatct 300
gccagcccag ttgtttgcta tcagtccaac cgtgatgagc tccgacgtcg catcatccaa 360
tggctggaan ctgagatcat tccagatggc tggttctcta aaggcagcaa ctacagtgaa 420
atcctagaca agtattttaa agaactttga taatggtgat tctcgcctgg actccaagtg 480
aattcctgaa gtttgtggga acangaatga aactgccatc aatattacaa cgtttccagn 540
accaagggag aacaacaagt ttgcctaang ggactccggt ngttgatgcc tctcaatttg 600
aactggtctg gatgaaaaat gcctgattgg gnaattnaag cttcccaant agtttcncca 660
aatg 664

<210> 293
<211> 719
<212> DNA
<213> Homo Sapiens

<400> 293
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caagttaaat gcaatatana agcctactaa atacaaatac aagttcacaa acacatatgc 120
aacagaaact tgtttanatt gtttcttgaa gtttgactac ttaaaaacat aggtgtaaag 180
gaaagacatt cagactggtc cacgtgggct tgttagcagg canaggaacc ctgctttcca 240
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gcagaactca agaagaatgt ggatttgctc ttgggantte aatgttgcag ggtanantaa 600
tcttgggatg ataaccatgt tctaaatgac tagtgaanaa acctgtggtt tcttgctttt 660
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<210> 294
<211> 762
<212> DNA
<213> Homo Sapiens

<400> 294
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ggcctgtgtg tggcagtaat ggcaagacct acctcaacca ctgtgaactg catcgagatg 180
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ccgtaagtcc atctgccagc ccagttgttt gctatcagtc caaccgtgat gagctccgac 300
gtcgcatcat ccagtggctg gaagctgaga tcattccaga tggctggttc tctaaaggca 360
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gaactgtctg gatgaaaatg ctgattggna actcagcttc caagagtttc tcaaagtgcc 600
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<210> 295
<211> 708
<212> DNA
<213> Homo Sapiens

<400> 295
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aacagaaact tgtttanatt gtttcttgaa gtttgactac ttaaaaacat aggtgtaaag 180
gaaagacatt cagactggtc cacgtgggct tgttagcagg cagaggaacc ctgctttcca 240
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ctaagcccta tgcttttaga gggctgaagg aaccaaacct agtttaatcc tgtttgtttg 420
ctccatgcaa aactttatgg aagactcccc agactaggct atttagcagc ttccatgaat 480
ggtcctcaga tcatgtgatt ctacggcata gacgacagct gccctattta cacagaagct 540
gcagaactca agaggaatgt ggatttgctc ttgggagttc aatgttgcag ggtaaaagta 600
gtcctggatg ataaccatgt tccaaatgac taagtgaaga gacactgtgg gttcctgcct 660
tttaacaaaa tggggtact cctgcccctc ctccccanaa atgtccaa 708

<210> 296
<211> 652
<212> DNA
<213> Homo Sapiens

<400> 296
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caagttaaat gcaatataga agcctactaa atacaaatac aagttcacaa acacatatgc 120
aacagaaact tgtttanatt gtttcttgaa gtttgactac ttaaaaacat aggtgtaaag 180
gaaagacatt cagactggtc cacgtgggct tgttagcagg cagaggaacc ctgctttcca 240
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ctccatgcaa aactttatgg aagactcccc aagactaggc tatttagcag cttccatgaa 480
tggtcctcag atcaagtgat tctacggnat anacgacaag ctgccctatt tacacagaag 540
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aaaagttant cttgggntga ataaccaggt ttctaaaatg accaaattga aa 652

<210> 297
<211> 879
<212> DNA
<213> Homo Sapiens

<400> 297
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aacagaaact tgtttagatt gtttcttgaa gtttgactac ttaaaaacat aggtgtaaag 180
gaaagacatt cagactggtc cacgtgggct tgttagcagg cagaggaacc ctgctttcca 240
aaaactgata tagtccagag tcacggcatg tgggaatgtt tccatggaca ctggatctta 300
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gcagaactca agaggaatgt ggatttgctc ttgggagttc aatgttgcag ggtagaagta 600
gtcctggatg ataaccatgt tccnaaatga ctagtgaaga gacactgtgg tttcctgcct 660
ttaacaaant ggtgtactcc ttgccctcct ccaatantgt ccaaagggct ggtaaaaacc 720
ctttgattaa aggcgtgctg cctgttgagt tccccaangg nacttgggac angggancccg 780
catttcaaga ccggaacaaa ttgggagttt tgaaaaaagt ttttaaatng ggaatgggtt 840
acataaaaan gcttgaaatg gctaaaacaa aggngggaa 879

<210> 298
<211> 697
<212> DNA
<213> Homo Sapiens

<400> 298
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gtgaaaacaa ctatggaaag tatatctaat acgtctacgc agtctctcac agcagaaaca 120
aaggacatag ctttggaacc taaggaacaa aaacatgaag acaggcagag caatacacct 180
tctcctcctg ttagtacctt ttcatcaggt acttctacca ccagtgatat tgaagtttta 240
gatcatgaaa gtgtaataag tgagagctca gcgagctcga gacaagagac tacagattca 300
aaatcaagtc ttcacttgat gcagacatct tttcagcttc tctctgcatc tgcttgtcct 360
gaatataatc gtttagatga tttccaaaaa ctcactgaga gttgctgttc atctgatgct 420
tttgaaagaa tagactcatt tagtgtacag tcattagata gccggagtgt aagtgaaatc 480
aattcaagat gatgaattgt caggcaaggg gatatgcttt agtgcctatt ataagttaat 540
tcttcaactc caaaagtcta aaacagttga atctgccgaa ggaaaatctg aagaagtaaa 600
tgaaacatta agttatacca ctgaggaagc agaaatggga agaaaagtgg gcgaaagtgg 660
caactccccg gttaacngng aaaangcctg gatatcc 697

<210> 299
<211> 510
<212> DNA
<213> Homo Sapiens

<400> 299
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aatacttcnt ccaaatcntt taaatgttnt naangccntt gcnaaatcct tataaataaa 120
ttttcncccct tatccaancn catcnanaaa acattgaata tgttcaggtt tcncnggann 180
ggtnccnaaa ggnncncnt tttatacnga cttaattgtn aaagcngggt gaaataaatt 240
ttccnatcna aattttttt aagtttaaat cnttccccncn ttaaatttcn nanagtgtcc 300
gtgtnactcc tacttttaaa ggaaaaaaat tantttaaaa tttaatancc cccgatttaa 360

taattttta ctttaacncn taatgttcnt tttcctgaac nntaattaan aaatgttgaa 420
attttaaatg tnaaanantc caantttccg tntgttaaca ttacncctcc aatgttcnta 480
atatatntnt taacccntnc caattatnga 510

<210> 300
<211> 625
<212> DNA
<213> Homo Sapiens

<400> 300
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tgctttagtg cctattatag ttaattcttc aactccaaag tctaaaacag ttgaatctgc 120
tgaaggaaaa tctgaagaag taaatgaaac attagttata cccactgagg aagcagaaat 180
ggaagaaagt ggacgaagtg caactcctgt taactgtgaa cagcctgata tcttggtttc 240
ttctacacca ataaatgaag gacagactgt gttagacaag gtggctganc agtgtgaacc 300
tgctgaaagt cagccanaan cactttctga caaggaanat gtttgcaata cagttgaatt 360
tctgaatgaa aaagcnggaa aaaagggang ctcagttatt atctcttagt aaggaaaaag 420
cacttctagg aagaagcttt ttgatacctg aananatgaa atgttcacag tngaaaggaa 480
naanngcagt ancatttccn tccttgaaan gattnngttt actcaaagga attngnnnaa 540
nccngtanta gaaaagtttc aaacctaagn ccggnaaaag aggaagagat gcctggccta 600
aaaaaaggga aatccacnga ccatt 625

<210> 301
<211> 792
<212> DNA
<213> Homo Sapiens

<400> 301
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tttnctccat tatccaatca catctaaata acattgaata tntacaggtt nctctggata 180
ggtaccaaaa ggtaccacnt tttatacaaa cttaattgtg aaanctgggt gaaataaatt 240
tncaaatcaa aatttttttt aantttaaat catncactct ttaaatttca aacagtgtca 300
gtgtgacnct tacttttaaa ggaaaaaaat tagtttaaaa tttaatancc acanatttaa 360
taattttta ctttaacact taatgtacat tttcatganc agtaattaaa atatnttgaa 420
attttaaatn tgaaaaattt caaagtttca gtatnttaac attacncttc aaatgttctt 480
aatatatata taaacactta caaattataa atacaactag ttgtntntct acaatacata 540
tntgaacacc attcttcttc tctagccatn tttatntgan gataaagtaa taaatctctg 600
tgctattcaa gggaaaaaaa atgaatgctt taaaaaataa atctttaaaa aataattcca 660
aaaataaagt tcaaatattg cacaaaaata atttaactgt aaatattact ncntagtgta 720
aacaatttta aaaaaatttt acactctaca ntaaatccnc ttctnattct ttaaaaaaat 780
tatgggaaat cc 792

<210> 302
<211> 738
<212> DNA
<213> Homo Sapiens

<400> 302
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ttttctccat tatccaatca catctagata acattgaata tgtacaggtt tcnctggata 180
ggtaccaaaa ggtaccacat tttatacaga cttaattgtg aaagctgggt gaaataaatt 240
ttcagatcaa aatttttttt aagtttaaat cattcactct ttaaatttca gacagtgtca 300
gtgtgactct tacttttaaa ggaaaaaaat tagtttaaaa tttaatagcc acagatttaa 360

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ctggtgctat tcaaggnaaa aaaatggaat gccttaaaaa aataaaatcc ttaaagaata 660
ggttcaaaaa ataaagttca aaatantngc ccaaaaataa attaacnngg taatattaac 720
tacataaggg taaaacaa 738

<210> 303
<211> 635
<212> DNA
<213> Homo Sapiens

<400> 303
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gacagaacca gccgagtgga aaaggggagc gaagccgttc ctctgcaccc ttccccaggc 120
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caactgatgt ccagaccatt cagaagagtc cagtggtatc aaaacctcca ncataatcac 540
aacnaccang nagaangaan tgaaaancan cttacatgaa tccttgcaca ttggncaant 600
caagaaactt cctgaaacaa ctgaaatcac aaagt 635

<210> 304
<211> 847
<212> DNA
<213> Homo Sapiens

<400> 304
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taacctccac ctcccaggtt caagcaatgc tcctgcctca gcctcccgag tagctaggat 120
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<210> 305
<211> 767
<212> DNA
<213> Homo Sapiens

<400> 305
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aactgaaagg naaacaacga agaaaactgt ttaatnaaag aatccgg 767

<210> 306
<211> 1659
<212> DNA
<213> Homo Sapiens

<400> 306
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<212> DNA
<213> Homo Sapiens

<400> 307
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<210> 308
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<212> DNA
<213> Homo Sapiens

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<210> 309
<211> 1320
<212> DNA
<213> Homo Sapiens

<400> 309
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840

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<210> 310
<211> 1030
<212> DNA
<213> Homo Sapiens

<400> 310
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ccaaaatgac aggttcagca ccacccctt ctccaacacc taacaaagag atgaagaaca 180
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ggggttaacc 1030

<210> 311
<211> 546
<212> DNA
<213> Homo Sapiens

<400> 311
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gctaaaataa aaagcacaga aggaaaaaat aattgatttg tacataagct aaattataat 180
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gtttatatga atatgttgtt aacagtgaga tttctgatat ggtataacaa agtatatgat 300
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ccggcc 546

<210> 312
<211> 518
<212> DNA
<213> Homo Sapiens

<400> 312
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gggaggaatg gggtggggct naccccctgna acccatnata aacctattct nctnagggtg 120
ctgggaaana attggggtct ggaataaanc tncaaatggg tcnccngctt cactaaaacc 180
ttggcaacta aggctcattt ttccaaaggg gttnctnang tcnnctccct ntnaaatcnt 240
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nctctgcccc ctttactnnt gccaannctt tcccccccgg ttaggataaa aattccccctn 480
aacctccnac ctttggttan cgggggtccc ctnccccc 518

<210> 313
<211> 660
<212> DNA
<213> Homo Sapiens

<400> 313
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gtacaacctt ctcagctaca aatacttgaa gaaacaagac aangggactc aagccantgg 600
gagtcatggg ccctggcctc angggctgcc aacaacgggc cccgtgttct ggccccgttt 660

<210> 314
<211> 516
<212> DNA
<213> Homo Sapiens

<400> 314
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aggctgctta gcccacccag cctatcacac tgcccgctcc acgttgggca gccacataaa 180
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gtgcattttt ttaatattgt acaaaatatg ttaactagga aaaattagct gtactgtgac 300
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acctctaaaa ggtggagctg tncaaaccaa aaaaaatcta aacgatttta agaanagcag 420
caactcaata ctgctttagt tcatttaaat tttctttccc aaaaatacac tcctaaatat 480
acaaactata caatcttatt attttaatgc tggttt 516

<210> 315
<211> 677
<212> DNA
<213> Homo Sapiens

<400> 315
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aaatttgttc tcaaaacaaa tatactcatt tcaaagaact tccaactctt ctccactgtg 180
cagcaaaatt tggcttaaag aacctggcta ttcatttgct tcaatgttca ggagcaacct 240

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gtcacaaaga actcaagaaa atcttcgaag acttttcaat ccaagaaatt gacataaata 360
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<210> 316
<211> 843
<212> DNA
<213> Homo Sapiens

<400> 316
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taataacctc cttaatgatc ttcctgcaca naaaccaaat tcttttcaac ttggggtcaa 780
caagaaccta ttgctgaatt ttcatataaa actatttcct gttggcagtt tcctaccccc 840
gga 843

<210> 317
<211> 835
<212> DNA
<213> Homo Sapiens

<400> 317
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aatgtcaaaa gccgttttca agttccaaat ccagnttcat naagnttgcc ttaaa 835

<210> 318
<211> 582
<212> DNA

<213> Homo Sapiens

<400> 318
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canagctcac caagttcncn ccgtatcaaa tttccanaat acccacaaga tttcttcacc 180
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aaatagactg aatcanccta nacataattt cattagggnt gcaaaccacc cangggaaag 420
tagcacaatt ataccanttt gtaatccaca ttcacaagaa gtttgcnaca caaatgaaga 480
aaactttgng cccatagaca acttattttt taaaatatca ctccccaaaa gtagccatgt 540
ttccactttt ggtccccttt ccanatcaaa aataccaact tg 582

<210> 319
<211> 827
<212> DNA
<213> Homo Sapiens

<400> 319
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ataataactc attacaaggc ccagaagacg atgattcaga aggatttgga caaagagttc 240
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caatcctggt tgccggcttc tccaatacca aaacaaccct ccggactccc aagggaaaat 720
tacncctaac ggtttacctt caaagggacc ctgaaaagac ccncctggtt caatgaccaa 780
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<210> 320
<211> 598
<212> DNA
<213> Homo Sapiens

<400> 320
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<210> 321
<211> 808
<212> DNA

<213> Homo Sapiens

<400> 321

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<210> 322
<211> 629
<212> DNA
<213> Homo Sapiens

<400> 322

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tacattgcct ttttgcctgt agagaaccca tgaggagagg ggttctcagc cttcccagtg    180
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<210> 323
<211> 798
<212> DNA
<213> Homo Sapiens

<400> 323

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tagattttcc cagagctgct gaaggagcct tgatatggga aaatgaattt ttattaccaa    720
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ggagccaagg agaaaagg 798

<210> 324
<211> 754
<212> DNA
<213> Homo Sapiens

<400> 324
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tctctctaca taaccttgta aggcttcagt aactaaaatg taaaaccaaa caaaacaaaa 180
ccccaaaaca aaacaaaaac cccagcctat tagtttacag tttattttaa aaattccgaa 240
agacactgca agttctaaac ttttagtagt gctacccata cacaaccatc tggttaagaa 300
cccagtaaaa gagccccctt ccaaggaagc tttgcaacag tagagttgtg caatatggat 360
gtttcttact acaagaaaaa aattatacat ggcacattct cattcatatt ctgtaatgta 420
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atggtaatac ccagcgtggg tacactgcta caaaactcaa aacagaagga gtaaacttga 600
aatgttttcc ataataaaga tctagcanca tgactatcct aatgccgttt tatcccgaat 660
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caaaaaatat ccttttacaa gaaagaaacc cgtt 754

<210> 325
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<212> DNA
<213> Homo Sapiens

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tgagaagaag gcagctgttg aagattcagg gaccacagtg gaaacaatta agctaggagg 180
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acanggaatt gacaagatct tcctcaggaa aaagcatcgc aaccatggtc tcaaggngtt 780
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tggaagtcca anga 854

<210> 326
<211> 760
<212> DNA
<213> Homo Sapiens

<400> 326
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catagctcac caagttctct ccgtatcaaa tttccagaat acccacaaga tttcttcacc 180
agctcagtcc tgactcaacc tcttcaatct ttatttcatt agaagacaaa gggtcatatt 240
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ttaaataact ttaacaagaa agccagctga tcttaacaag ttactctgct agtaaatggg 360
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<210> 327
<211> 852
<212> DNA
<213> Homo Sapiens

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ccctgtgcct gtgtatatcc cagttcctat gcacatgtac agtcagaata ttcctgttcc 180
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tacagagttg cttacaatga cggatatgat gagtgaagac gaggggaaaa cagagacaac 360
caacatcaac agtgtaatta ttgaaacaga tataattggt tcagaccttt tgaagaactc 420
tgacccagag acacagtcca gcatgcctga tgtaccatat gaaccaagat ttggatatcg 480
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atgcagcntt cctttcaaat tatacgtatg ggcgtaaatg catgggnaac accgggtcaa 720
aaactaagnn acttggatga aagatcntcc gggnaattag aatgagttaa aatccttcca 780
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aggggttaa cc 852

<210> 328
<211> 799
<212> DNA
<213> Homo Sapiens

<400> 328
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tctctctaca taaccttgta aggcttcagt aactaaaatg taaaaccaaa caaaacaaaa 180
ccccaaaaca aaacaaaaac cccagcctat tagtttacag tttattttaa aaattccgaa 240
agacactgca agttctaaac ttttagtagt gctacccata cacaaccatc tggttaagaa 300
cccagtaaaa gagccccctt ccaaggaagc tttgcaacag tagagttgtg caatatggat 360
gtttcttact acaagaaaaa aattatacat ggcacattct cattcatatt ctgtaatgta 420
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gttaagtatc ctaaaaccac tacatagaat aatggcaact ttcactcaca gattatttac 540
atggtaatac ccagcgtggg tacactgcta caaaactcaa aacagaanga gtaaacttga 600
aatgttttcc ataataaaga tctagcaaca tgactatcca atgctgtttt atcccgattg 660
cttctgcaac gttcctttta atccgtgtct catccagttc anaantgtcc ttatcaanaa 720
taacctttac tagaagaaac cgtncaagca tattttcaan gggtttccgg tccaattgaa 780
gttanacgtn taccaaaca 799

<210> 329
<211> 978
<212> DNA

<213> Homo Sapiens

<400> 329
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cagaacataa attattagga aacattaaaa atgtggccaa gacagctaac aaggaccact 180
tggttacagc ctataaccat ctttttgaaa actaagcgtt ttaagggtac tgaaagtata 240
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cactacaaga tgggactgtt tttgatacta atattcaaac aagtgcaaag aagaagaaaa 480
atgccaagcc tttaagtttt aaggtcggag taggcaaagt tatcagagga tgggatgaag 540
ctctcttgac tatgagtaaa ggagaaaagg ctcgactgga gattgaacca gaatgggctt 600
acggaaagaa aggacagcct gatgccaaaa ttccnccaaa tgcaaaactc acttttgaag 660
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<210> 330
<211> 1017
<212> DNA
<213> Homo Sapiens

<400> 330
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caggagacct ggaccagacc acgatgtgga aacgctggct cgcgctcgcg ctcgcgctgg 120
tggcggtcgc ctgggtccgc gccgaggaag agctaaggag caaatccaag atctgtgcca 180
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attacgatgg acactgcaaa gagaagaaat ccgtaagtcc atctgccagc ccagttgttt 420
gctatcagtc caaccgtgat gagctccgac gtcgcatcat ccagtggctg gaagctgaga 480
tcattccaga tggctggttc tctaaaggca gcaactacag tgaaatccta gacaagtatt 540
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ttaggggact ctgtgttgat gctctcattg aactgtctga tgaaaatgct gattggaaac 720
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aggggcccca gacccagacn gaggangaga tgancngata tgtccaggag ctccaaagct 960
taggaaacag cttgaaaaga nccagagagg gagcccccaa agagattatg aggaggc 1017

<210> 331
<211> 799
<212> DNA
<213> Homo Sapiens

<400> 331
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gcctggaagc caagccaaaa acgagacagc caagccgatg atcccgaaaa cattaaaacc 120
caggagcttt ttagaaaagt tcgaagtatc ttaaataaat tgacaccaca gatgttcaat 180
caactgatga agcaagtgtc aggacttact gttgacacag aggagcggct gaaaggagtt 240

attgacctgg tctttgagaa ggctattgat gaacccagtt tctctgtggc ttacgcaaac 300
atgtgtcgat gtctagtaac gctgaaagta cccatggcag acaagcctgg taacacagtg 360
aatttccgga agctgctact gaaccgttgc cagaaggagt ttgaaaaaga taaagcagat 420
gatgatgtct ttgagaagaa gcagaaagaa cttgaggctg ccagtgctcc agaggagagg 480
acaaggcttc atgatgaact ggaagaagcc aaggacaaag cccggcggag atccattggc 540
aacatcaagt ttattggaga actctttaaa ctcaaaatgc tgactgaagc catcatgcat 600
gactgtgtgg tgaagctgct aaagaaccat gatgaagaat ccctggagtg cctgtgtcgc 660
ctgctcacca ccattggcaa agacttggac tttgaaaaaa gccaaagcca cgtatggacc 720
cagtacttta atcagatgga gaaaattgtg aaaggaaaga aaaacctcat ctaggatcgg 780
gtcatgcttt caggaggtt 799

<210> 332
<211> 881
<212> DNA
<213> Homo Sapiens

<400> 332
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caggagacct ggaccagacc acgatgtgga aacgctggct cgcgctcgcg ctcgcgctgg 120
tggcggtcgc ctgggtccgc gccgaggaag agctaaggag caaatccaag atctgtgcca 180
atgtgttttg tggagccggc cgggaatgtg cagtcacaga gaaaggggaa cccacctgtc 240
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ttaagggact ctgtgttgat gctctcattg aactgtctga tgaaaatgct gantggaaac 720
ttagctttca agaagtttct caagngcctt naacccatct ttnaaccttc ttgagaagaa 780
tgtgcccttg gaggatgaaa cgtatgccan atggagcttg aaancgaggt ggactgtaan 840
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<210> 333
<211> 810
<212> DNA
<213> Homo Sapiens

<400> 333
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gcagcaacta cagtgaaatc ctagacaagt attttaagaa ctttgataat ggtgattctc 360
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tgtcagccat gacctgtgac ngaaagaatc agaagggggc ccagacccag acngaggang 720
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agggagcccc caaagagatt atgaggaggc 810

<210> 334

<211> 808
<212> DNA
<213> Homo Sapiens

<400> 334
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caagttaaat gcaatataga agcctactaa atacaaatac aagttcacaa acacatatgc 120
aacagaaact tgtttagatt gtttcttgaa gtttgactac ttaaaaacat aggtgtaaag 180
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gcagaactca agaggaatgt ggatttgctc ttgggaagtt caatgttgca gggtaaagta 600
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ttaacaaatt ggnggactct tggcccttct tcccatagng tccaagggct ggtaaaacct 720
ttggattaag gcgtgnctgc ttgggagttc ttccaaggca ctttggacca gggaacctgc 780
atttcaaact ggaccaagtg gaggtttg 808

<210> 335
<211> 758
<212> DNA
<213> Homo Sapiens

<400> 335
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aggctaaaat agaagaacaa gaagagcaaa ggaaggtcca gcaactcatg accaaagaga 120
agagaagacc aggtgtccag agagtggacg aaggtgggtg gaacactgta caaggggcca 180
agaacagtcg ggtactggac ccctcaaaat tcctaaaaat cactaagcct acaattgatg 240
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gaggtgtgga tgtggagagg aacagccttg agctgaaccg aaataaacaa gggagtcagc 660
aaaaccccga aanttcagca atgtcagctt attgacaagg gttgattatc agaagaggac 720
tgganaggaa gtccaaatct atcatggtna attttttc 758

<210> 336
<211> 785
<212> DNA
<213> Homo Sapiens

<400> 336
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ctgagtcaat ttctttttgt ttttttaaat atttgttcta tgtatttaca agccttaaag 120
ttgctctaaa gatttcaaga gtattaagag tacttttctc agggtagcac tttttttttt 180
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cattttttta agtatgagtc cttgtttaaa aagaaaagat taaaacagaa aatattttct 600
ataaatacnt gnattttggg tttaagggct cccgccctaa ggnttgaagg ttacttttat 660
cccaggaccc tttttcctcc atggaacccc ttttttcnc ttttcccttt tcccacttcg 720
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aaacc 785

<210> 337
<211> 643
<212> DNA
<213> Homo Sapiens

<400> 337
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agctgcccaa gaaggacatt atcaagtttc tgcaggaaca cggttcanat tcgtttcttg 120
cagaacataa attattagga aacattaaaa atgtggccaa gacagctaac aaggaccact 180
tggttacagc ctataaccat ctttttgaaa actaagcgtt ttaanggtac tgaangtnta 240
nntaaagtgt ctgancaagt naaaaatgnn aancttantg aagataancc caaagaaacc 300
aagtntgang agaccctgga tgagggtcca ccnaaatata ctaaatctgn tctgaaaaag 360
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ctacaagatg ggactgtttt tgatactaat attcaaacaa gtgcaaagaa naagaaaaat 480
gccaagcctt taagttttaa ggtcggagta cgcaaaagtt atcanaggat ggggatgaag 540
ctctcttgac tatgagtaaa ggagaaaagg ctngactgga aaatggaccc aaaatggctt 600
accggaaaga aagggacagc ctgatnccaa aatttcccca aat 643

<210> 338
<211> 831
<212> DNA
<213> Homo Sapiens

<400> 338
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aagttctcct tgaccagtat tttacacagc tgtaggaaag tattttagac cagggattca 120
taagggattt atctctcaaa agctgggacc aagtaaacaa atttattaa ctccttgaat 180
tttccagttg actcttcctt tacaatagta acaagttcta actagttgng taaatttctt 240
caaggccaag ttttatcatt gttgctaata tccttagagc tgaagcactg ctatttcaat 300
caatatccac taattccact tcaaaagtga gttttgcatt tggnggaatt ttggcatcag 360
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agttggtttt atctcccttt ttcagaacag gatttagtat attttggggg accctcatcc 660
agggtctctt cagacttggt ttctttgggt ttatcttcat ttaagcttca catttttac 720
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<210> 339
<211> 758
<212> DNA
<213> Homo Sapiens

<400> 339
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cagtagctgt cagagggaaa gactgtgcag taattgtcac acagaagaaa gtacctgaca 180
aattattgga ttccagcaca gtgactcact tattcaagat aactgaaaac attggttgtg 240

tgatgaccgg aatgacagct gacagcagat cccaggtaca gagggcacgc tatgaggcag 300
ctaactggaa atacaagtat ggctatgaga ttcctgtgga catgctgtgt aaaagaattg 360
ccgatatttc tcaggtctac acacagaatg ctgaaatgag gcctcttggt tgttgtatga 420
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tagtgacagt tgaaaatcct aaattcagga ttcttacngg aagcagagat tgatgcttac 720
cttgtgnttt agcngagagg agacttaacc attggccg 758

<210> 340
<211> 840
<212> DNA
<213> Homo Sapiens

<400> 340
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ggtaagtggc atcacggatc tggtaaacta acgacaatgt ttagtctctc tctgctagag 180
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nccaataatt tggcaggnac ctttctttct ggggngacaa ttactggccc agtcttttcc 780
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<210> 341
<211> 793
<212> DNA
<213> Homo Sapiens

<400> 341
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aacagaaact tgtttanatt gtttcttgaa gtttgactac ttaaaaacat aggngtaaag 180
gaaagacatt canactggtc cncgngggct tgntagcagg cagaggaacc ctgctttcca 240
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ttaggggaaa naacccntgg gggtntcntt ggnnttttaa caaaattggg gggncntttt 720
ggnccttcct cccaaaaggg ggcccanggn ctgnggaaaa aaccttttgg antaaggggg 780
gncccnnctt gga 793

<210> 342
<211> 906
<212> DNA

<213> Homo Sapiens

<400> 342
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cagtagctgt cagagggaaa gactgtgcag taattgtcac acagaagaaa gtacctgaca 180
aattattgga ttccagcaca gtgactcact tattcaagat aactgaaaac attggttgtg 240
tgatgaccgg aatgacagct gacagcagat cccaggtaca gagggcacgc tatgaggcag 300
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actactgtgg gtttaaagcc actgcagcgg gagttaaaca aactgagtca accagcttcc 540
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cttacctgtg tgtttggtaa caacaaacca acatcatgga ggtccctgga ttgaaaaagg 840
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ttttgg 906

<210> 343
<211> 875
<212> DNA
<213> Homo Sapiens

<400> 343
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tcgaggtgtt tttaccacca agactaaaaa aagataggaa aaacttgttg gagacccgat 120
tgcacatcac tggcagagaa ctgaggtcca aaatagctga aacctttgga cttcaagaaa 180
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tccccntaaa nggaattgtg gggaaaagag aangtctggt tctaagactn tacttacttt 840
nagggatccg aacttttcca gggggaatga tgtaa 875

<210> 344
<211> 629
<212> DNA
<213> Homo Sapiens

<400> 344
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cgcatgatcc atcctgtctt cagtcagtgc cttctggaag ggagggaaag tcttggatgc 180
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tcccactggg cacacatcta cagaggagtg cgtggcgcag tgaggacggt tactgctgga 300
gccgacacac agcgaactac atacttttag aaagagcctc tgtcacatgg ctagaacaac 360
aacaacaaca aagaaaaccc acaaaaaacc tggagaaaat atatctaaat ctctgatagg 420

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tctcttagct agcagtgagt tcagtatgac agcacagagt ctaaaaatat taattaaaaa     480
taaattgctt tggttagcat ttaaaccttt cccattcaat agaagatttc tgtaatgagg     540
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<210> 345
<211> 724
<212> DNA
<213> Homo Sapiens

<400> 345

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aacacaaagt aaattaatgt tnatactgnt ttttcacctg agtcatgtaa aaggtgactc     120
ctttcatttt aaaaagttat atttaatttt tgggggcctt aattaaaatt taacatttaa     180
ccatgngtnn tttttttgta aacagtctac atgtcaacaa atggataagg gttaacaaag     240
gcaaatnctg acttcatttg tgttttaaac acgattatat gaatttttct tttttaatta     300
aaaaaatgac ataaaaccat tcatataggt cctcttctct caactgcttt gagatatagc     360
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aaaaaaataa aggaacttat ttccttccta aggtctcagc tagtttctta ngtcttttct     480
tcagctccaa tggaaattnc tcatagcact tcttacagac tggcttcatg tcaaactcca     540
caaacttatt cttgantgtt aatttagtgt tgcaggtana acaggcaaag cagttcacgc     600
accaggcctt attaagagca gagacccccca tcaccttcta taacacgatt gcagtgggaa    660
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tcaa                                                                  724
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<210> 346
<211> 907
<212> DNA
<213> Homo Sapiens

<400> 346

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agccgaaagt gttcttaaga agcctgtagt tgactgtgtt gtttcggttc cttgtttcta     120
tactgatgca gaaagacgat cagtgatgga tgcaacacag attgctggtc ttaattgctt     180
gcgattaatg aatgaaacca ctgcagttgc tcttgcatat ggaatctata agcaggatct     240
tcctgcctta gaagagaaac caagaaatgt agtttttgta gacatgggcc actctgctta     300
tcaagtttct gtatgtgcat ttaatagagg aaaactgaaa gttctggcca ctgcatttga     360
cacgacattg ggaggtagaa aatttgatga agtgttagta aatcacttct gtgaagaatt     420
tgggaagaaa tacaagctag acattaagtc caaaatccgt gcattattac gactctctca     480
ggagtgtgag aaactcaaga aattgatgag tgcaaatgct tcagatctcc ctttgagcat     540
tgaatgtttt atgaatgatg ttgatgtatc tggaactatg aatagaggca aatttctgga     600
gatgtgcaat gatctcttag ctagagtgga gccaccactt cgtagtgttt tggaacaaaa     660
ccaagttaaa gaaagaagat atttatgcag tggagatagt tggtggtgct acacgaatcc     720
ctgcggtaaa aggagaagat cagcaaaatt tttcggtaaa gaacttagta caaccnttaa     780
atgctgatga aactgcactc gaggctgggc cattgcantg ggccatctta tcgcctgctt     840
tcaaagtccg agaantttct atcactgatg tagtaccata tccatatctc tgaaaaggga     900
atcttcc                                                               907
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<210> 347
<211> 711
<212> DNA
<213> Homo Sapiens

<400> 347

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gggttgtctc cttgnccatc cactggtcca ttctgctctg catttttttg ttcctntttt 180
ggaggttcca ctttgggttt gggctttgaa attatagggc tacaagtact tgncagctcc 240
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attattttca tatactgntg aatctgnttc cctagttctt caaataattt tggtcgttct 480
tnaaattcct ggaaacgtat nttaataggt tgacctaaat tttttaattc agccaactta 540
tcaacataaa cttgctttgg ctggcttctc catcctcata caaccaattt tcagtatctt 600
ccagtttcaa agtaaaactg ttacgancat nttcactnnc aaacttctca tattcnccac 660
taaagcttgg ctctcatttc ataccccata tttcctccca ctggggtctt a 711

<210> 348
<211> 862
<212> DNA
<213> Homo Sapiens

<400> 348
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tgtcatttgc aatgactact gcagtctgga gatcagcctg aaactgccgc cattccgcag 120
attcttcccg aagtcttctg tggagtgtct ttatttctct ttccatgtcg tgcttttggt 180
cctggagttt tttaactgta ttctctagat cagaaataat gaggttgtca tgaagtttca 240
cagcacgatg ttgttctact tcatcttcaa gttcaaagat ggtttctttc atgtcactcc 300
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aaggaaagct ggttcccggt tc 862

<210> 349
<211> 832
<212> DNA
<213> Homo Sapiens

<400> 349
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caaatggttc aaataatgcg gaacacgaaa cattgactaa tacaagtgct ttaaatatga 120
aacaaaatta ttttttaaaa aagcaaaaga ataaagaata tatacaaaag ggacctggaa 180
tctgtaagct gattccaaaa acgaaataag tagaaaatcc atggtgaaac ctgaacattc 240
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gtgaagttca actcttgatg agccgcttac aacagcagtt ccttaggagc caacatgaca 480
ggtgggtcag atttccctat gagaaacaaa actggccacc tacagcaaaa tatcaaaatg 540
ggtaagtcct tccttcctct tcctcctgat tatatacaac atatctcctt tcaagactat 600
tatttccatc atgcttattc cttcacaaat ctaaaccttg aggtgatatg aaggaaacca 660
acatcangaa aagaaaactc aattcagaaa tgaagaaaac tggcaggtat acaatacacc 720
cccagaacat ctcaatatcc ctggccagta caattcaagt gnactgggta caggcccata 780
ggattaaata attgggcagc ttgggaataa agctcatttt tttnccctca gg 832

<210> 350
<211> 782
<212> DNA
<213> Homo Sapiens

<400> 350
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tnaaanaang cgnancacna ancatngact aatncaaggg cttnaaatat gaancaaaat 120
nattttttaa aaaagcaaaa naataaanaa tatatncaaa ngggaccngn aatcngnaag 180
cngatnccaa aaccnaaata agtaaaaaan ccangggggaa nccngancat tcnacctnng 240
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ncnatncata ancttcagnc attttngctn gggcaaaatc atcccaatnt tcccaanact 360
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caactntnga nganccgttt acaacagcag ttccttagga nccancatga caggggggnc 480
aaatttccct atgagaanca aaacnggcca cctacagcaa aatatcaaaa ggggnaagnc 540
cttccttcct cttcctccng attatatnca ccatatctcc tttcangact atnatttcca 600
tcaggctnat tccttcacaa atntaaacct tgaggggata tgaaggaacc caacttcngg 660
aaangaaaac tcaattcana aattgaagaa acctggcagg tatacaatac ccccccaggn 720
catntcaana tccctggcac aagnnccaat tcagggncct ggtaccagcc ccatagaana 780
aa 782

<210> 351
<211> 775
<212> DNA
<213> Homo Sapiens

<400> 351
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cagtctttgt gcttgncttc aacccagtcc ttnttcagat tccttacccc cagaggtgtc 720
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<210> 352
<211> 865
<212> DNA
<213> Homo Sapiens

<400> 352
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tcaaataatg cggaacacga aacattgact aatacaagtg ctttaaatat gaaacaaaat 120
tatttttttaa aaaagcaaaa gaataaagaa tatatacaaa agggacctgg aatctgtaag 180
gtgattccaa aaacgaaata agtagaaaat ccatggtgaa acctgaacat tctacctctg 240
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nggaaaagaa aacctcaatt tcagaaatgg aagaaaaact ggcagggtat accaatacac 720
ccccccagag catttttaaa atatccctgg ncacaagtnc caattcaagg gnacctggtt 780
ccggnccata gaataaaana ntgggcactt tggaaaaaag cnccattttt ttcccttcag 840
ggggggttaa aagggccccc aaacc 865

<210> 353
<211> 875
<212> DNA
<213> Homo Sapiens

<400> 353
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caaaattatt ttttaaaaaa gcaaaagaat aaagaatata tacaaaaggg acctggaatc 180
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ccccagagca tcttcaatat cccctgggca cagtncccaa ttcagggact gggtacaggc 780
ccataagaat naaataattg ggcagctttg gaataaagcc tcattttttt cccttcaggn 840
gggttaaagg ggccccccaa accaaaaact ggggc 875

<210> 354
<211> 705
<212> DNA
<213> Homo Sapiens

<400> 354
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caaaattatt ttttaaaaaa gcaaaagaat aaagaatata tacaaaaggg acctggaatn 180
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<210> 355
<211> 862
<212> DNA
<213> Homo Sapiens

<400> 355

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accgcaatgg ggcctctatc cacgagttct gcatcaacct gcggcagctc tacggggaca 180
gccgcaagtt cctgctgctt ggtctgaggc ccttcatccc tgagaaggac agccagcact 240
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<210> 356
<211> 750
<212> DNA
<213> Homo Sapiens

<400> 356
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accgcaatgg ggcctctatc cacgagttct gcatcaacct gcggcagctc tacggggaca 180
gccgcaagtt cctgctgctt ggtctgaggc ccttcatccc tgagaaggac agccagcact 240
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aaggagctgc cagacctgcg tgtcaaccct tggtggtggc cagggagagg cgcccggtgc 600
agatggcccc gggccggccc aagtcctcta ctgtgaagga acagggagct tgccgangga 660
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ccttgcaatg nggccccgct tcggggaagg 750

<210> 357
<211> 725
<212> DNA
<213> Homo Sapiens

<400> 357
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ccccgagcgg ggacacactg cagggcttgg ctganccctg gtggacaagg caaagagcct 180
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cggtcatcag agctgcccgt ggccctgttc ccattggtgg tggaactgga tgtggtgctc 540
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atggtctnca ggaagttctc gaantgctgg ctgncctttn tcagggatga anggccttan 660
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acttc 725

<210> 358
<211> 813
<212> DNA
<213> Homo Sapiens

<400> 358
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ataaaaaacg cagtgaaatt ccttgttatt gggaaaatca gccaacagga tgtcaaaaat 180
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gcaaaactgt gttgcccact gtgcctgagt caccagaaga ggaagtgaag gctagccaac 300
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gagtttccag tcttttactt caccсttgag ccccgntcca ngtcctgaaa aagaaaatgt 720
caaggactgt ggtgangaca gtactntttt caccaaccaa ggagaagaac ccttggttag 780
atgagtctta ctgagagact ggggaaacca aaa 813

<210> 359
<211> 756
<212> DNA
<213> Homo Sapiens

<400> 359
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gggccagggc agaggaggaa gagaaggcta aggtagaaga gcagaaacgt aacaagcagc 120
tagaagagaa aaaacgtgcc atgcaagaga caaagataaa aggggaaaag gtagaacaga 180
aaatagaagg gaaatgggta aatgaaaaga aagcacaaga agataaactt cagacagctg 240
tcctaaagaa acagggagaa gagaagggaa ctaaagtgca agctaaaaga gaaaagctcc 300
aagaagacaa gcctaccttc aaaaaagaag agatcaaaga tgaaaagatt aaaaaggaca 360
aagaacccaa agaagaagtt aagagcttca tggatcgaaa gaagggattt acagaagtta 420
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gccctggagg gagggccagc gtggacacca aggaggctga gggcgccccc caggtggaag 540
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gagaagctca aacagaagca gcaggaggcg gctttggagc tggaggaact caaggaaaaa 660
ganggaggag agaaggaagg tcctgganga ggaagagcag aggaaggaac aggaggaaag 720
ccgatcggaa aaccttcaag aggaggaaga agaaga 756

<210> 360
<211> 706
<212> DNA
<213> Homo Sapiens

<400> 360
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gatcttctgt tgacttcana tgnggttggt atcactgctc aaatacagag ttatgatgat 180
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gcagtacttt taccatgaac atctntanac tgggattatt aaatatagng ataatataca 300
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gttctttctg gaactgtctc aaaccttagt gggggaagtg accttatcca canattgctt 480

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706

<210> 361
<211> 726
<212> DNA
<213> Homo Sapiens

<400> 361
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gagcgagtga acatgccgcc cgcggtggac cctgcggagt tcttcgtgct gatggagcgt 120
taccagcact accgncagac cgtgcgcgcc ctcaggatgg anttcgtgtc cgaggtgcat 180
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gccgagcacc gcnagctgat ggcctggaac caggcggaga accggcggct gnacgagctg 300
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gcccgcaagg ccgaagaggt gcangcctgg gcgcagcgca aggagcgnga antgctgcag 420
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gcattggact cccggaagaa ctacaactgg gccatcacca gagaggggct ggtggtcagg 540
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tatcatggcg gaagagttgc ccttgactgg aattaaagca attggtgttg cttatgagga 660
aaggtt 720
726

<210> 362
<211> 747
<212> DNA
<213> Homo Sapiens

<400> 362
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acatgctagt cagctngcag ttttacctcg taaagatanc aganaattat agncaaacca 120
gtaaacangg aattnacttt tcaaaagatt aaatccaaac tgancaaaat tntaccctaa 180
aacttactcc atccaaatat tggaataaaa gtcagcaggg atncattctn ttctgaactt 240
tanattttnt anaaaaatat gtaatagnga tcaggaggag ctnttgttca aaagtncaac 300
aaagcaangt taccttacca taggccttaa ttcaaacttt gatccatttc actccaanga 360
cgggagtcaa ngctacctgg gacacttgta tttgtaaatt ctgatttagc ttatngtaaa 420
cttgggccta ctttgncatg agggtttgac ttcngcattn ttcggggntt tccttccttt 480
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gactttgtaa cgcanatgtc acttttaatg ccagccctgc cctggttagc ncttctggag 600
gaatactgca gataagaaaa atagttattt gggaggctcc ctcagngggg tanggaattg 660
gggactaacc ncaattttng gttaaag 720
747

<210> 363
<211> 1227
<212> DNA
<213> Homo Sapiens

<400> 363
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gaccaccaaa tggtgccagc aaggaaatac cagaattgga agaagaaaaa acaattccta 120
ccaaagagcc tgagcagata aaatcagaat acaaggaaga aagatgcaca gagaagaatg 180
240

aagatcgtca tgcactacac atggattaca tacttgtaaa ccgtgaagaa aattcacact 300
caaagccaga gacctgtgaa gaaagagaaa gcatagctga attagaattg tatgtaggtt 360
ccaaagaaac agggctgcag ggaactcagt tagcaagctt cccagacaca tgtcagccag 420
cctccttaaa tgaaagaaaa ggtctctctg cagagaaaat gtcttctaaa ggcgatacga 480
gatcatcttt tgaaagccct gcacaagacc agagttggat gttcttgggc catagtgagg 540
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tcagagtcta tttcnggaat ataccgg 1227

<210> 364
<211> 831
<212> DNA
<213> Homo Sapiens

<400> 364
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aggaggcggc ccgacacgga gcggctcgcc ctgcaggccc tcacggagaa gcttctcagg 120
tctgaggagt ccgtctcccg cctcccggag gagatccgga gactggagga agagctccgc 180
cagctgaagt ccgattccca cgggccgaag gaggacggag gcttcagaca ctcggaagcc 240
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agcccanggt tactagatga ccttggggaa tgatcnggat aggttgtttg t 831

<210> 365
<211> 785
<212> DNA
<213> Homo Sapiens

<400> 365
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caggggctgc gcttcaggaa accaaccaaa tgcagaagca gagaacttaa atattgtaaa 180
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tcatgagaaa ttggacttta aatccgcgcc ctgcacacgc aattcattta gaccttttcg 360
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gcttggtcct gactgagcag cgtgtgcacc tgctcctgcc ctttctggga gtgattccac 660
ggtgctgggg agctngccca cacttcctct tcagcttctt ccacgtcacc cgtaaaagca 720
cccagctggg tctcgnccaa gcttcntacc gtgctgggcc aggcccatcc tggnctggct 780
tttga 785

<210> 366
<211> 816
<212> DNA
<213> Homo Sapiens

<400> 366
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gcgatacgag atcatctttt gaaagccctg cacaagacca gagttggatg ttcttgggcc 120
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ataactttgg acagtccaga tgaaattgac atcaatgtgg atgaacttga taccccgat 720
gaagcagatt cttttgagta ccctggccca tgaagaatcc cacagccaca aagattctgg 780
cccaagaagt cagagtctat ttcnggaata taccgg 816

<210> 367
<211> 803
<212> DNA
<213> Homo Sapiens

<400> 367
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ttcaaagatg gagagaggct ttggaagttg aggaaagtgg ctcagatgac ctcttaataa 180
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ttattacaca aagggaaaca gaaaataacc aaatgacatc agaaagtgga gccacagcag 300
gaaggcaaga agtggataac accttttgga atggctgtgg agattattac caactctatg 360
acaaagatga agatagttct gaatgcagtg atggggaatg gtctgcttct ttgcctcatc 420
gattttctgg tacagaaaaa gatcaatcct caagtgatga aagctgggag actctgccag 480
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tacagtacaa tgaagtcaat gaaagcagca gtgatgaagg gaaatgaacc tgccaatgaa 660
tttgcacagc cagctttcat gttggatggt aacaataacc tggangatga cttccgtgtg 720
aagtgaagac ttagatgtgg attggagcct attttgatgg ctttgcaaat gggcctagga 780
gttgctggaa gctttttcat aag 803

<210> 368
<211> 809
<212> DNA
<213> Homo Sapiens

<400> 368
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ggctggggtt atagaacaat aaaccaacca ttacatttag acctgggctt ttgaaaaact 120

tgcattccat tttaacaatt cgtatgtatc taacaaatac ataaatccag atcacaaata 180
atcttaagag ttaaacaatt aagaaacaca aagaatacca catagatcta cctttaaata 240
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aacataaaat agagaaataa gataaatgct attttattaa tattcatact tatttctaat 360
ttaccttcat atagtcttaa ctttttcaaa aggatccaag atatgatcaa ataatatttt 420
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aaaaccctct taacaactgg cagataatag cttaaatctt tacaggccaa ggaagaaata 720
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aaatattaan gggnggcttt aattttagg 809

<210> 369
<211> 826
<212> DNA
<213> Homo Sapiens

<400> 369
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gaccaccaaa tggtgccagc aaggaaatac cagaattgga agaagaaaaa acaattccta 180
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gttagaaccc gaggcanggc tgggcccgga tgcagtaccc cntgacagtg gaatgggnaa 780
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<210> 370
<211> 783
<212> DNA
<213> Homo Sapiens

<400> 370
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cagacacttt attctgagca atccaatgca tgatagaaaa acctttagat atataaaaga 180
ttaatttgtg cacatctaaa tgtttctaag ggaacaaact actgaggcat tgtgataaga 240
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aagagctaga gagctaaatc atgtgaatgg ttacctctgn ctacctatct gcttanggat 660
tatttttcta nggattcatc taggattcta tttaccttgg gggtgaaatg gacatggtag 720
cttttcctta gccccatgcc aattaaaatt naatttgggc ntttaaagaa taattaaaat 780
tgc 783

<210> 371
<211> 793
<212> DNA
<213> Homo Sapiens

<400> 371
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caccaagcat ccctccagta atgtcaagac ctgttagctc ttcctccatt tccactccct 180
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<210> 372
<211> 804
<212> DNA
<213> Homo Sapiens

<400> 372
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cccactactg ctattcacac acagtacttc cacggcacaa tacattagga gatctaaaaa 180
tgctcaccct gtactctagg ctgcttagga aatgtgaaaa ctagtaacat ttataatggc 240
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ctctttgggc tcactgcttt gtccagagac tatggcagca tttacctccg ctttgggctg 720
gcaacagang cctgcaatgc tgngggttga agttcctttt gagactaaat tctggcgacn 780
gggctttgct gggggtaaag ttct 804

<210> 373
<211> 792
<212> DNA
<213> Homo Sapiens

<400> 373
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aactgaaaga ggcaaagcac attgctgaag atgccgaccg caaatatgaa gaggtggccc 420

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aactaaantt ggagaaaaag catttgatga cttagaagaa gaaagtggct tcatgcccaa 720
agaagaaaan cttatatgca tcaanatgct ggatcagact ttactggagt taaaccacat 780
gtgaaaaact tc 792

<210> 374
<211> 745
<212> DNA
<213> Homo Sapiens

<400> 374
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acaaccaatt ttacctgact ttgatcctgc tcttggaatg atgactggaa ttccaccaat 180
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cacaggcaga ctccacgttg atttcgcaca ggctcgagat gacctgtatg agtgggagtg 600
taaacagcgt atgctagcca gagaggagcg ccatcgtaga agaatggaag aagaaagatt 660
gcgtncacca tnttcacccc cagtggtcac tatttagatc atgaatgcag cattggtgct 720
gaaaaaataa aaggaggatt ccaaa 745

<210> 375
<211> 734
<212> DNA
<213> Homo Sapiens

<400> 375
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atttacaaag tatttttgtg aaatactctc cattggcttt gcttgctcag tacattcttt 120
tatcttcaat tgagactcaa gggagggtat gcttgcatta ttataaatac cacaaccacc 180
accacacaca ataaagacca tctctgcctc aggacattcg ccccaaacct ccatcctctc 240
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ccagagggga aagaatatta atataaatcc cttctgccac tgtgtgccgt gccgtgtgtg 600
tgtttgtgcg tgtgtgccca cacatgagca tattttaatt cacagaaaaa ctgaaacatg 660
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atactggaaa cttg 734

<210> 376
<211> 822
<212> DNA
<213> Homo Sapiens

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accacctcga caagcaacag gttcaactcc tggcagagat gtgtatcctt attgatgaaa 120
atgacaataa aattggagct gagaccaaga agaattgtca cctgaacgag aacattgaga 180
aaggattatt gcatcgagct tttagtgtct tcttattcaa caccgaaaat aagcttctgc 240
tacagcaaag atcagatgct aagattacct ttccaggttg ttttacgaat acgtgttgta 300
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aaatggtggg ataacttaaa tcatttgaat caagtttggt gacccatgag aaaatatacn 720
gaatggggaa tatgtaggta aatggattac ccgaaaaaan ttatctgntt aacaaactta 780
gaaaggcttt ttncctttta aattaagttc tatcattaaa tt 822

<210> 377
<211> 812
<212> DNA
<213> Homo Sapiens

<400> 377
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tacaattttt aacattaata tacacattcc ataatctcat ctatttaaca ttaacacagg 180
cctttgttgt tgttattttt ttctccctac aatatttcct gactctgtag gacagtggtc 240
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gctaactggt aaatactatt tacaagaaga ttcaacctaa tcaatatcac ttatcaaaag 480
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812

<210> 378
<211> 870
<212> DNA
<213> Homo Sapiens

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gttcagctct caacattgct ggttgagttt ggaaccaaaa cctcttaaca actggcagat 180
aatagctaaa tcttaacaga caaagaagaa atattttctt tgggacagct gctatctaga 240
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cccataaaag gatacncagt attttgctgn aaataccagg accacattta caatatatgc 720
aaaaaattag aatgcagngg taagntcctt anatttaagc cctcatatgn gncaacaggg 780
gaaaattcca tttattttta agaaaggaaa aanggagacn gggatataaa tactcggaga 840

aattccccga attaagaagn aacctctgca 870

<210> 379
<211> 837
<212> DNA
<213> Homo Sapiens

<400> 379
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aggagaagtt caagcaggcc ctttctggaa ttctcattca atttgagcag atagtggctg 180
tgtaccattc cgcctccaag cagaaggcat gggaccactt cacaaaagcc cagcggaaga 240
acatcagcgt gtggtgcaaa caagctgagg aaattcgcaa cattcataat gatgaattaa 300
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aagaagctga acttgaaaaa ctcaaagatg acaagttaca ggtggaaaaa atgttggaaa 660
atcttaaaga aaaggaaagc tgtgcttcta ngctgtgtgc ctcaaaccag gatagcgaat 720
accctnttga gaaagaccat gaacagcagt cctatcaaaa tcttgaaccg tgaagcactg 780
gttagtgggg gattatcttc cacanttcct tcatggtcac cccatttgga gccagcc 837

<210> 380
<211> 793
<212> DNA
<213> Homo Sapiens

<400> 380
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agacacaatt ttttttaatt ttcatgaagt ccaatttgtc tatttttttt cttttgttgc 180
ctattttgtg tcatcctcaa gaaaccatta ccaaatccag tgttttgaag cttttcccat 240
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tataataagt agcctgaagt gggcaagtaa tgaaacaaac ttgagaatta cataaccttn 720
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cttttcacca ggc 793

<210> 381
<211> 807
<212> DNA
<213> Homo Sapiens

<400> 381
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gatgtttgac aaggatgtag taatgcttca gacaggtgtc tccatgatgg atccaaatca 180
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aagggcagaa cagtccaagg cagaagaagc gcaacggaaa ttgaaaagac naaatagaga 660
agatacagca cttccacctt ccggggttgn ctncattctg gcctctggtt gcaagcctgg 720
gtaacanttt gcagtcagat gtcatggtgn gcatcatggg gaaccaattn tgcaatgggc 780
tgtggaacca taaanggata tgcctgg 807

<210> 382
<211> 800
<212> DNA
<213> Homo Sapiens

<400> 382
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cagtcaatgc caaccagtgt ctgattggct tcctgtgcat gtccaatttc ctctgtgaca 180
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<210> 383
<211> 1203
<212> DNA
<213> Homo Sapiens

<400> 383
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<210> 384
<211> 2651
<212> DNA
<213> Homo Sapiens

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<210> 385
<211> 804
<212> DNA
<213> Homo Sapiens

<400> 385
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cataaagaat ggcccttgtg gataagcaca aagtcaagag acagcgattg gacagaattt 180
gtgaaggtat ccgcccccag atcatgaacg gcccccctgca cccccgcccc ctggtggcgc 240
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<210> 386
<211> 782
<212> DNA
<213> Homo Sapiens

<400> 386
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ga 782

<210> 387
<211> 865
<212> DNA
<213> Homo Sapiens

<400> 387
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tcagatacat ttgggaccna gagatagtga aaaatgatga acttagagaa aaaggaatat 780
gaaggncttt ggaactggat cttggactta tgcatcattg atgcttgcaa gtggttaaaa 840
ctnccaggag ctttgaaaac tggaa 865

<210> 388
<211> 753
<212> DNA
<213> Homo Sapiens

<400> 388
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ancagtttca nggttcactt ccctcccttg anccaggncc aggncatttn gctttggggn 180
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agccattatt tttcngcttg gggacaattt taaagntttt cttttggccc aaaaaccngg 660
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gattcncaaa aanactggng aaatagaaca tgg 753

<210> 389
<211> 737
<212> DNA
<213> Homo Sapiens

<400> 389
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tgcttaaggg tccgttg 737

<210> 390
<211> 775
<212> DNA
<213> Homo Sapiens

<400> 390

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<210> 391
<211> 776
<212> DNA
<213> Homo Sapiens

<400> 391
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<210> 392
<211> 909
<212> DNA
<213> Homo Sapiens

<400> 392
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<210> 393
<211> 769
<212> DNA
<213> Homo Sapiens

<400> 393
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<210> 394
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<212> DNA
<213> Homo Sapiens

<400> 394
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<210> 395
<211> 762
<212> DNA
<213> Homo Sapiens

<400> 395
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<210> 396
<211> 822
<212> DNA
<213> Homo Sapiens

<400> 396
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<210> 397
<211> 812
<212> DNA
<213> Homo Sapiens

<400> 397
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gaccttttg acaagctacc aagcaccccg ca 812

<210> 398
<211> 751
<212> DNA
<213> Homo Sapiens

<400> 398
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<210> 399
<211> 800
<212> DNA
<213> Homo Sapiens

<400> 399
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<210> 400
<211> 810
<212> DNA
<213> Homo Sapiens

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ttccagaaga aagggagaac tttcttcagc aattgtacaa atttatggaa gatagaggta 180
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<210> 401
<211> 860
<212> DNA
<213> Homo Sapiens

<400> 401
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<210> 402
<211> 779
<212> DNA
<213> Homo Sapiens

<400> 402
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gaaccaaggg ataaaactcc tacaaaaaga aaatactgta agtattaatg ctaggttatc 540
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gcatgcctta tgaggaatga cttaaaggga ctagaggtaa cagcagctca aaagtaagaa 720
ctgaggggga aaacccccca ctgnaccata tntnaagggc cgttaaagaa ttgcagaat 779

<210> 403
<211> 1443
<212> DNA
<213> Homo Sapiens

<400> 403
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cgcaaaaagg cacaagcaga attagctagc ttcaaagtcc tgctagatga cactcaaagt 240
gaagcagcaa gggtcctagc agacaatctc aagttgaaaa aggaacttca gtcaaataaa 300

gaatcagtta aaagccagat gaaacaaaag gatgaagatc ttgagcgaag actggaacag 360
gcagaagaga agcacctgaa agagaagaag aatatgcaag agaaactgga tgctttgcgc 420
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<210> 404
<211> 819
<212> DNA
<213> Homo Sapiens

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gaacatgaca agcagatttg ggagtccaag gcccagacag aggtccagct tcagcagaag 180
gtctgtgata ctctacaggg ggaaaacaaa gaacttttgt cccagctaga agagacacgc 240
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aatatgaaag agcaaaagat tataagcctg ctttctggca aggaagaggc aatccaagta 540
gctattgctg aactgcgtca gcaacatgat aaagaaatta aagagctgga aaacctgctg 600
tnccaggagg aagaggagaa tattggttta gaagaggaga acaanaangc ttgtggttaa 660
aacccaatca gcttatggga acacttgaaa accatcaaaa nggaaacatt tagncaaaag 720
gcncagttgg attccttggt naaatcctgn cttctnttcc aaatggatcc gagaaccgcn 780
tagtgggggg actattcacc agctgggaan agccgactt 819

<210> 405
<211> 761
<212> DNA
<213> Homo Sapiens

<400> 405
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ttaggganag gctaggcagt gaacacatca tgtatgcaat ganaaaataa ccaactggta 180
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gtncttcaag aggtcaggag ttgcagtgtg gtgttanacc agtcanactc ctggctgaaa 420

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ggaatnttca natnttcctg gaatgacaag aattggaacc ctgctgncca tagacacttc 540
tccctgccct ttggtgaaag gaaagacttt gggccccttt aataccttan tatcccatgt 600
gatcaagggc caaaagccaa aggggattct tatccttata gcctaagacc ctgaaattct 660
tcccttccca attatatctg gaaattggcc aggggaanaa aaatgctgnc cttcccatgn 720
ggaatctacc aggnttaaaa ccccnttaag ggagttccct t 761

<210> 406
<211> 758
<212> DNA
<213> Homo Sapiens

<400> 406
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gtcccattca ctgngctcta accggctgga tctgctcctc ggccacagga gagagcattt 660
ttcagcagcc actctttggc cncggtcttt cttccagcag cttcctttaa atcattcctt 720
tcttggctgg nggttgccat aactgctggt tggacctt 758

<210> 407
<211> 778
<212> DNA
<213> Homo Sapiens

<400> 407
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aggtatcaag agaaaattag tgctctggag agaactgtta aagctctaga atttgttcaa 120
actgaatctc aaaaagattt ggaaataacc aaagaaaatc tggctcaagc agttgaacac 180
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gaagataatt gcagtgtcta aaggacactt agacagatgt ccttcntatg gaagaattaa 720
agantaccat ttcaggcttt gaccatgaca gcagatttgg agtccaggnc caaccaga 778

<210> 408
<211> 752
<212> DNA
<213> Homo Sapiens

<400> 408
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nttttacngg accncaaaan atcagggncc tgcaaaatct cancaaatnt taggctcanc 120

aaaccaaang ngattntnaa attaancaaa ancgttcagg ctcagggcag taaaaaaaag 180
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ttccatccaa cgccantccg ggtccttcga caactgtngc ttgtaanatc tattaacagg 540
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ctgggggttg caaaacntgc tggntgacct tt 752

<210> 409
<211> 736
<212> DNA
<213> Homo Sapiens

<400> 409
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gctcagccaa gatcaagtta aagagcagtg agctgcaggc catcaagacg gagctgacac 120
agatcaagtc caatatcgat gccctgctga gccgcttgga gcagatcgct gcggagcaaa 180
aggccaatcc agatggcaag aagaagggtg atggaggtgg cgccagcggc ggcggcggcg 240
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gccaggacac agacgcggat gatggggcct tgcagtaagc agcctgacag gagcaatggc 480
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caccccccag cgggtaccag aggaaagctg cagcaggccg cctcctcccc caacgcatnc 600
cagccagtgc catgtcctct gcaggtggag ttactggcct actccttccc atgaaccctt 660
ccttgtctgc acttgccagg ccagagggta gagcacangg gtttccccat acttaccttc 720
ccttcccagg acactt 736

<210> 410
<211> 766
<212> DNA
<213> Homo Sapiens

<400> 410
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<210> 411
<211> 812
<212> DNA

<213> Homo Sapiens

<400> 411
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<210> 412
<211> 857
<212> DNA
<213> Homo Sapiens

<400> 412
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gaccaaagga agcaacaggc aatgtggcga agtgccctct gatttaaaga tgctaaaaag 660
actcaaaact caaatggccc gaagttcgat gtatgaaaac tgatgtaaag gaatacactt 720
tcagaaataa aaagcacagt gctgcttctg gagacatgcn gacaagnctt tttttgctga 780
nccagcagnt ntggctgatg tggactgaaa cttttggcag aatgcaggat ttggatggac 840
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<210> 413
<211> 790
<212> DNA
<213> Homo Sapiens

<400> 413
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cgtgtntaca gggccaggaa cgtaatgaat ccatgttaac ttaatttcat ttaaaattnc 540

atttgtagaa gtcncncaac agaaagatcc atgcggttga acagtgtgcc tgtncttgac 600
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catagnggct acagggcana atctttttca aaagcaattt tctggtccct aaatctacag 720
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taagctttta 790

<210> 414
<211> 1063
<212> DNA
<213> Homo Sapiens

<400> 414
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taatganctn nacttgnctt gagacagcct angggagacc acggatgntc tattannngn 180
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ggngcccntt tttcaatttt cngactcccg gagcttttaa aaaccggggg ccttaggttn 1020
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<210> 415
<211> 824
<212> DNA
<213> Homo Sapiens

<400> 415
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taaatatcac aggaaataca ntgcattttc aagntgnana gacnaatact tnctcattca 180
cagngnttga catanganag cctatttaca tancnatctg tataaagtca tgctctnant 240
ancaggntat ncagngctgn gccancacaa tgntttnaga angtgaagaa ccggncaaac 300
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cannaatgnc ttgngccctt taggtggcac tggctgtgga agtggttaag ctgctgctga 420
actcaattcg tggactgnag aattaggaat ggganccagg cggttnggat gaccattgcc 480
cactcnanca natnccaaag nnctnagaan gggaacnctc caancctgct tnatggngat 540
taancatnct tcttcttttg cttaacccat ggattananc acancagcna gtacngactt 600
ggntttaccc ncttcngttg gaaataagga ttcttgatng actaaannnc agctggtnaa 660
aacntaactn tccctcaatt tagcnttatt ntatgaancc ggggcctant ntcntgttca 720
aaaangngnt tttaagttcc ggtaatccta ccggnaatta nttgggggct ntgaattcan 780
cncccttana anatttnggn ttaccatttn aatccaaagg ccac 824

<210> 416
<211> 838
<212> DNA

<213> Homo Sapiens

<400> 416

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aaatacacaa ttttactagc aaatgcctct actgtaatcg ctatttaccc acagatactc     180
tgctcaacca tatgttaatt catggtctgt cttgtccata ttgccgttca actttcaatg     240
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aaacagattc tactttgagt tttgatttga cattgcagca gggtagtcac actaacatcc     360
atctcctggt aactacatac aatctgaggg atgccccagc tgaatctgtt gcttaccatg     420
cccaaaataa tcctccagtt cctccaaagc cacagccaaa ggttcaggaa aaggcagata     480
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aatgnatcca ttggcttggt gngnatacca gcaacatgga ncggctnaac tatcacttct     720
gnatctagnt cactggangg gccgtttggn aagganccca aatgggccag gataagacaa     780
aaggcnccct ttngggttaa tcagncttcc aagtctngca cctgtgnaac gcacttac       838
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<210> 417
<211> 880
<212> DNA
<213> Homo Sapiens

<400> 417

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acaaaattat acatactaca acagtgtgtc atatattaga tggtataaat gaatccacca     120
tgatggtgtt gaactaaaga taaaactaaa tatccaaaat gcagcactca ttggtttgct     180
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taaactagat agagcgttta ttacacagca agggcaacac taaaaaaaga aatctatgat     540
gggcacacag taacaggatc atgagcatca cttgaatagg tctaaaagac tgtcaaatat     600
acatttcaac tattcagaat gaatacatga aaaaaaatcg cttttcccaa aggtctacta     660
tacncattan actgggagct tgnatgttgg gccctacact accatgggga attangttta     720
acacttntta aaaacatttg gccaatcatt tcncagangg gaaagaaatg ttgaaaaggc     780
cgataaaata aacccttggg ttttcctcgg gggattcatg gagtcacccg ccttaatggg     840
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<210> 418
<211> 763
<212> DNA
<213> Homo Sapiens

<400> 418

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agaagatggc ggaagcggaa tttaaggacc atagtacagc tatggatact gaaccaaacc      60
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cctcctctcg aatgcagcag ccacagatct ctgtctacag tggttcagac cgacatgctg     180
tacaggtaat tcaacaggca ttgcatcggc cccccagctc agctgctcag taccttcagc     240
aaatgtatgc agcccaacaa cagcacttga tgctgcatac tgcagctctt cagcagcagc     300
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tgcatagaag atagggcatt gactcactca gacctggctt gcccagcatg cattgcaaca     540
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ataatgtgca agttattaaa gacatgagtg aattcgtgac agattgtcag aaaagaaaca 600
agagttttct acaacaaaaa actggcttat ggaacatata cttctgcttg agttgaatgt 660
gttggggctg agtgtaagaa aatgcaagct gcaaatctgg cttacatgtg gaaccaaagc 720
tggaaatgng tgctttaaan gcaacttgta aaattggatt tcc 763

<210> 419
<211> 753
<212> DNA
<213> Homo Sapiens

<400> 419
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ttgaaatagt agngtaacac ttcacaaata gagtaaaaac cttataatct tccatttttc 300
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tgatatacnc acattatcat ttttgcttta catactcaat tatcttttaa ataaaataaa 420
aattgaggag aaaatccgtt atattatcta cacatttact gtttccagca cttttcattt 480
ctttgngtag attcaaattt ctgncatctt ccctttgccc aaagaacttc ttttcatctt 540
tcttatagtt caggtctgct ggcaaccaat tagctcagcc tttggtttgc taaaaaagtt 600
catatattat cttgattttc aaatggnatt taagctctat ataggaattc ttaggtgact 660
ttaattcctt catcattggg aagangtcat aaagggcttg caaaggacta gaaatctgct 720
tacatttttt natttggtaa tctttcttac cca 753

<210> 420
<211> 799
<212> DNA
<213> Homo Sapiens

<400> 420
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acttgatgat atcctaccct tcttacaaca aattccatcc aaggaacctg cggtcctcat 180
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aaaattagca aaagaacaag agcaggcaca gaagctgaaa agccagcagc ctcttaaacc 660
ccaagtgcac acacctgttg ctactgttaa acagactaag gacttgacag acacactgat 720
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tctttcactt ctggtcctt 799

<210> 421
<211> 770
<212> DNA
<213> Homo Sapiens

<400> 421
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aggaaaacca ttgtgtaaaa cagtaggcgg atctttcaga gactccaaat cattgacaat 180

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ntgaagcttg aaccgtaggt caatgacata cctcaaacgg naccataaga tccaggcccg 720
actaccacaa tctcantgga gtcacagcan aactggtggg attctcttga 770

<210> 422
<211> 733
<212> DNA
<213> Homo Sapiens

<400> 422
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ctgtggccgc cgggggtgac ggncctttgc aggggctcat ccccgctcca ctgcacatta 180
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tgccaccttg gcacacatgg tcttccctgn gctgcggagg gcagaggttc atggagcaaa 660
agccaccgag tactccaacg gggnagccag acagggcagn cagggtcctt tcanaacatc 720
aacccagccc gaa 733

<210> 423
<211> 862
<212> DNA
<213> Homo Sapiens

<400> 423
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cagaccatct tggaaaaact tgaacagaaa gccattgatg tccangtcaa gtccaggtct 720
atgaacttca agccaagcaa ccnttgaagc agatcaagcc cctggaggca atcatggaaa 780
agggtgccgt ggcagcaaga caagggcaag aaaaatgctt ggaaatggcn gaagatcccc 840
acacnggaaa ccagcaggcc cg 862

<210> 424
<211> 859

<212> DNA
<213> Homo Sapiens

<400> 424
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cagatattcc tatggctcct ggcacatttt actctctcta aagtcaggta ttttaattat 120
gagatgaaga aaatcatctc attaaaatgg caacatttct gataaatgtt tcatatttat 180
gtgatgggta attgactccc catctacccc tccagtccag agctacaaaa gacagtgcac 240
aaccacagct aacaggtggt gggggtgccc aagtagacag ggctgcagaa caagcaacgg 300
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gttgctgggg ctggagttca ttagacctgg accttggccc tgggacatca aagggctttc 780
tggtcaaggt tttccaaga agggcctgga accttcctgg acancggntt tttctgggcc 840
tggacgcnca attggggtt 859

<210> 425
<211> 837
<212> DNA
<213> Homo Sapiens

<400> 425
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actaattgag gattatgaag gcaagttgaa taaagctcag tcctttatg aacgtgagct 120
tgatactttg aaaaggtcac agctttttac agcagaaagc ctacaggcca gcaaagaaaa 180
ggaagctgat cttagaaaag aatttcaggg acaagaagca attttacgaa aaactatagg 240
aaaattaaag acagagttac agatggtaca ggatgaagct ggaagtcttc ttgacaaatg 300
ccaaaagctt cagacggcac ttgccatagc agagaacaat gttcaggttc ttcaaaaaca 360
gcttgatgat gccaaggagg gagaaatggc cctattaagc aagcacaaag aagtggaaag 420
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agaatcagaa aaatcgagag tcaatgagag attatctcaa cttgaagagg aaagagcttt 600
tttgcgaagc caaaacccaa agtctggatg aagagcagaa gcnacagatt ctaagaactg 660
ggagaagaaa gtaaatgaac caagagactc agcaggaata ttatgaaagg gaacttaaaa 720
anctgcaagt agaatggaag aagaggggct taattaacga nggccattct aagacttttg 780
gaagaattag cttggaacnc cttttggcaa ttgaacttgt cncaggtaat gccattt 837

<210> 426
<211> 724
<212> DNA
<213> Homo Sapiens

<400> 426
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aaaaataaca gttataatta cacacataat atagtacctt atagaatgat tccaataaat 120
atcacaggaa atacagtgca ttttcaagtt ggagagacaa atactttctc attcacagtg 180
tttgacatag gaaagcctat ttacataaca atctgtataa agtcatgctc ttagtaacag 240
tctatacaga gctgtgccaa cacaattctt tcagaatgtg aagtaccggg caaaccactc 300
ctggcgctgg ggatctggag aagccactgg agaagcttca ctctgagcag gactcaaaaa 360
tgtcttgggc cctttaggtg gcactggctg tggaagtggt ttgctgctgt tgaactcaat 420
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accagattcc agagcactta nattgggaac actcacaaac ctgtttgttg gtgatttatc 540
attcttcttc ttttgcttag ccaatggatt aataacacca acagtaggac ttgagttaaa 600
cactttggtg aaagttagtt tctcgaattg actaattcca gctgataaaa cttattatcc 660
tcaattagtt tctttatgan ctgggcctct ttctgtaagc atggctttta attctggaat 720
catc 724

<210> 427
<211> 981
<212> DNA
<213> Homo Sapiens

<400> 427
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acacacacac acacaactca aagagttana atcattacnt ncaaatgaaa gtcgtaatga 120
tagatgatga tagntncaat gaanctgnga ncatanatta angaaacana naacantncn 180
aaaggtccac aaatctggtc ctatgaaaag agtaaaatta ccaagactng gtgaaagan c 240
ccannaaaan ncanagagag anagagagag agagaganac anagagagag aganaaaggg 300
aaggcacacn taancnatat cagcaataaa angggnnact ttantacana ttctgcaanc 360
attannnnna taatganagg atattatgaa cagttgtatg gcnatatgtt tgaaaactta 420
gatgccgata tgtttgaaaa cttaaatgaa acggaaaaat tccttgaaga accacaantt 480
aaatttgaca caggtagaaa atntgaatgc agttngncct tcagtatctg tggggaaatc 540
ggttncagaa ccactccccc antaccnaaa tttataattg ctcaagttcc tgatataaaa 600
tggcaaagta tttgcatata ncctatccct accctttttac atactttaaa taacctntga 660
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ttttnaaaat tatnttantt ttggaatagg nngtantatt tcctggggct ttttttttcc 780
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catangattt tgggaanggn ccaacttggg gccttngtaa ctttttaaag aaatngggaa 900
ttctttgntn aanaattctt ncncccaaag aaaacccctt tggccccana agttntttna 960
aatggggaaa tttncccaaa c 981

<210> 428
<211> 655
<212> DNA
<213> Homo Sapiens

<400> 428
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ttttattcat ccaagaaata ttcattagag aaattggcat gggatttttt tttcattgta 180
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tggtgaaatt cacaattgaa gacatctggg cctagcgtgt tctttgtagg aagaatatta 360
agaaagaatt ccatttcttt aaaagttacg agcacagttg gccttccaga tctatggatc 420
ccacatgagt tccagattca accaattgtg tattaaaaat atttgggaaa aaaagccaca 480
agaaataata caactataca aaataatata atttttaaaa tacaatataa caacgattta 540
cacagaatgt nccattatgt taggnattat aagtaactca gaggntattt aaagnatgtg 600
agaggnnatg gataggctat atgccaaata ctttgccant cttatantca gggaa 655

<210> 429
<211> 788
<212> DNA
<213> Homo Sapiens

<400> 429
gagcagcaga gatttttgct gtgagaatta attaccagta acagttcaat atgggggaca 60

ttctggctca tgaatctgaa ttacttggac tagtgaaaga gtatttagat tttgctgaat 120
ttgaagacac cttgaaaaca ttttcaaaag aatgcaaaat aaaaggaaaa ccactgtgta 180
aaacagtagg cggatctttc agagactcca aatcattgac aattcagaag gatcttgtcg 240
ctgcatttga caacggagac cagaaggtgt tcttcgatct gtgggaggag cacatttcaa 300
gttccatccg agatggggac tcctttgccc agaagctgga attctatctc cacatccatt 360
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agtttcttcc tttctatgcc cttccttttg ttcccaaccc tatggtgcac ccctcattta 540
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aaagtaccaa gaaatcttgc agcagcttca ccacagctgg ttgaagctga acgtaggtca 720
gngccttcct taaacgggcc aattaagaat ccaggccgac taccacaatc ttantggggg 780
tcccagca 788

<210> 430
<211> 655
<212> DNA
<213> Homo Sapiens

<400> 430
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aaagcttaan aaagtcaatt cccgnttcct ttanccctga cttacnctgg gtncccgttt 120
ntggggccnc cgggggngac gggcctttgc aggggctcat ccccgntcca ctggacatta 180
nccagcccct tccgccttgg cttccccgng ttggtcatga nccccaggtn ctccgnggtc 240
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ancatttcag cattgccttn tttgaagaac cancgtagga nggtttccat tcccattggt 480
nttgnttcct cacgaatgga tggaacanaa aggatgctnt acananctcc attcacatac 540
ggntgnatnt catggntttc atggccaana anaatcccaa aggctttgag cccaggnctg 600
gcccttggca caaatgttnt tcctggcttc cgaaggccaa ggttcattga ccaaa 655

<210> 431
<211> 844
<212> DNA
<213> Homo Sapiens

<400> 431
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cctgtcacta gagaatttga tgttggtcga cacattgcca gtggtggcaa tgggctagct 180
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cctttagaag aatccaggga ttgcttggca ttttgtacag aaccagtttt tgccagttta 420
gccaatgttc ttggtaactg ggaaaatcta ccttccccta tatctccaga cattaaggat 480
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ttctgaacaa gagcctaaat ttccttgtaa agaatgggac ccaaatttac cttcattgng 720
tcttncaaat cctgaatatt tggcttctga atcctacttt ctgngaactt gtgaaaccag 780
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gaaa 844

<210> 432

<211> 807
<212> DNA
<213> Homo Sapiens

<400> 432
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ctttttcttt catgtgtaaa aacaaccatg tgaggtattt tacaggtcaa aagaaaacaa 120
aaactacttc cttattcagt gtaaaggagg cttataagca ttccaaaata aaaacaaaca 180
aaaaccagac aagtacatag tctatttcca tttcctttta tacatcctct ctatatatca 240
cacatttagc aataggagaa tagagaacta attcaaatgc aagggaatct tttttgtaga 300
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tgtcttcagt acgtgaaata attttaaggt gatctagtac tttgaaaatt tcattcactt 420
aagaacactt aagctgaaaa atagcactat ttttcagagg caatttctca acagaaaaag 480
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catactggat ttttttcaaa tgacttattt tcatatttag tagttcaagg tctataagct 660
ggtatattaa gctttctttc tggttaagag ntcaacactt acatcatggt attttacnaa 720
attaaaaacc aatttcttaa ataaaccgng gctcctaaaa tggtaccaag gaaaaattct 780
tcaataccta atttaattcc ataagga 807

<210> 433
<211> 866
<212> DNA
<213> Homo Sapiens

<400> 433
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caggaccagc gccagcattc cagccatttt tcttcactgg agcatttcca tttaatatgc 360
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taagtgaaaa taattttctg ttcanaaatg ctgcatccac actgactgaa aggccttgct 660
ataacaggag agcttcaaaa actgacttac taatgcacag ggacttttat cactggagta 720
ttatgacagt gngcatcacc ttntgggccc aaggaccaag ccattggtct aaaaggcctc 780
aaaatgcccc ggganggcct ctggtggcca tggcattagt atatactaac catcattctg 840
gccaggtaag gaagcccctg gacccc 866

<210> 434
<211> 764
<212> DNA
<213> Homo Sapiens

<400> 434
caaaataacc tttatttttg atacaaaaat aaagatgcta actcctttag ctcagtttcc 60
cacaataacc tttaaaatag caacagattc agtctcaaaa attgcttttc atttgtagtg 120
gaaaatgaaa gtggagaaca tggaacagca atatttgngc tcttctcata ggatgcagtt 180
acacacacat atgactggaa tcacttcaga gtaaaaaaaa agtgggctgg gtgcagtggc 240
tcacacctgt aatcccagca ctttgggagg ccaaggacag gagcatcact taaggccaga 300
agtttgagac cagcctgggc cacatagtga gaccctgtct ctatgggcgg ggtggggtg 360
gggggcattg taaaaaagca gttgttcttt tanaaggcat cagagagccc tntagtgacc 420

acgaagggga gttaatgcag agatgactcg agacagagaa gcagtcatga gtgtttacaa 480
aggaaaaagt gagggaggga aagctctttt ggttaacagc atatttacaa ttagttaact 540
gnattcttaa atacttttaa cctgagtaac atttataaat atgttatagg aaacctcaca 600
gtcacaagtc acactagaat ccatctgtcc agtatctggg ctttccccac accagaatcc 660
atctgtccag tatctgggct ttcccgagtc ttcctcttct cataagttcc caanggcagc 720
anaagtgtga agcatgcaca ccaaggaaaa acgcattcca gccc 764

<210> 435
<211> 834
<212> DNA
<213> Homo Sapiens

<400> 435
agattttgtt aattttccta caaaaaatgg atttgctact aaccaaaacc cctcctgatg 60
agataaagaa cagtgttcta cccatggttt acagagcact agaagctcct tccattcaga 120
tccaggagct ctgtctaaac atcattccaa cctttgcaaa tcttatagac tacccatcca 180
tgaaaaacgc tttgatacca agaattaaaa atgcttgtct acaaacatct tcccttgcgg 240
ttcgtgtaaa ttcattagtg tgcttaggaa agattttgga atacttggat aagtggtttg 300
tacttgatga tatcctaccc ttcttacaac aaattccatc caaggaacct gcggtcctca 360
tgggaatttt aggtatttac aaatgtactt ttactcataa gaagttggga atcaccaaag 420
agcagctggc cggaaaagtg ttgcctcatc ttattcccct gagtattgaa aacaatctta 480
atcttaatca gttcaattct ttcatttccg tcataaaaga aatgcttaat agattggagt 540
ctgaacataa gactaaactg gagcaacttc atataatgca agaacagcag aaatctttgg 600
atataggaaa tcaaatgaat gtttctgagg agatgaaagt tcaaatattg ggaatcagca 660
aattggcaaa gtttttaaca acattggagc agaccttntg actggcagtg agtccgaaaa 720
taaagangac gggttacaga ataaccttaa aagagcatcc ttaccacttg gaggaaaaac 780
caaaatttgc caaaagaacc aggaccggcn ccgaagctgg aaaagccgca ggct 834

<210> 436
<211> 812
<212> DNA
<213> Homo Sapiens

<400> 436
acagaagtaa agtttattac atttgaaaca atacagcaga aacctcaaaa gtttactcat 60
aaatatagtt taattcttac aaatcttctt ttgaaaatgc aattcatata tgctgcaacc 120
tcagaagttt gaatttgaaa tgaaatatga aggtagtagt cagggaagtc acatcagagt 180
gccttgtcaa atatccaaac aaatcagcac atacctcttc cttgatacag gaggaaaaaa 240
gtgattctaa atatatccaa gtgaatgcag aaaaatacat tactatttga ggcagaccat 300
gctaaaatat aatttacaat gattagtttg cacttaagat ggttaataac gcatttaaac 360
caatgaaatg aaggttaagt tgaattttgt agtatttgct cagtctctgt actaaacaat 420
agttcatctg aaaagtttgg aaaaagcaaa taacctgata cttctcttta tgcttatcat 480
tttctcactg tcatcttaaa tgcaaacaaa tcaatacagc atcaagattt tttacatatt 540
aaaatgaaga ctaatgactc atagactgng taccatatag tacttaatag atgagcttgc 600
aatgaccatc acctcaattt tttaaataac accaagatcc acaagccaaa ataaacattt 660
gattaaaaag ttatggtatt caagataact cagtttcctt tttctctttg agattgggna 720
anggctgggt ctttaaaaaa ccctggaaaa gggagttggg taaagaggga aaaaaatcct 780
tcaangcttt taaaaaaact tcnactgggt ta 812

<210> 437
<211> 842
<212> DNA
<213> Homo Sapiens

<400> 437

gtggaagagg cgtacctatt tgcaaagtgc agagcaggca tggattgcca attctggaac 60
agagcaaagc cccaacttgc cctccactgg tgatgtcaca cccacccatg aagagcctgc 120
ctctagggtt gttgaatgtt gggtcacgaa gatctcaacc tggccaaaga agagaaccca 180
gaaagatcat cacagtttct gtaaaagaag atgtacacct gaaaaaggca gaaaatgcct 240
ggaagccaag ccaaaaacga gacagccaag ccgatgatcc cgaaaacatt aaaacccagg 300
agctttttag aaaagttcga agtatcttaa ataaattgac accacagatg ttcaatcaac 360
tgatgaagca agtgtcagga cttactgttg acacagagga gcggctgaaa ggagttattg 420
acctggtctt tgagaaggct attgatgaac ccagtttctc tgtggcttac gcaaacatgt 480
gtcgatgtct agtaacgctg aaagtaccca tggcagacaa gcctggtaac acagtgaatt 540
tccggaagct gctactgaac cgttgccaga aggagtttga aaaagataaa gcagatgatg 600
atgtctttga gaagaagcag aaagaacttg aggctgccag tgctccagag gagaggacaa 660
ggcttcatga tgaactggaa gaagccaagg acaaaagccc ggcggagatc cattggcaac 720
atcaagttta ttggagaact cttttaaact caaaatgctt gacttgaagc catcattgca 780
tgactgtgtg gtgaagctgc ttaagaaccn ttgatgaaga atccctggaa tggcctgtgt 840
cg 842

<210> 438
<211> 678
<212> DNA
<213> Homo Sapiens

<400> 438
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ctgagncaat ntctttttgt ntttttaaan atttgtncta tgtatttaca ngccttaaag 120
nngctctaaa gatntcaaga gnattaanag nacttttntc agggnagcac tntttttttt 180
ttaaacantt nttggngttc tgtggnccac annatttcct tntgtntcaa ngtnatgtat 240
gtnttgatna cnatngngat nttttaaann ttntgaanca agctgagagg cnngcanaaa 300
gatntgangc cnnaaaaaaa aaaatctttn ttaccttgtn caccccaaac tttttcaaat 360
ctggnctaaa tgctntacct taaaacanac atgaggggca tcttgaaggg gagggaaant 420
tatttctctg cntttctatn atacangtng tttacanaaa ctgngaatta naaaattaca 480
ctggnatttg cngaccttaa aataaattaa aagtnctcaa ctnttttttt ttttgntaaa 540
cnttttttta agnatgannc cntggttaaa aagaaaagnt ttaaaccgaa aatattttct 600
ataaataata cctggatttt ggntttaggg cccccgccct aaggnttgna ggttactttt 660
ntccnangac cttttcc 678

<210> 439
<211> 826
<212> DNA
<213> Homo Sapiens

<400> 439
gacccttac caacaaatga aaatgatgat gatatatgca agaaaccctg tagtgtagca 60
cctaatgata ttccactggt ttctagtact aacctaatta atgaaataaa tggagttagc 120
gaaaaattat cagccacgga gagcattgtg gaaatagtaa aacaggaagt attgccattg 180
actcttgaat tggagattct cgaaaatccc ccagaagaaa tgaaactgga gtgtatccca 240
gctcccatca cccctccac agttccttcc tttcctccaa ctcctccaac tcctccagct 300
tctcctcctc acactccagt cattgttcct gctgctgcca ctactgttag ttctccgagt 360
gctgccatca cagtccagag agtcctagag gaggacgaga gcataagaac ttgccttagt 420
gaagatgcaa aagagattca gaacaaaata gaggtagaag cagatgggca aacagaagag 480
attttggatt ctcaaaactt aaattcaaga aggagccctg tcccagctca aatagctata 540
actgtaccaa agacatggaa gaaaccaaaa gatcggaccc gaaccactga agagatgtta 600
gaggcagaat tggagcttaa agctgaagag gagctttcca ttggcaaagt acttgaatct 660
gaccaggata aaatgagcca ggggtttcat cctgaaagag acccctntgg cctaaaaaaa 720
gtgaaaagct gtggaagaaa atggagaaga actgagccag accgtaatgg ggcctgaaag 780
ggttctgang gtgaaggaat agatgcttaa ttcangcttc cccaga 826

<210> 440
<211> 689
<212> DNA
<213> Homo Sapiens

<400> 440
aaatatttgt tctatgtatt tacaagcctt aaagttgctc taaagatttc aagagtatta 60
agagtacttt tctcagggta gcactttttt tttttaaac aattcttgga gttctgtggt 120
ccacagcatt tccttctgtt tcaatgttat gtatgttttg attactattg tgattttttа 180
aattttctga agcaagctga gaggcaggca gaaagatttg atgccaaaaa aaaaaaaatc 240
tttcttacct tgttcacccc aaactttctc aaatctggac taaatgctat accttaaaac 300
aaacatgagg tgcatcttga aggggaggga aatttatttc tctgcttttc tattatacaa 360
gttgtttaca gaaactgcaa attaaaaaat tacactggca tttgcagtcc ttaaaataaa 420
ttaaaagttc tcaacttttt tttttgcta aacatttttt taagtatgag tccttgttta 480
aaaagaaaag attaaaacag aaaatatttt ctataaataa tacatgtatt ttggttttag 540
tgctcccgcc ctaaggtttg aagtttactt ttatccagta ccttttcct ccatgatcac 600
ctttttttct ctttcccctn ttccactcgg gcacacgtgg ggggtttctg cnanaattgg 660
ccttgctgca ctgngaatgg gcnaaaacc 689

<210> 441
<211> 883
<212> DNA
<213> Homo Sapiens

<400> 441
ctttttatcc tggaccagga cctggggact tccccaatgc ttatggaacg cctttttacc 60
caagtcagcc ggtgtatcag tcagcaccta tcatagtgcc tacgcagcaa cagccgcctc 120
cagccaagag agagaaaaaa actataagaa ttcgggatcc aaaccaggga ggtaaagaca 180
taacagagga gattatgtct ggaggtggca gcagaaatcc tactccaccc ataggaagac 240
ccacgtccac acctactcct cctcagcagc tgcccagcca ggtccccgag cacagccctg 300
tggtttatgg gactgtggag agcgctcatc ttgctgccag caccсctgtc actgcagcta 360
gcgaccagaa gcaagctcaa atagctataa ctgtaccaaa gacatggaag aaaccaaaag 420
atcggacccg aaccactgaa gagatgttag aggcagaatt ggagcttaaa gctgaagagg 480
agctttccat tgacaaagta cttgaatctg aacaagataa aatgagccag gggtttcatc 540
ctgaaagaga cccctctgac ctaaaaaaag tgaaagctgt ggaagaaaat ggagaagaag 600
ctgagccagt acgtaatggt gcttgagagt gtttcttgag ggtgaaggaa tagatgctaa 660
ttcaggcttc acagatagtt ctggtgatgg gggtacattt ccatttaaac cagaatnctg 720
gaagcctact ggtacttgaa ggtaagaaca gtatgaccag ggagtttctg gtggactttc 780
cagttcatgc ctggctgnat tccaaaancc naagggcctg gcttctatta anggatgngg 840
ttnttgacag gatcaaccaa ncccaaatgg ccaatgggga act 883

<210> 442
<211> 777
<212> DNA
<213> Homo Sapiens

<400> 442
gctaaacatt tttttaagta tgagtccttg tttaaaaaga aaagattaaa acagaaaata 60
ttttctataa ataatacatg tattttggtt ttagtgctcc cgccctaagg tttgaagttt 120
acttttatcc agtacctttt tcctccatga tcaccttttt ttctctttcc cctctcccac 180
tcgtgcacac gtgggggttt ctgcgagaat tggccttgct gcactgtgat tggcgaagac 240
gtgaaacttt ttaaaaaaat acttaaattg tttcttttgt ttcattttgt gtatttgaag 300
ttttagttat cctcagactc ctcttctgct tcccgcagcc acgtgaagaa tgccgtgaca 360
gatttcagag ccacgcccctt cccattctgc tctgcagggt ccttgctgct ctcccatttg 420
tagaaggcat cctcggagat cacctcctcg tcatatagac aatcaaaaaa catccgcagc 480

aaattggcag gttgatcaag ttttactatc gatgcttgta gtgcataaag tgcttgcagt 540
tccttctctg natctgagtc taggtacttg agtaagatcg gcactctctg cttgaaacag 600
cagtgtccac ttcttgaang tagaagaagt cggctattaa tagctggttt acaaacagca 660
gtcatttaaa gctctaagga atggtaggtg aactcntctg ggatttcggc taagaataag 720
ccctttancc aggccaaaga acctggtcan tcaattcgct tttggccctc caataaa 777

<210> 443
<211> 875
<212> DNA
<213> Homo Sapiens

<400> 443
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taaagcagat gatgatgtct ttgagaagaa gcagaaagaa cttgaggctg ccagtgctcc 120
agaggagagg acaaggcttc atgatgaact ggaagaagcc aaggacaaag cccggcggag 180
atccattggc aacatcaagt ttattggaga actctttaaa ctcaaaatgc tgactgaagc 240
catcatgcat gactgtgtgg tgaagctgct aaagaaccat gatgaagaat ccctggagtg 300
cctgtgtcgc ctgctcacca ccattggcaa agacttggac tttgaaaaag caaagccacg 360
tatggaccag tactttaatc agatggagaa aattgtgaaa gaaagaaaaa cctcatctag 420
gattcggttc atgcttcaag atgttataga cctaaggctg tgcaattggg tatctcgaag 480
agcagatcaa gggcctaaaa ctatcgaaca gattcacaaa gaggctaaaa tagaagaaca 540
agaagagcaa aggaaggtcc agcaactcat gaccaaagag aagagaagac caggtgtcca 600
gagagtggac gaaggtgggt ggaacactgt acaaggggcc caagaacagt cgggtactgg 660
acccctcaaa antcctaaaa atcactaagc ctacaattga tgaaaaaant cactggacct 720
aaagccagct aggcagctgg ggaaaaggca gcagtggtgg accaangcaa gtgaaactga 780
gccntacggc aagtgcttnc agttaaacag atctntgncc tgaaccttca gaaccttang 840
gtcccgccat cacgcctgta aagttggatt cccga 875

<210> 444
<211> 756
<212> DNA
<213> Homo Sapiens

<400> 444
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tagtactgag tcaatttctt tttggttttt taaatatttg gtctatgnat ttacnagcct 120
taaagttgct ctaaagattt caagagtatt aagagtactt ttctcagggt agcacttttt 180
ttttttttaa caattcttgg agttctgngg nccacagcat ttccttctgn ttcaatgnta 240
tgtatgtttt gattactatt gggatttttt aaattttctg aagcaagctg anaggcaggc 300
ngaaagattt gatgccnaaa aaaaaaaaaa aatctttntt accttggtca ccccaaactt 360
tntcaaatct ggactaaatg ctataccttta aaacaaacnt gaggggcatn ttgaagggga 420
gggaaattta tttctctgnt tttctattat acnagttgnt taccgaaact gnaaattaaa 480
aaattaccct ggcntttgca ggccttaaaa taaattaaaa gntctcaact tttttttttt 540
gccaaacatt tttttaagta tgagnccttg nttaaaaaga aaagattnaa nccgaaaata 600
ttttctataa ataatacntg natttttggtt ttaaggctcc cgccctaang nttgaaggtt 660
acttttatcc nagnnccctt tttccctcca tgaanacccc tttttttcnc ctttcccctt 720
ttcccacttn gggccccccc tngggggggtt tttgcg 756

<210> 445
<211> 783
<212> DNA
<213> Homo Sapiens

<400> 445
cagaaaatgg tgcttaccaa ctacatgttc cctcaacagc caaggactga ggatgttatg 60

tttatatcag ataatgaaag ttttaaccct tcattgtggg aggaacagag gaaacagcgg 120
gctcaagttg catttgaatg tgatgaagac aaagatgaaa gggaggcacc tcccagggag 180
ggaaatttaa aaagatatcc aacaccatac ccagatgagc ttaagaatat ggtcaaaact 240
gttcaaacca ttgtacatag attaaaagat gaagagacca atgaagactc aggaagagat 300
ttgaaaccac atgaagatca acaagatata aataaagatg tgggtgtgaa gacctcagaa 360
agtactacta cagtaaaaag caaagttgat gaaagagaaa aatatatgat aggaaactct 420
gtacagaaga tcagtgaacc tgaagctgag attagtcctg ggagtttacc agtgactgca 480
aatatgaaag cctctgagaa cttgaagcat attgttaacc atgatgatgt ttttgaggaa 540
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gaaacctcta ttaaccagcc aaaagtcgta gcacttagta ataacaaaaa agatgataca 660
aaggaaacag attctttatc agatgaagtt acacacaata gcaatcagaa taccagcaat 720
tggtcttctc catctcggat gtctgattca gttctcttaa tactgatagt agtcaagaca 780
cct 783

<210> 446
<211> 866
<212> DNA
<213> Homo Sapiens

<400> 446
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tatccataaa aatcaattcc tatgtaaata gtactgaaaa tcaactaaaa tgagttaaaa 120
tttacaaaga gttgttaaag ggtttcaatc aaaattatta aaactataca gtacaataac 180
caattgataa catcttgaaa gaagtgcaat atttgagttc acatattttt aaaagtgctg 240
cctacttact ctgactagca agaatggaaa gtgagtccaa ctcacttttg caaaaataat 300
gttggttggt gttttaagct agtcttataa aagtcttaat taaaatcaag gttgataaac 360
aaagcataac agattaaaaa ttcccaaatt gcatttctta gtaaataaaa atgaagtgca 420
ataaccaaat attgctctaa tgaaaggttc cagactagcc tcaactaaac agttattggt 480
cttctatggc actttttttct ggtccaaata accatgcatt aatccttacc attacatgtt 540
actcaaattt tatttgatta catagaacaa aaacaaataa aattaatggt ctggataaac 600
aaaattaata aacctctatc atcaaatatt tgttacagta actaggaaca aagaaaggca 660
gtttggtggg taaaacacta ttacactgat ccccatagga aacccctttta aagactctgg 720
aagtgttgag ttcacattta atggtacctg tagaaacagn cctttatttg gacaccttta 780
cccactggca ngccctaang gacccatccc tttgctctat aacttttcac aagcaattct 840
ctaatcctgg gccagtttnc aaaagc 866

<210> 447
<211> 789
<212> DNA
<213> Homo Sapiens

<400> 447
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tttcagaaaa attgccagag aagtgggaga gcgtgaaact cctgtttgtg aaaactgaga 120
aatcggctgc acttcccatc ttttcctcgt ttgtcagcaa ttgggatgaa gccaccaaaa 180
gatctttgct taataagaag aaaaaagagg caaggagaaa acgaagagaa agaaattttg 240
aaaaacaaaa ggagaggaag aagaagaggc agcaggctag gaagactgca tcagttctta 300
gtaaagatga tgtggcacct gaaagtggtg atactacagt gaagaaacct gaatcaaaga 360
aggaacagac cccagagcat gggaagaaaa aacgtggcag aggaaaagcc caagttaaag 420
caacaaatga atccgaagac gaaatcccac agctggtacc aataggaaag aagactccag 480
ctaatgaaaa agtagagatt caaaaacatg ccacaggaaa gaagtctcca gcaaagagtc 540
ctaatcccag cacacctcgt gggaagaaaa gaaaggcttt gccagcatct gagaccccaa 600
aagctgcaga gtctgagacc ccagggaaaa gcccagagaa gaagccaaaa atcaaagaag 660
agcagtgaag gaaaaaagtc cttcgctggg gaaaaaagat gccgaagaca gacttcaaaa 720
aagccagang ccaggttttc ccactcctag taaatctgtg agaaagcttt ccacaccccc 780

aaaaaatgg 789

<210> 448
<211> 820
<212> DNA
<213> Homo Sapiens

<400> 448
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cctgcctcag cctccctagt agctgggatt acaggtgtcc accaccatgc ccaattaatt 180
tttgtatttt tggtacagac agggtttcac catgttggcc aggatggtct cgatctcgtt 240
gaccttgtga tccgcctgcc tcggcctccc aaagtgctgg gattacaggc gtgagccacc 300
gcccctggac tacttatgga ggttttaaaa aatcttttaa gtccaggcct gacgtttaga 360
gaaggttaca aaggcggcca ggatctgagt atttccaaaa agctctggag gcagcattga 420
ggtttccttc cagttgaatc actgacttta ggtcgactgg ggtactttgg gtttttttggg 480
ccattttttg gggggtgtggg aagcttttct cacagattta ctaggagtgg tgaaaaactt 540
ggcctctggc tttttttggag tctgtctcgc atcttttttc cccagcgaag gactttttttc 600
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actctgcagc tttttggggg tcttcaanat gctggcaaaa gccttttctt ttcttcccac 720
gagggggngc ctggggatta ggactctttt gcctgggana cttcttttct tgngggnang 780
tttttgaaac nntacttttt ccaatttagc ctggaggcct 820

<210> 449
<211> 936
<212> DNA
<213> Homo Sapiens

<400> 449
aaaagaagga aacagttact caactccaaa atatcattga ggctaattct cagcattacc 60
aaaaaaatat taatagtttg caggaagagc ttttacagtt gaaagctata caccaagaag 120
aggtgaaaga gttgatgtgc cagattgaag catcagctaa ggaacatgaa gcagagataa 180
ataagttgaa cgagctaaaa gagaacttag taaaacaatg tgaggcaagt gaaaagaaca 240
tccagaagaa atatgaatgt gagttagaaa atttaaggaa agccacctca aatgcaaacc 300
aagacaatca gatatgttct attctcttgc aagaaaatac atttgtagaa caagtagtaa 360
atgaaaaagt caaacactta gaagatacct taaaagaact tgaatctcaa cacagtatct 420
taaaagatga ggtaacttat atgaataatc ttaagttaaa acttgaaatg gatgctcaac 480
atataaagga tgagtttttt catgaacggg aagacttaga gtttaaaatt aatgaattat 540
tactagctaa agaagaacag ggctgtgtaa ttgaaaaatt aaaatctgag ctagcaggtt 600
taaataaaca gttttgctat actgtagaac agcataacag agaagtacag agtcttaagg 660
aacaccatca aaaagaaata tcagaactaa atgagacatt tttgtcagat tcagaaaaag 720
gaaaaattaa cattaatggt tgaaattcaa ggtcttaang gacagtgtga aaacctaccg 780
ccaggaaaag caagaagcca ttttaaantt ntgagagntt acccagagga ttttggaaat 840
ttcccaancn gaactggggg gaatctgctg ggaaaaatag gtcaggagtt cgaatcatgg 900
aaccaccagc aggcctttga ngtcatgacc tgagca 936

<210> 450
<211> 806
<212> DNA
<213> Homo Sapiens

<400> 450
aactcaaaac agtgttaagt tcctatgctg ttagtactgt atcttgtcca cacctcaaac 60
aacagtgaga tctctgagca catggtctgt acctcaacca cttttctatc accagggtct 120
agaatagttg ggcatttaaa taaaatttgc taaatgaatg aaaaatccaa aataaatcat 180

gaagccattt ataaatcaca ccaatcttgc ttgggttaaa caatagaaag taacactttt 240
gaaagagaag gcaaacaggt gttagagggg caagaatgtg agctcgagga aaagacagct 300
acgaactgtg tttttaacaa ctcattattt ggctactata tttcccaatc tattctaaca 360
ctaacaagaa tctgtctaat taattgtgac aacatctgca aaaccatagt tacctatttt 420
ttcttccaac tcttttactg aagacagagg atcatttttt acagaaggtg attttgctaa 480
ggaatccttt aatagtatca actctgctct cctatctcgt aattcttttt gntctagtag 540
tggctttagg ttttcatgtt cctttataaa acatttttct ttttcattat ggatttcact 600
tttgctacat gtttgagata cttctttcaa cttgaattaa aagaatctga ttttcaagcc 660
ttggtttttc attagcattc ttcatttcta gaagatccag actgcanggn ctctttttct 720
ggactggaat tcttctaact cttttccttt aagaagaacc tttttcttgg ntcataggcc 780
tcttcaatta aggacttaag gtcttt 806

<210> 451
<211> 909
<212> DNA
<213> Homo Sapiens

<400> 451
ctgagctctt ccagggcaag aaatatgacg ggccagaagt ggatgtgtgg agtctggggg 60
tcattttata cacactagtc agtggctcac ttccctttga tgggcaaaac ctaaaggaac 120
tgagagagag agtattaaga gggaaataca gaattccctt ctacatgtct acagactgtg 180
aaaaccttct caaacgtttc ctggtgctaa atccaattaa acgcggcact ctagagcaaa 240
tcatgaagga caggtggatc aatgcagggc atgaagaaga tgaactcaaa ccatttgttg 300
aaccagagct agacatctca gaccaaaaaa gaatagatat tatggtggga atgggatatt 360
cacaagaaga aattcaagaa tctcttagta agatgaaata cgatgaaatc acagctacat 420
atttgttatt ggggagaaaa tcttcagagc tggatgctag tgattccagt tctagcagca 480
atctttcact tgctaaggtt aggcccgagc agtgatctca acaacagtac tggccagtct 540
cctcaccaca aagtgcagag aagtgtttct tcaagccaaa agcaaagacg ctacagtgac 600
catgctggac cagctattcc ttctgttgtg gcgtatcccg aaaaggagtc agaccagcac 660
tgcagatagg tgaccctcaa agaagatggg aaatttcctt ccnggaaatc aaagtggcag 720
tgctggttgg aaggaaangg gaattgcttc cagccaggtc ccatgctttg ggnaatgcca 780
ggtaatncct aataaggcgg atattcctgg aacgccagga aaagctccac tggnccctag 840
tagtancnca gcatctggtg ggaatgacnc gaccgaaatt ncttaaggtt tgcagtggag 900
agaacttcc 909

<210> 452
<211> 672
<212> DNA
<213> Homo Sapiens

<400> 452
actgaaaaaa agtgaanttt naattatntt gtnaatnnac tnaaaaaacc ncacncaagc 60
aatgttcaca antntaaatt naaacctttt gcactaaaaa ancacaaaan ancaaacaca 120
aaaccacagg cntgaactgn aaacctgtct taactatgaa ctggncttaa ggttaattct 180
tannngccat tcantatttc nntccttggn aactgtaatg ttntagcacc ggatgatctc 240
ccgnanaggt nctagaanng acngnctgcc agngnangga gatncttccn tatacaccac 300
ttnanacnca taccgtcnan tttcanaccn acccagacgg nangcacatg gngatggggc 360
cncacnccna ctntnanggn aacggaagta gggcaggngg cgcatnggtt gcacatcttt 420
aatgtattgc attcgnaaaa aaaaggccag ntttcnatcc caggcgtgct ctngacctna 480
gactttaatn ncatgattta naanatncag nacgntattg cctaaatntt attctataca 540
tttccatcag tggttnagga aaacacttta aatgcaactn anttccacat cananncact 600
gnggttacag ntttagctca ttgggcaatt tttngaagca attttttnng aaangctntt 660
ggaatgnccc cc 672

<210> 453

<211> 834
<212> DNA
<213> Homo Sapiens

<400> 453
aagaagccaa gaagtctgaa gaaccaagaa ttcggaagaa gccgggaccc aagcccggat 60
ggaagaagaa gcttcgttgt gagagggagg agcttcccac catctacaag tgtccttacc 120
agggctgcac ggccgtgtac cgaggcgctg acggcatgaa gaagcacatc aaggagcacc 180
acgaggaggt ccgggagcgg ccctgccccc accctggctg caacaaggtt ttcatgatcg 240
accgctacct gcagcgccac gtgaagctca tccacacaga ggtgcggaac tatatctgtg 300
acgaatgtgg acaaaccttc aagcagcgga agcaccttct cgtccaccaa atgcgacatt 360
cgggagccaa gcctttgcag tgtgaggtct gtgggttcca gtgcaggcag cgggcatccc 420
tcaagtacca catgaccaaa cacaaggctg agactgagct ggactttgcc tgtgaccagt 480
gtggccggcg gtttgagaag gcccacaacc tcaatgtaca catgtccatg gtgcacccgc 540
tgacacagac ccaggacaag gccctgccct ggaggcggaa ccaccacctg ggccaccgag 600
cccctctgtg accacagacg gccaggcggt gaagcccgaa cccacctgag gacggcagtg 660
aggatgagca cctctagcag cctggacttc gcagtggctg tgtcaagcct caccccttcgt 720
gtgcacccgc atgggagggt cggagggttg cttgccgncc ttggtgctgg angcgggctt 780
ggtgtccggc tcaagtagcc ttctttgntc ttgggaccag tgggttattt tccc 834

<210> 454
<211> 703
<212> DNA
<213> Homo Sapiens

<400> 454
cccgtgtaaa taatttatta caagcataac atggagctct tgttgcacta aaaagtggat 60
tacaaatctc ctcgactgct ttagtgggga aaggaatcaa ttatttatga actgtccggc 120
cccaagtcac tcagcgtttg cgggaaaata aaccactggt cccagagcag aggaaggcta 180
cttgagccgg acaccaagcc cgcctccagc accaagggcg ggcagcaccc tccgaccctc 240
ccatgcgggt gcacacgaag ggtgaggctg acacagccac tgcggagtcc aggctgctan 300
aggtgctcat cctcactgcc gtcctcaggt gggttcgggc ttcaccgcct ggccgtctgt 360
ggtcacagag gggctcggtg gcccaggtgg tggttccgcc tccaggggca gggccttgtc 420
ctgggtctgt gtcagcgggt gcaccatgga catgtgtaca ttgaggttgt gggccttctc 480
aaaccgccgg ccacactggt cacaggcaaa gtccagctca gtctcagcct tgngtttggt 540
catgtggtac ttgagggatg cccgctgcct gcactggaac ccacagacct cacactgcaa 600
aggcttggct nccgaatgtc gcatttgggg gacgaaaaag gtgcttccgc tgcttgaaag 660
gnttggccca attnggtaca agatatagtt ccccaccttt ggg 703

<210> 455
<211> 825
<212> DNA
<213> Homo Sapiens

<400> 455
atggcaatca ggaaaaggtg ccagaacccg aggctttgga ccttccagat gacttgaacc 60
ttgacagtga agacaagaat ggtggtgagg acaccgacaa tgaagaagga gaagaagaga 120
atcctttgga gataaaagaa aaaccagaag aagcaggtca tgaagctgag gaaagaggag 180
agaccgagac cgaccagaac gaaagtcaga gtccacagga gcctgaggaa ggccccagtg 240
aagatgacaa ggcagaaggg gaagaggaaa tggacacagg agctgatgac caagatggag 300
atgctgctca gcatcctgaa gaacactctg aggagcagca gcagtctgtg gaggaaaaag 360
acaaggaagc cgatgaagaa ggtggagaga atggccctgc tgaccaaggt ttccagcccc 420
aggaggaaga agaacgggag gactctgata cagaggagca ggtgccagag gctttggaga 480
ggaaggagca tgcctcctgt gggcagactg gtgtggagaa catgcagaac acacaggcca 540
tggagctggc tggggccgca cctgagaagg agcaggggaa agaggaacac ggaagtggag 600

ctgcagatgc aaaccaggca gaaggccatg aatcgaattt cattgcccag ttggccttcc 660
agaacacacc aggaaaaaca cacagagttt taagaggaaa cctgggcagg cttgacaatt 720
gaacgttnca tgggtgatca caattgaacg tgtgcacaag aagctganga cttgtggaat 780
ccggacaggc attgccaacc aggggccagc ttaacaagcc ccagg 825

<210> 456
<211> 740
<212> DNA
<213> Homo Sapiens

<400> 456
acatcaacaa cagtggtata tgttttaata gttttcagaa tataagctgc atagcttttt 60
agaataaaaa atgatataac ttcaggtaca tgctttggga cacttggtta aacaaggaat 120
ctgtgtcttt gatgaccacc tcaaaagggt cgcagacttc acagtgtaac ttggaaacag 180
acaaggagat agatgattac atcatgacat actgcctaca aaagaacatt ctgacagaac 240
attaagtaga acagagcaca cagtttcaag tattcagcac tgctttctgg ccaagtaaaa 300
actgcctaaa gatcagtttc tttcgactgg aaaaaataga tggagctgct gagttctgga 360
cacagcgttt ctttcccaga atgagactgg ctcagtccag cttgaaagca gtgtgaggaa 420
tcactcttcc ccttgactgt taagaaaaaa aaaaatgaac taaacaaata aattactaca 480
acaacaggga ccatggcact gaatgaaata aaggggcaat caccttccca tcattgcata 540
gtctcccgaa gcagcaagtg tgaaagagga tactgaaaag ccacttcatt tttacacagc 600
ccaagggatc gtttttatng atgacctggg cacctataat gnccagttgc tttatgagaa 660
ccacacacac accacattct tcctaccctn taagagaagg taggttcctt tcacaataag 720
gaaaaccccc ccttatactt 740

<210> 457
<211> 726
<212> DNA
<213> Homo Sapiens

<400> 457
aaaatgtagt caactttatt ctccttaaac cacaaaatag agtctttggt tgtacaaaca 60
tcactagtta cagtctcgcc gaggtctcgg ctggggtggg gcagttagtt agtcacaggc 120
cagaactcct gtggggtctc tttaaaatgc taacacccag gttaaaagac ttggggcaag 180
ggtggtgctg gagctggcag ggcccccacc ccaagtctgg gggaggtgcc tgctcctcta 240
ggagggcaca gggcccaggc cacggcgccc aggccttacg gggcggcggc tgctgcacag 300
tgccacatct tcagggccca cagcgccggg tgagggcctg cccagaagca ccagagccac 360
ttctccatcc tcctcctgcg ggccagggct gggagatggt tccagggacc tcaactcctc 420
agcaaagtcc ggtgacaggc gtcccgggga ggtgctggtc tgggggccga ggtcttccac 480
aggggtgggc gacggggtgg gcccagggga aggggcctcg gccagtcgct ccaggggccc 540
ccgcgtgccc cggcctttct gggacctgct gaggaccatc tgtgctcgga gagcgtcctg 600
ttccaatgac ttcatcctgg ctggccttca caagcgcacg cttctcggnc ttcagggccc 660
cggacttcgg caaggggaca nggcacgctt cgggtgccgg tggcttccgg actttggacg 720
ccgcaa 726

<210> 458
<211> 870
<212> DNA
<213> Homo Sapiens

<400> 458
cgcggcctct ccgccgggtg taccacctgt cgcggcgcga gacctctggt gaaagaaaag 60
atgttgtccc ggttaagagt agtttccacc acttgtactt tggcatgtcg acatttgcac 120
ataaaagaaa aaggcaagcc acttatgctg aacccaagaa caaacaaggg aatggcattt 180
actttacaag aacgacaaat gcttggtctt caaggacttc tacctcccaa aatagagaca 240

caagatattc aagccttacg atttcataga aacttgaaga aaatgactag ccctttggaa 300
aaatatatct acataatggg aatacaagaa agaaatgaga aattgtttta tagaatactg 360
caagatgaca ttgagagttt aatgccaatt gtatatacac cgacggttgg tcttgcctgc 420
tcccagtatg gacacatctt tagaagacct aagggattat ttatttcgat ctcagacaga 480
ggtcatgtta gatcaattgt ggataactgg ccagaaaatc atgttaaggc tgttgtagtg 540
actgatggag agagaattct gggtcttgga gatctgggtg tctatggaat gggaattcca 600
gtaggaaaac tttgttgnat cagcttgtgc aggaatacgg cctgatagat gcctgccagt 660
gtgtattgat gtgggaactg ataatatcgc actcttaaaa ganccatttt acatgggctt 720
gaccagaaac gagatcgcac ccacagttga tganctgatg gatgagttta tgaaagcttt 780
actgacagat atggccggaa cacctttatt cagttcgaag acnttggaaa tcataangcc 840
ttcaggtctt tgagaaagtc cggggaaaaa 870

<210> 459
<211> 761
<212> DNA
<213> Homo Sapiens

<400> 459
aaatgtaaga tatttattaa ataaaaaggt tacactatga tttttataca ctgttgaaaa 60
caatgacttt tatttactta aagccagcag tagttcccat tactctcata atgttatagt 120
taaggcttga tttagttcca gaaaataaat agggtaaatt tttaatattt ccctagctct 180
gtctgctata gggaatttca gagtatgaag gtaagatgaa gcagatatat aagaacattt 240
ttagataatg acaatttttc cttaaaattt ggtgaaaatt tagtttcttc tcaaaattct 300
gtacttctat ccataaaagt aaatttctat tttagtagct ctgtaagaac taggccagag 360
aagagtatta cccataatag taaatagcaa atactttggc aagtctgaat tagagtacaa 420
gtgaagacat tcacaaacac actttttaca tctcctggat gtggtacggg ctgtatgtta 480
gaattaaagc atcacaacta tctgattgta gggtgctggt gggcaatgca atcaatcaac 540
acgtctaccc caacagatgt ggagacccat ggaaaaaata catcaaccaa agtggtcagg 600
gagaacaaaa ccccagaaaa caccccttaaa actgaagaca ttatctcttc ttggctgaaa 660
aaaggggttc cctggagcac angaaaggtt ttatcaaggg aggcttctat tcngtaatca 720
caggaaggct tgatgcanat tcctggccat tcatacccca t 761

<210> 460
<211> 876
<212> DNA
<213> Homo Sapiens

<400> 460
ctgagctcct gaagcgccct aaggagtaca ctgtgcgctt cacttttcca gacccccac 60
cactcagccc tccagtgctg ggtctgcatg gtgtgacatt cggctaccag ggacagaaac 120
cactctttaa gaacttggat tttggcatcg acatggattc aaggatttgc attgtgggcc 180
ctaatggtgt ggggaagagt acgctactcc tgctgctgac tggcaagctg acaccgaccc 240
atggggaaat gagaaagaac caccggctga aaattggctt cttcaaccag cagtatgcag 300
agcagctgcg catggaggag acgcccactg agtacctgca gcgggggcttc aacctgccct 360
accaggatgc ccgcaagtgc ctgggccgct tcggcctgga gagtcacgcc cacaccatcc 420
agatctgcaa actctctggt ggtcagaagg cgcgagttgt gtttgctgag ctggcctgtc 480
gggaacctga tgtcctcatc ttggacgagc caaccaataa cctggacata gagtctattg 540
atgctctagg ggaggccatc aatgaataca agggtgctgt gatcgttgtc agccatgatg 600
cccgactcat cacagaaacc aattgccagc ttgtgggtgg tggaggaaca gagtggtagc 660
ccaatcgatg gtgactttga agactacaag ccgggaggtg ttggaagccc tgggtgaagt 720
catgggcagc cnggccccga naagtgaagc tttnctttcc agaagtntcc gagagaacat 780
aattgggggg gcctaaaann cctctggggg cttcccttct tttgaanaat gctntggnct 840
gcaantgact tggcaaccat ttaggcccct taaagg 876

<210> 461

<211> 689
<212> DNA
<213> Homo Sapiens

<400> 461
gcaaacaaga tccatttagt ggggaagagg ggactattaa aagctgctag aaaactgaat 60
aaagcaaatc aagactgaga acagttccaa ctcccatcaa tctccaaaca gtgacaggtc 120
ggcagcaact cctttccttt atttcttccc cttgtaaagg gaaattcaag ttcagcagca 180
ttcctttcct gccccaagtc ctcaaccaga caagaggctg caggcaccaa atcttgggct 240
ggataatggc aaaggcctca gaagctcacc tccagctctg agcttcaaca gctgtttgta 300
ccagtgagtc agcattaaat ccaccagaaa agaacagcac cacccaaaga ctgggggca 360
gctgggcctg aagctgtagg gtaaatcaga ggcaggcttc tgagtgatga gagtcctgag 420
acaataggcc acataaactt ggctggatgg aacctcacaa taaggtggtc acctcttgtt 480
tgtttagggg gatgccaagg ataaggccag ctcagttata tgaagagaag cagaacaaac 540
aaagtctttc agagaaatgg atgcaatcag aagtgggatc cccggncaca tcaaggtcac 600
actccacctt catgtgcctg aaatggttgc caggtcagct gcaggcccan aggcagtctt 660
canaaggaag gggagaccac agaggactt 689

<210> 462
<211> 840
<212> DNA
<213> Homo Sapiens

<400> 462
aggagccttt ggagttccat gccaagcggc cttggcgccc cgaggaggca gtagaagatc 60
cggacgagga ggatgaggat aatactagtg aagccgagaa tgggttctcc ctggaggaag 120
tgttacggct cggaggcacc aagcaagatt accttatgct ggctactttg gatgagaatg 180
aggaagtgat agatggaggc aaaaaaggag caatcgatga ccttcagcaa ggtgaattgg 240
aagcatttat tcaaaatctt aatttggcga agtatacaaa agcttcctta attgaagaag 300
atgaaccagc tgaaaaagaa aattccagca aaaaagaagt aaaaatacct aaaataaata 360
ataaaaatac agcagaaagt caaaggacat cagttaataa ggtgaaaaat aagaataggc 420
cagaaccaca ttctgatgag aatggcagta ccacaccgaa agtaaagaaa gataaacaga 480
acatctttga attttttgag agacagactt tgttacttag gcctggaggc aaatggtatg 540
atctggagta cagcaatgaa tattctttga aaccccagcc tcaggatgtt gnatctaagt 600
acaaaaccct tgctcagaag ctgtatcagc atgaaatcaa cttattcaaa agtaagacga 660
atagtcaaaa gggagcctct tctacctgga tgaaaggcaa ttgtgtcatc ggggaccact 720
aggtgacagg atggcagcca ttgattcttc ttattcagga tgatgcccgt tcacaccact 780
ttcagnttgt agnaaactct tggggaaccc ttggtaaaaa ggaanggcna caaaacagca 840

<210> 463
<211> 784
<212> DNA
<213> Homo Sapiens

<400> 463
agatgtaagt agaattttaa tctataattt acattaataa ctcatttcct ttgtttttta 60
gtttttgag tggttttaat cctcttcttt ttaaaatgtt tctttttctt gatgatactt 120
tttgcatctc tgttgtgtag ccagtcatca cgttcagcct cccatctaag ctgtttgaga 180
cttgcattat ctttgttagc catggcattc atgccaatgt tatcaaactt ggatcccata 240
ttttcatcca atagatggcc aaactcttca gcagatacaa ataggctgga atcatttaag 300
tttcttttct tttttcttgg cccttgaaat gagccagcaa agtcaaaatc atctgtacct 360
tttctcttgc ttttcttagt actgactttg gagtggactt caagttctgg aacactctca 420
ctttcatcat ctaacacatc catgaatgtt cctccatctt catcaacttc agcaaattct 480
tcatcatcca tacttcctaa agaaacttca tcgtcatcca ggttaccaag ttcatcatca 540
ctaccttctg aatcttcatc taatgtgtta tccttagctc cttttggtct ctttttcacg 600

tttccagcaa aaatccatat catcctttnc agagctgaaa cagttatcat cttcaaatgt 660
gtcaatcagc tcttcaaatt ctttcatcat ccacgtcctt ctaatacttt cttcaatctg 720
catccccgtt tttggnttct cttttaanca gcaacttttt ttatnaaacc ctgggggaaa 780
aaac 784

<210> 464
<211> 850
<212> DNA
<213> Homo Sapiens

<400> 464
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ctgagggccc aggcaaggag aaggagctgc ctggacagac cctgcactgg gggcccgagg 120
ccacagaagc cgcaggtcgg ggtctgcagc ccctgaagct ggactaccgc gccctggccg 180
ccgtgcccag cgctggcagc gtgcagaggg taccgtctgg agcagctgga gggaagatgg 240
ctgaatctcc ctgctcccct agtggccagc agccgccctc cccgccttct ccggatgagc 300
tgcccgccaa tgtgaagcag gcctacaggg ccttcgcggc cgtgcccact tctcacccgc 360
ctgaggatgc ccctgcccag cccccccacgc ctgggcctgc agcctccccg gagcagctgt 420
ccttccggga gcggcagaag tactttgagc tggaggtgcg cgtgccccag gccgagggcc 480
cccctaagcg cgtgtccctg gtgggtgctg acgacctgcg gaagatgcag gaggaggaag 540
ccagaaaact acagcagaag agagcgcaga tgctgcggga ggcggcagaa gctggggccg 600
aagcgaggct ngccctggac ggggagacgc tgggcgagga ggaacaggan gatgagcagc 660
caccctgggc cagcccgagc cccacttaag gcagaacccg gcgtcccccc ggccctggaa 720
gtggcgcccc ggtgcggacg gncaaaagct gaacggggcc ancaggaacc ggttgccctt 780
canagtnccg gacccaccgg gaccccancg tgccctggtc ccttgcccaa cttccgggcc 840
ctggaaggcc 850

<210> 465
<211> 759
<212> DNA
<213> Homo Sapiens

<400> 465
aaaatgtagt caactttatt ctccttaaac cacaaaatag agtctttggt tgtacaaaca 60
tcactagtta cagtctcgcc gaggtctcgg ctggggtggg gcagttagtt agtcacaggc 120
cagaactcct gtggggtctc tttaaaatgc taacacccag gttaaaagac ttggggcaag 180
ggtggtgctg gagctggcag ggcccccacc ccaagtctgg gggaggtgcc tgctcctcta 240
ggagggcaca gggcccaggc cacggcgccc aggccttacg gggcggcggc tgctgcacag 300
tgccacatct tcagggccca cagcgccggg tgagggcctg cccagaagca ccagagccac 360
ttntccatcc tcctcctgcg ggccagggct gggagatggt tccagggacc tcaactcctc 420
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ccgcgtgccc cggcctttct gggacctgct gaggaccatc tgggctcngg aaagcgtcct 600
tgttccaatg acttcatcct ggctgcccctt cacagngcac gcttntcggc ttcagggccc 660
ggagctttgg cangggggaca aggcaacgct tcgggtgccc ggtgggttcc ggacttttga 720
acgcgccaan ccggttcctt ggngggcgcc cgtttcaac 759

<210> 466
<211> 1240
<212> DNA
<213> Homo Sapiens

<400> 466
gtggtagtgg tgccggagct ggaggcggag gcatgtttgg tagtggcggt ggaggagggg 60
gcactggaag tacaggtcca gggtatagct tcccacacta tggatttcct acttatggtg 120

ggattacttt ccatcctgga actactaaat ctaatgctgg gatgaagcat ggaaccatgg 180
acactgaatc taaaaggac cctgaaggtt gtgacaaaag tgatgacaaa aacactgtaa 240
acctctttgg gaaagttatt gaaaccacag agcaagatca ggagcccagc gaggccaccg 300
ttgggaatgg tgaggtcact ctaacgtatg caacaggaac aaaagaagag agtgctggag 360
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<210> 467
<211> 885
<212> DNA
<213> Homo Sapiens

<400> 467
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tccatcctgg aactactaaa tctaatgctg ggatgaagca tggaaccatg gacactgaat 180
ctaaaagga ccctgaaggt tgtgacaaaa gtgatgacaa aaacactgta aacctctttg 240
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caaaaanggc agcactactt tnttgaccac cccaacggg ggacggtctt gaatgccatt 840
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<210> 468
<211> 748
<212> DNA
<213> Homo Sapiens

<400> 468
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atgctgtggt cagaaggaat gccaggtggc gaccgtgata cctttaatga caataggaac 180
gtagcagagg gacaacagca atgacaacag aaagcagctg tgatccagca gcagctggca 240
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tgagtttgcg gaaggatgtc tccacgccgc ttgtcgcaga cactgtcact ggcttcggag 660
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gngggcnttc actggctgg aaggcttg 748

<210> 469
<211> 770
<212> DNA
<213> Homo Sapiens

<400> 469
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atgctgtggt cagaaggaat gccaggtggc gaccgtgata cctttaatga caataggaac 180
gtagcagagg gacaacagca atgacaacag aaagcagctg tgatccagca gcagctggca 240
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atactatctg taagtgaacc aaactaaaat tcatttatga accaagaaag gaagccaagt 360
tgaaaaggtc tcgagttaaa tcgagaatga ttcaggcggg ccggctctct gagcaccttt 420
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tgggagctcn gctattttgc ttgcccttgt ggangcaggc caaaanaagc caacgaatgg 720
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<210> 470
<211> 892
<212> DNA
<213> Homo Sapiens

<400> 470
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agcgccatct cactgctgtg caggatgaga atggggacag tgtcttacac ttagcaatca 180
tccaccttca ttctcaactt gtgagggatc tactagaagt cacatctggt ttgatttctg 240
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ctaagcagga agatgtggtg gaggatttgc tgagggctgg ggccgacctg agccttctgg 360
accgcttggg taactctgtt ttgcacctag ctgccaaaga aggacatgat aaagttctca 420
gtatcttact caagcacaaa aaggcagcac tacttcttga ccaccccaac ggggacggtc 480
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ccttctatga cctggatgac tcttgggaaa atgcaggaaa aggattgaag gagttggnct 840
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<210> 471
<211> 759
<212> DNA
<213> Homo Sapiens

<400> 471

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atgctgtggt cagaaggaat gccaggtggc gaccgtgata cctttaatga caataggaac     180
gtagcagagg gacaacagca atgacaacag aaagcagctg tgatccagca gcagctggca     240
aagcttagta agcaacctca tccccagatg catccgctca gccagtgttg tgattgctag     300
atactatctg taagtgaacc aaactaaaat tcatttatga accaagaaag gaagccaagt     360
tgaaaaggtc tcgagttaaa tcgagaatga ttcaggcggg ccggctctct gagcaccttt     420
ggatgcactt cagcttctgt cttgtggaca acgcagtgga attttagggc tttggtttac     480
acggtgtggg aaattgtcag caggctaaat tttgccttct agaggtcctt cctgcccata     540
atcatggggc atttgttga gagttagcag tgaggcacca ctggtcagag actcggtaaa     600
gctgagtttg cggaaggatg tctccacgcc gctgtccgca gacactgtca ctgnctcgga     660
gctcgtctat ttgctgcctt gtggaggcag gcgananagg caacgagtgg gccctgaaaa     720
gnggtcttca ctgggctgga agcttgnctg gatcacttt                            759
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<210> 472
<211> 852
<212> DNA
<213> Homo Sapiens

<400> 472

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gcactggaag tacaggtcca gggtatagct tcccacacta tggatttcct acttatggtg     120
ggattacttt ccatcctgga actactaaat ctaatgctgg gatgaagcat ggaaccatgg     180
acactgaatc taaaaaggac cctgaaggtt gtgacaaaag tgatgacaaa aacactgtaa     240
acctctttgg gaaagttatt gaaaccacag agcaagatca ggagcccagc gaggccaccg     300
ttgggaatgg tgaggtcact ctaacgtatg caacaggaac aaaagaagag agtgctggag     360
ttcaggataa cctctttcta gagaaggcta tgcagcttgc aaagaggcat gccaatgccc     420
ttttcgacta cgcggtgaca ggagacgtga agatgctgct ggccgtccag cgccatctca     480
ctgctgtgca ggatgagaat ggggacagtg tcttacactt agcaatcatc caccttcatt     540
ctcaacttgt gagggatcta ctagaagtca catctggttt gatttctgat gacattatca     600
acatgagaaa tgatctgtac cagacgccct ttgcacttgg cagtgatcac taagcaggaa     660
gatgtggtgg aggatttgct gaagggctgg ggcccgacct tgagcctttc tggacccgct     720
tgggtaactc tgttttgcac cctaacttgc caaagaaggg cattgataaa ggtcttcaag     780
tatcttactt cagcccaaaa anggcagcac tacttntttg accaccccaa cgggggacgg     840
gcttgaatgc ca                                                         852
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<210> 473
<211> 804
<212> DNA
<213> Homo Sapiens

<400> 473

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atgctgtggt cagaaggaat gccaggtggc gaccgtgata cctttaatga caataggaac     180
gtagcagagg gacaacagca atgacaacag aaagcagctg tgatccagca gcagctggca     240
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tgaaaaggtc tcgagttaaa tcgagaatga ttcaggcggg ccggctctct gagcaccttt     420
ggatgcactt cagcttctgt cttgtggaca acgcagtgga attttagggc tttggtttac     480
acggtgtggg aaattgtcag caggctaaat tttgccttct agaggtcctt ccttgcccat     540
aatcatgggg catttgttg agagttagca gtgaggcacc acttggtcaa gagactcggt      600
naagctgagt tttgcggaag gatgtctcca cgcccgctgt cgcagacact gtcactgtct     660
tcggaactcg nctatttgct gncttgtgga agcaggcnaa nanaagcanc gaantggggc     720
cctgaaaagn gggtcttcac ttggnctgga aggcttgccc tgggatcnct ttnaatgggc     780
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ttcggnggaa ccccattttg tctt 804

<210> 474
<211> 819
<212> DNA
<213> Homo Sapiens

<400> 474
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gcctagcggg aaaagtaaaa gatgtctgaa tatattcggg taaccgaaga tgagaacgat 120
gagcccattg aaataccatc ggaagacgat gggacggtgc tgctctccac ggttacagcc 180
cagtttccag gggcgtgtgg gcttcgctac aggaatccag tgtctcagtg tatgagaggt 240
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gttgtcaact atccaaaaga taacaaaaga aaaatggatg agacagatgc ttcatcagca 360
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aaaacaaccg aacaggacct gaaagagtat tttagtacct ttggagaagt tcttatggtg 480
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gaatatgaaa cacaagtgaa agtaatgtca cagcgacata tgatagatgg acgatggtgt 600
gactgcaaac ttcctaattc taagcaaagc caagatgagc ctttgagaag cagaaaagtg 660
tttgtggggc gctgtcagag gacatgactg aggatgaagc tgcgggagtt cttcttttca 720
gtancgggga tgtgatggat ggtcttcatn cccaagccat tcagggcctt tggctttggt 780
catttgcaga tgaatcagat gcgccagtct ctttgtgga 819

<210> 475
<211> 721
<212> DNA
<213> Homo Sapiens

<400> 475
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gcacaggaca cagaactgca gcaaacagca ttcttatggg tagctaacag acattagaac 120
ttccaccctt ctttgagaca cctgagctca ctggtgaact ctgcttcaag tcctcctgca 180
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attcgtacat tatttgctat cattgctctc tgcacactct ctcaccaaag ccacaggatt 480
gagagacaca tctcgccaag ttaaaaaata tccattatgc accaccaagt ctctgcacgc 540
gctctctcct tttctcgctc atactagcct ttcatgcctc ggcaccacca tcaatcccac 600
acaaggtttc aaaagttcag acagccttct ggttccatat cacaggcctt gcgttcatag 660
cggtgatacg acttcctgga aattaagagt ancggataaa aatgggacac ccaccggtaa 720
a 721

<210> 476
<211> 442
<212> DNA
<213> Homo Sapiens

<400> 476
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ncncaggacn canancngca gcaancagcn ttntnanggg tagntancan acnttaaanc 120
ttccaccntt ntttganacn ccnganctna nnggggganct nngnttcang ncctccngca 180
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nttncntatc agtaccagaa gagaccncnc nccntncagc nttcncagca gtngncaaag 300
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naccaaaanc tcanttaaan gtnttccanc anangnggan gnccttngaa ngcaaaaanc 420
nttcgnccat nattggctat ca 442

<210> 477
<211> 878
<212> DNA
<213> Homo Sapiens

<400> 477
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gcggcctagc gggaaaagta aaagatgtct gaatatattc gggtaaccga agatgagaac 120
gatgagccca ttgaaatacc atcggaagac gatgggacgg tgctgctctc cacggttaca 180
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tggaaaacaa ccgaacagga cctgaaagag tattttagta cctttggaga agttcttatg 480
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ttaaagggaa tcagcggttc attatattcc aatggccc 878

<210> 478
<211> 768
<212> DNA
<213> Homo Sapiens

<400> 478
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ttcaaaatct tcttagggta aaataaatac ccgtatctat gcagtaccat aaacatgtta 180
ataaaaggcc actcaacatt gaaagccttc tatgaccagt aactgaaatt tacacaagtg 240
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<210> 479
<211> 815
<212> DNA
<213> Homo Sapiens

<400> 479
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tcgttttacg gaatatgaaa cacaagtgaa agtaatgtca cagcgacata tgatagatgg    600
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<210> 480
<211> 812
<212> DNA
<213> Homo Sapiens

<400> 480

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cttcaaaatc ttcttagggt aaaataaata cccgtatcta tgcagtacca taaacatgtt    180
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tgctgagtaa tagtgcaagt gcattttagg tgcggtcacc cagacttatt caaaactaga    420
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ctgggtatca ggtgtcaatg catgacaggt gatgaatcca tttgacttga gacaactttt    540
caaataagtt tatttgaagc aaaataaact actgccaaga aactttatga aaagttccat    600
cttcaaaagg ggtcaaaaaa ggggaattaa ctgctatgaa ttctttgcat tcanggctgc    660
aaaacaaaga ccccatatta tttaaaatcc agtttattta agaatttncc accntggaca    720
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<210> 481
<211> 1127
<212> DNA
<213> Homo Sapiens

<400> 481

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gagaatccga agaagaaaat ctcaataaat ctgaaataag tcaagtgttt gagattgcac    180
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agccacagac aagcccagaa tatggccagg ggatcaatcc gattagccga ctggcccaga    480
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cgcgccgcag ggagtttgtg atgcaggtga aggttggaaa ccacactgca gaaggaacgg    600
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tgatagcccg agagttgttg tatgggggca cctcgcccac agcccgagac cattttaaag   1020
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aataacatct cttcaggcca cgtaccccat ggacctctca cgagaccctn tgagcaactg 1080
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<210> 482
<211> 773
<212> DNA
<213> Homo Sapiens

<400> 482
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cccagatcca gcaggcaaaa aaggagaagg agccagagta cacgctcctc acagagcgag 180
gcctcccgcg ccgcagggag tttgtgatgc aggtgaaggt tggaaaccac actgcagaag 240
gaacgggcac caacaagaag gtggccaagc gcaatgcagc cgagaacatg ctggagatcc 300
ttggtttcaa agtcccgcag gcgcagccca ccaaacccgc actcaagtca gaggagaaga 360
cacccataaa gaaaccaggg gatggaagaa aagtaacctt ttttgaacct ggctctgggg 420
atgaaaatgg gactagtaat aaagaggatg agttcaggat gccttatcta agtcatcagc 480
agctgcctgc tggaattctt cccatggtgc ccgaggtcgc ccaggctgta ggagttagtc 540
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ctgccatgat agcccgagag ttgttgtatg gggcacctc gcccacagcc cgagaccatt 660
ttaaagaata acatctcttc aggccacgta ccccatggac ctctcacgag accctntgag 720
caactggact atctttncag agtccaggga ttncaggttg aataccaaga ctt 773

<210> 483
<211> 794
<212> DNA
<213> Homo Sapiens

<400> 483
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ggcaagttgg gaggggacca acctagcagt agnggcattt ganaataaat tancaaaaaa 180
atttagtatt accattnatt gatgacaaac acttaagttt tacttacatt ccatggggag 240
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caaaagcaac acagntgtat acagaaacgt aggtcattct tttcagccct aanggagatg 420
taattaacag tatcgagcac tntggaaaat cactctgcag gtttatatgg actacatgga 480
gatcatatcc tgtagtgtag tgaaagctaa gtcctcaaga gccatatgta tagatncaca 540
atgtttttta ataatcttta aaacagagat caaagttcat ttaagncctg tttgcattac 600
caaaaataaa aatgaaataa aaatggaacc aaatgaacat ctaangttta aaattcctaa 660
atnggccaat ttatncaact ggnggggaga cttattcaag ggttttgaaa gtccaggaac 720
tggtttcaag ctggaaccca gggggcccc acaatttggc attcnctgga aactggccct 780
ggggttaagc caaa 794

<210> 484
<211> 788
<212> DNA
<213> Homo Sapiens

<400> 484
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gttcaaaggt ccagagactt ctgagtatgt tgatggatgt aaaaacatgc aatgaggtgg 180
acctggagaa ttctgcagat tgggaagtga agacaataac aagtgccttg aaacagtatt 240
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ccaaaagcgg cagcccagaa tctcgtgtta atgcgatcca tttcttggta cacaaactgc 360
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tgaggccaca ggaagaaact gtcgctgcct catggacttg aagtttcaga atattgttgt 540
ggaaatctta attgaaaacc atgaaaagat ttttcggacg ccgnccgata ctacattccc 600
tgagcccacc tgcctgtcag catcaccccc aaatgcgcca ccaangcagt cnaagagaca 660
aggncagaga accaagaagg cccgtgggcc gtctacaatc tttggctgga gctggaaaga 720
tggtgacaat ccttaccctt tccanggagg acacccctta ccacagtctg gactcacttt 780
tcttcccg 788

<210> 485
<211> 430
<212> DNA
<213> Homo Sapiens

<400> 485
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agtgcagtga gtgtggggtc ctgcaggtgg ccgtctagga agggcaggct tgagacgcgc 180
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taggctgcca cagccaagca cacactctgc aaacctatca ctgcgagtng tacagttccc 300
tttanaatcg nagcagcang tgctcaggga ggagagggag ccnnngtggc tctggtggcg 360
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atgctgngat 430

<210> 486
<211> 831
<212> DNA
<213> Homo Sapiens

<400> 486
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ttatggtgac aaaaccagtg caggaatata aaaggaata cacagtgcag caggccttgt 120
tttgtacttc tggaattgtt acttctatac cggtgccctt ggcaggaagt gcccttctcc 180
catatcatat ttcatctact gcatgtcagg ccaaggctca tctgtcatct gatgatagta 240
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ttattagcaa cttttctgca gcagtggtgc atacgatagt aaatgaaact ttagagtcaa 480
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taaaggagaa aacccctcca ttttcccact gtgatcaggc agtgctgcaa tgcagtgaag 600
ctagtagcaa taaggacatg tttgctgacc ggttatctaa atctattatt aaacattcca 660
tagataagag caaatcagtg atcccaaata tagataaaaa tgcagtatac aaggaaagct 720
tgcctgtttc tggagaagaa tcacagttga cacccagaaa agtcttncca aatttnctga 780
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<210> 487
<211> 728
<212> DNA
<213> Homo Sapiens

<400> 487
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atctctgcct cccaggttca agcaattctc ctgccttagc ctcccaagta gctgggatta 120
caggtgcctg ccaccacgcc tggctaattt ttgtattttt ggtagagacg gggtttcacc 180

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cttcccagag ttctgggatt acaggcgtga atcaccgcgc ccagcccaaa tcgccgaagt     300
ctttatctcc taccttgatc tctgtagcag aaaagaacag tatagatatc aattgtcatc     360
aacagatgca acatatcttg taaatcaata tattttcaag tgaggtctct gaatcacctg     420
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caatcctgga tgagccccgc tttttctctg tgccagaacc ttaatgccac gcagcattac     600
attaagtcac attacaactt tggtcaatgg aaacacaggg tctttttctg acaaaatgcc     660
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taaaatgc                                                              728
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<210> 488
<211> 788
<212> DNA
<213> Homo Sapiens

<400> 488

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tggacttcac ccaggaagaa tggtaccatg tcgaccctgc tcagaggagc ttatacaggg     180
atgtgatgct ggagaactat agccacctgg tttctcttgg atatcaagtt tccaagccag     240
aggtgatctt caaattggag caaggagaag agccatggat atcagaggga gaaatccaac     300
gacctttcta tccagactgg aagaccaggc ctgaagtcaa atcatcacat ttgcagcagg     360
atgtatcaga agtatcccac tgcacacatg atctcttaca tgctacatta gaagactcct     420
gggatgttag cagccagtta gacgggcaac aggaaaactg gaagagacat ctgggatcag     480
aggcatccac ccagaagaaa ataattacac cacaagaaaa ttttgagcaa aataaatttg     540
gtgaaaattc tagattgaac accaatttgg ttacacaact gaacattcct gcaagaataa     600
ggcctagtga atgtgagacc cttggaagca atttgggaca taatgcagac ttacttaatg     660
agaataatat tcttgcaaaa aagaaaccct tttagtgnga taatgtagaa aagnctttan     720
tcatagatca tcgnttacta aaccttgaga aaacccctta anggaaaagg gagctttcct     780
aatgggac                                                              788
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<210> 489
<211> 875
<212> DNA
<213> Homo Sapiens

<400> 489

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gttaattttt ttaatggtga aatcttttct ttgcacataa aatgagccag tgcatgttgc     180
ttctctgagt acaagacaaa atttatggca atgggcaatt agacttatac ttttctgcaa     240
gaaaattaac gggaaaattc tcctcttagt tttctgttgt tttcccattg atctgatact     300
gtaggcttaa gaaagtgctt tttcatgggc atgccataaa aagtacaata aggggactta     360
atagttctgt gaaactggca tatgttagct gaaagtataa ttgtaactgg gaaaagggga     420
aaaaagtcac tagtagttca accatctaca gtttctgtta aattgtggtt tgtaagcctc     480
caagaagttg ctttaaatag tttgtgataa atttgcatac attttgctcc cacttatact     540
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atcttaaaat ttattttaaa gccctctgag tcccaaaaat aacctttca ctggcaaggc     660
catgggggccc caaatccagg aaaccctggc atttttaacc caacttttac ccttataggc     720
tggaatcata ctgngggaaa cccacttcac atcttttggc tttcagtctt caatctgncc     780
cnaatggaaa atgggttggg cctagttgga actaaattct tttgaatggg ggactttcct     840
ggaaattggg aactnggttt ccatgggga aagtt                                 875
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<210> 490

<211> 844
<212> DNA
<213> Homo Sapiens

<400> 490
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gtggcccacc ccacatgaag aactttgtga ccaaggtttc ggttggggag tttgtggggg 120
aaggtgaagg gaaaagcaag aagatttcaa agaaaaatgc cgccatagct gttcttgagg 180
agctgaagaa gttaccgccc ctgcctgcag ttgaacgagt aaagcctaga atcaaaaaga 240
aaacaaaacc catagtcaag ccacagacaa gcccagaata tggccagggg atcaatccga 300
ttagccgact ggcccagatc cagcaggcaa aaaaggagaa ggagccagag tacacgctcc 360
tcacagagcg aggcctcccg cgccgcaggg agtttgtgat gcaggtgaag gttggaaacc 420
acactgcaga aggaacgggc accaacaaga aggtggccaa gcgcaatgca gccgagaaca 480
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taagtcatca gcagctgcct gctggaattc tttccatggt gcccgangtc gcccaagctg 720
taggaagtta gtcaaggaca tnacacccaa gattttacca ggcagcttcg aatcttgcca 780
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ggga 844

<210> 491
<211> 825
<212> DNA
<213> Homo Sapiens

<400> 491
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ttgcccagat ggaatcacaa gcattacaaa gttttttctt aaaaataaaa aaaggatagg 120
ggcaagttgg gaggggacca acctagcagt agtggcattt gagaataaat taacaaaaaa 180
atttagtatt accatttatt gatgacaaac acttaagttt tacttacatt ccatggggag 240
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tccatacgga ccacacgcag agcctcagtg cacacacttc tgtgtacagt aacacaacat 360
caaaagcaac acagctgtat acagaaacgt aggtcattct tttcagccct aatggagatg 420
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aatggtccaa tttatacaac tgggggagac ttattcaagg tttttgaaag tccaggactg 720
gtttcagctg aaccagangg cccccaattt gcatcactgg aactgncctg ggtttagcca 780
aggaaattaa aaaagnctta acccccttcc cctgggattt gaacc 825

<210> 492
<211> 946
<212> DNA
<213> Homo Sapiens

<400> 492
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gagaatccga agaagaaaat ctcaataaat ctgaaataag tcaagtgttt gagattgcac 180
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agaagatttc aaagaaaaat gccgccatag ctgttcttga ggagctgaag aagttaccgc 360
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agccacagac aagcccagaa tatggccagg ggatcaatcc gattagccga ctggcccaga 480
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atgggcttgt antaaagagg atgagttcag gatgncntat ctaagtcatn aacacttgct 840
gctggaaatc tttccatggg ggccgaggtc ncccagcttt taggagttat canggccntt 900
ccncccaaga attttcccgg gcagtttcca atctgccaag gccccg 946

<210> 493
<211> 804
<212> DNA
<213> Homo Sapiens

<400> 493
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ttcctgattt tgcatgttct cattcccaaa gtagtctacc ttagtttaca ctcaaaggta 180
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gtaagagaaa gcccaatccn ggaatggagt tcntccattt tcagactaac cctgggcncn 720
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nggnaagtaa ttngctttgg gtaa 804

<210> 494
<211> 856
<212> DNA
<213> Homo Sapiens

<400> 494
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ttcttcccct ttgggaccag catgaaacaa ggtggctttt ccttcaaagc caccggatga 780
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gatacccggg aacttc 856

<210> 495
<211> 757

<212> DNA
<213> Homo Sapiens

<400> 495
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gttcaaaaac tttgctttta ttacgaagaa catntggact gtagacacct ntaacgaaac 240
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tattctttca taatcaaatc tttcaatgga tttctaagac tggnttctac agcctgngng 660
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<210> 496
<211> 1759
<212> DNA
<213> Homo Sapiens

<400> 496
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accaggaaga gcagctgaca gtgaattcaa aggcattaga gattcttgac aagatttctc 180
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caaagaccaa gaccctgaga gagggaatca ttgtcactgg aaagcggctg ggactctgg 960
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acctgacaga aagcattttg agaggaattt tctctgttcc tggaggacac aatctctact 1380
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angaaaggga aaaccntntc agagagcctt gaaaaggttg ctaaaacaca agcttgaagg 1740
tncagaagaa aatgcttaa 1759

<210> 497
<211> 842
<212> DNA
<213> Homo Sapiens

<400> 497
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<400> 514

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<211> 790
<212> DNA
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<211> 747
<212> DNA
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<212> DNA
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<211> 789
<212> DNA
<213> Homo Sapiens

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<211> 827
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<213> Homo Sapiens

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<211> 710
<212> DNA
<213> Homo Sapiens

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<210> 522
<211> 638
<212> DNA
<213> Homo Sapiens

<400> 522
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<211> 833

<212> DNA
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<212> DNA
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<211> 837
<212> DNA
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<212> DNA
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<212> DNA
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<212> DNA
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<212> DNA
<213> Homo Sapiens

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<211> 789
<212> DNA
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<211> 901
<212> DNA
<213> Homo Sapiens

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<211> 761
<212> DNA
<213> Homo Sapiens

<400> 537

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ttcaaatcca tattttatct gaaatacatt tcctgcaaca aaacattatt agaagagtta     180
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<211> 869
<212> DNA
<213> Homo Sapiens

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gnagatgtcc ccaggatgtc ctggaagtat gttggantcg aaaagcagnt tgccaaancc     780
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catcctttaa aacggggatg atcccttgg 869

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<212> DNA
<213> Homo Sapiens

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<211> 874
<212> DNA
<213> Homo Sapiens

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<211> 729
<212> DNA
<213> Homo Sapiens

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<211> 830
<212> DNA
<213> Homo Sapiens

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<210> 543
<211> 733
<212> DNA
<213> Homo Sapiens

<400> 543
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<211> 852
<212> DNA
<213> Homo Sapiens

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<210> 545
<211> 414
<212> PRT
<213> Homo Sapiens

<400> 545
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35 40 45
Phe Leu Leu Ala Ala Asn Thr Cys Asn Arg Val Gly Gly Leu Cys Leu
50 55 60
Lys Cys Ala Gln His Glu Ala Val Leu Ser Gln Thr His Thr Asn Val
65 70 75 80
His Met Gln Thr Ile Glu Arg Leu Val Lys Glu Arg Asp Asp Leu Met
85 90 95
Ser Ala Leu Val Ser Val Arg Ser Ser Leu Ala Asp Thr Gln Gln Arg
100 105 110
Glu Ala Ser Ala Tyr Glu Gln Val Lys Gln Val Leu Gln Ile Ser Glu
115 120 125
Glu Ala Asn Phe Glu Lys Thr Lys Ala Leu Ile Gln Cys Asp Gln Leu
130 135 140
Arg Lys Glu Leu Glu Arg Gln Ala Glu Arg Leu Glu Lys Glu Leu Ala
145 150 155 160
Ser Gln Gln Glu Lys Arg Ala Ile Glu Lys Asp Met Met Lys Lys Glu
165 170 175
Ile Thr Lys Glu Arg Glu Tyr Met Gly Ser Lys Met Leu Ile Leu Ser
180 185 190
Gln Asn Ile Ala Gln Leu Glu Ala Gln Val Glu Lys Val Thr Lys Glu
195 200 205
Lys Ile Ser Ala Ile Asn Gln Leu Glu Glu Ile Gln Ser Gln Leu Ala
210 215 220
Ser Arg Glu Met Asp Val Thr Lys Val Cys Gly Glu Met Arg Tyr Gln
225 230 235 240
Leu Asn Lys Thr Asn Met Glu Lys Asp Glu Ala Glu Lys Glu His Arg
245 250 255

Glu Phe Arg Ala Lys Thr Asn Arg Asp Leu Glu Ile Lys Asp Gln Glu
260 265 270
Ile Glu Lys Leu Arg Ile Glu Leu Asp Glu Ser Lys Gln His Leu Glu
275 280 285
Gln Glu Gln Gln Lys Ala Ala Leu Ala Arg Glu Glu Cys Leu Arg Leu
290 295 300
Thr Glu Leu Leu Gly Glu Ser Glu His Gln Leu His Leu Thr Arg Ser
305 310 315 320
Glu Ile Ala Gln Leu Ser Gln Glu Lys Arg Tyr Thr Tyr Asp Lys Leu
325 330 335
Gly Lys Leu Gln Arg Arg Asn Glu Glu Leu Glu Glu Gln Cys Val Gln
340 345 350
His Gly Arg Val His Glu Thr Met Lys Gln Arg Leu Arg Gln Leu Asp
355 360 365
Lys His Ser Gln Ala Thr Ala Gln Gln Leu Val Gln Leu Leu Ser Lys
370 375 380
Gln Asn Gln Leu Leu Leu Glu Arg Gln Ser Leu Ser Glu Glu Val Asp
385 390 395 400
Arg Leu Arg Thr Gln Leu Pro Ser Met Pro Gln Ser Asp Cys
405 410

<210> 546
<211> 2885
<212> DNA
<213> Homo Sapiens

<400> 546
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aattt 2885

<210> 547
<211> 897
<212> PRT
<213> Homo Sapiens

<400> 547
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His Ser Leu Pro Gln His Pro Lys Cys Trp Gly Ala His His Ala Ser
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35 40 45
Ser Tyr Lys Leu Pro Leu Pro Gly Pro Tyr Asp Ser Arg Asp Asp Phe
50 55 60
Pro Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu Lys Val Arg Ser Arg
65 70 75 80
Leu Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg
85 90 95
Lys Asp Gly Thr Val Ile Ser Thr Phe Lys Lys Arg Ala Val Glu Ile
100 105 110
Thr Gly Ala Gly Pro Gly Ala Ser Ser Val Cys Asn Ser Ala Pro Gly
115 120 125
Ser Gly Pro Ser Ser Pro Asn Ser Ser His Ser Thr Ile Ala Glu Asn
130 135 140
Gly Phe Thr Gly Ser Val Pro Asn Ile Pro Thr Glu Met Leu Pro Gln
145 150 155 160
His Arg Ala Leu Pro Leu Asp Ser Ser Pro Asn Gln Phe Ser Leu Tyr
165 170 175
Thr Ser Pro Ser Leu Pro Asn Ile Ser Leu Gly Leu Gln Ala Thr Val
180 185 190
Thr Val Thr Asn Ser His Leu Thr Ala Ser Pro Lys Leu Ser Thr Gln
195 200 205
Gln Glu Ala Glu Arg Gln Ala Leu Gln Ser Leu Arg Gln Gly Gly Thr

210 215 220
Leu Thr Gly Lys Phe Met Ser Thr Ser Ser Ile Pro Gly Cys Leu Leu
225 230 235 240
Gly Val Ala Leu Glu Gly Asp Gly Ser Pro His Gly His Ala Ser Leu
245 250 255
Leu Gln His Val Leu Leu Leu Glu Gln Ala Arg Gln Gln Ser Thr Leu
260 265 270
Ile Ala Val Pro Leu His Gly Gln Ser Pro Leu Val Thr Gly Glu Arg
275 280 285
Val Ala Thr Ser Met Arg Thr Val Gly Lys Leu Pro Arg His Arg Pro
290 295 300
Leu Ser Arg Thr Gln Ser Ser Pro Leu Pro Gln Ser Pro Gln Ala Leu
305 310 315 320
Gln Gln Leu Val Met Gln Gln Gln His Gln Gln Phe Leu Glu Lys Gln
325 330 335
Lys Gln Gln Gln Leu Gln Leu Gly Lys Ile Leu Thr Lys Thr Gly Glu
340 345 350
Leu Pro Arg Gln Pro Thr Thr His Pro Glu Glu Thr Glu Glu Glu Leu
355 360 365
Thr Glu Gln Gln Glu Val Leu Leu Gly Glu Gly Ala Leu Thr Met Pro
370 375 380
Arg Glu Gly Ser Thr Glu Ser Glu Ser Thr Gln Glu Asp Leu Glu Glu
385 390 395 400
Glu Asp Glu Glu Glu Asp Gly Glu Glu Glu Glu Asp Cys Ile Gln Val
405 410 415
Lys Asp Glu Glu Gly Glu Ser Gly Ala Glu Glu Gly Pro Asp Leu Glu
420 425 430
Glu Pro Gly Ala Gly Tyr Lys Lys Leu Phe Ser Asp Ala Gln Pro Leu
435 440 445
Gln Pro Leu Gln Val Tyr Gln Ala Pro Leu Ser Leu Ala Thr Val Pro
450 455 460
His Gln Ala Leu Gly Arg Thr Gln Ser Ser Pro Ala Ala Pro Gly Gly
465 470 475 480
Met Lys Asn Pro Pro Asp Gln Pro Val Lys His Leu Phe Thr Thr Ser
485 490 495
Val Val Tyr Asp Thr Phe Met Leu Lys His Gln Cys Met Cys Gly Asn
500 505 510
Thr His Val His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser
515 520 525
Arg Leu Gln Glu Thr Gly Leu Leu Ser Lys Cys Glu Arg Ile Arg Gly
530 535 540
Arg Lys Ala Thr Leu Asp Glu Ile Gln Thr Val His Ser Glu Tyr His
545 550 555 560
Thr Leu Leu Tyr Gly Thr Ser Pro Leu Asn Arg Gln Lys Leu Asp Ser
565 570 575
Lys Lys Leu Leu Gly Pro Ile Ser Gln Lys Met Tyr Ala Val Leu Pro
580 585 590
Cys Gly Gly Ile Gly Val Asp Ser Asp Thr Val Trp Asn Glu Met His
595 600 605
Ser Ser Ser Ala Val Arg Met Ala Val Gly Cys Leu Leu Glu Leu Ala
610 615 620
Phe Lys Val Ala Ala Gly Glu Leu Lys Asn Gly Phe Ala Ile Ile Arg
625 630 635 640
Pro Pro Gly His His Ala Glu Glu Ser Thr Ala Met Gly Phe Cys Phe
645 650 655

Phe Asn Ser Val Ala Ile Thr Ala Lys Leu Leu Gln Gln Lys Leu Asn
660 665 670
Val Gly Lys Val Leu Ile Val Asp Trp Asp Ile His His Gly Asn Gly
675 680 685
Thr Gln Gln Ala Phe Tyr Asn Asp Pro Ser Val Leu Tyr Ile Ser Leu
690 695 700
His Arg Tyr Asp Asn Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Glu
705 710 715 720
Glu Val Gly Gly Gly Pro Gly Val Gly Tyr Asn Val Asn Val Ala Trp
725 730 735
Thr Gly Gly Val Asp Pro Pro Ile Gly Asp Val Glu Tyr Leu Thr Ala
740 745 750
Phe Arg Thr Val Val Met Pro Ile Ala His Glu Phe Ser Pro Asp Val
755 760 765
Val Leu Val Ser Ala Gly Phe Asp Ala Val Glu Gly His Leu Ser Pro
770 775 780
Leu Gly Gly Tyr Ser Val Thr Ala Arg Cys Phe Gly His Leu Thr Arg
785 790 795 800
Gln Leu Met Thr Leu Ala Gly Gly Arg Val Val Leu Ala Leu Glu Gly
805 810 815
Gly His Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser
820 825 830
Ala Leu Leu Ser Val Lys Leu Gln Pro Leu Asp Glu Ala Val Leu Gln
835 840 845
Gln Lys Pro Asn Ile Asn Ala Val Ala Thr Leu Glu Lys Val Ile Glu
850 855 860
Ile Gln Ser Lys His Trp Ser Cys Val Gln Lys Phe Ala Ala Gly Leu
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Gly Arg Ser Leu Arg Gly Ala Gln Ala Gly Glu Thr Glu Glu Ala Glu
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Met

<210> 548
<211> 1298
<212> DNA
<213> Homo Sapiens

<400> 548
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agaagaagaa agaagaaggg agaaggagaa gaaaagaagg agaagaggaa aaggaagaag 960

gagaaagaaa aggagaagga aaaggaaaag aaggagaaga aagaagaact aagaagaagg 1020
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aggaaagaag aggaagaact nagaagaaga aagaggagga aagaagaaag aagaataagg 1140
aacnagaaag aaggagaaga aagaataaga agaggaagaa gaaaaagaag aaaagaagaa 1200
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agaaagtata agaaggaaga agaagaaaga aggaaaaa 1298

<210> 549
<211> 236
<212> PRT
<213> Homo Sapiens

<400> 549

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35 40 45
Glu Ala Ile Ser Ser Leu Asp Gly Lys Asn Arg Arg Lys Leu Ala Arg
50 55 60
Ser Glu Ala Ser Leu Lys Val Ser Glu Phe Asn Val Ser Ser Glu Gly
65 70 75 80
Ser Gly Glu Lys Leu Val Leu Ala Asp Leu Leu Glu Pro Val Lys Thr
85 90 95
Ser Ser Ser Leu Ala Thr Val Lys Lys Gln Leu Ser Arg Val Ser Lys
100 105 110
Thr Val Glu Leu Pro Leu Asn Lys Glu Glu Ile Glu Arg Ile His Arg
115 120 125
Glu Ile Ala Phe Asn Lys Thr His Lys Ser Ser Pro Asn Gly Thr Leu
130 135 140
Ser Ser Val Leu Lys Asn Arg Gln Ala Glu Gln Leu Val Phe Pro Leu
145 150 155 160
Glu Lys Glu Glu Pro Ala Ile Ala Pro Ile Glu His Val Leu Ser Gly
165 170 175
Trp Lys Ala Arg Thr Pro Leu Glu Gln Glu Ile Phe Asn Leu Leu His
180 185 190
Lys Asn Lys Gln Pro Val Thr Asp Pro Leu Leu Thr Pro Val Glu Lys
195 200 205
Ala Ser Leu Arg Ala Met Ser Leu Glu Glu Ala Lys Met Arg Arg Ala
210 215 220
Glu Leu Gln Arg Ala Arg Ala Leu Gln Ser Tyr Tyr
225 230 235

<210> 550
<211> 2236
<212> DNA
<213> Homo Sapiens

<400> 550

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ttccagctta aaaaaa 2236

<210> 551
<211> 652
<212> PRT
<213> Homo Sapiens

<400> 551
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20 25 30
Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
35 40 45
Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
50 55 60
Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
65 70 75 80
Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
85 90 95
Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
100 105 110
Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu

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Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser
    130                     135                     140
Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
145                     150                     155                     160
Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
                165                     170                     175
Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
            180                     185                     190
Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
        195                     200                     205
Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
    210                     215                     220
Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
225                     230                     235                     240
Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
                245                     250                     255
Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys
            260                     265                     270
Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile
        275                     280                     285
Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu
    290                     295                     300
Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln
305                     310                     315                     320
Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu
                325                     330                     335
Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu
            340                     345                     350
Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu
        355                     360                     365
Lys Phe Lys Lys Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu
    370                     375                     380
Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg
385                     390                     395                     400
Lys Pro Lys Tyr Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp
                405                     410                     415
Asp Leu Asp Gly Gly Thr Glu Glu Gln Gly Glu Gln Asp Phe Arg Lys
            420                     425                     430
Tyr Glu Glu Gly Phe Asp Pro Tyr Ser Met Phe Thr Pro Glu Gln Ile
        435                     440                     445
Met Gly Lys Asp Val Arg Leu Leu Arg Ile Lys Lys Glu Gly Ser Leu
    450                     455                     460
Asp Leu Ala Leu Glu Gly Gly Val Asp Ser Pro Ile Gly Lys Val Val
465                     470                     475                     480
Val Ser Ala Val Tyr Glu Arg Gly Ala Ala Glu Arg His Gly Gly Ile
                485                     490                     495
Val Lys Gly Asp Glu Ile Met Ala Ile Asn Gly Lys Ile Val Thr Asp
            500                     505                     510
Tyr Thr Leu Ala Glu Ala Asp Ala Ala Leu Gln Lys Ala Trp Asn Gln
        515                     520                     525
Gly Gly Asp Trp Ile Asp Leu Val Val Ala Val Cys Pro Pro Lys Glu
    530                     535                     540
Tyr Asp Asp Glu Leu Thr Phe Leu Leu Lys Ser Lys Arg Gly Asn Gln
545                     550                     555                     560
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Ile His Ala Leu Gly Asn Ser Glu Leu Arg Pro His Leu Val Asn Thr
565 570 575
Lys Pro Arg Thr Ser Leu Glu Arg Gly His Met Thr His Thr Arg Trp
580 585 590
His Pro Trp Asp Leu Asn Leu Ser Pro Arg Asn Leu Lys Leu Pro Leu
595 600 605
Ala Leu Asn Gln Gly Gln Ile Arg Asn Ser Ser Gly His Phe Phe Glu
610 615 620
Gly Gln Cys Gly Gly Lys Gly Ala Ala Ser Arg Leu Gly Glu Asp Leu
625 630 635 640
Lys Asp Pro Asp Ser His Ser Phe Pro Leu Ala Gln
645 650

<210> 552
<211> 2162
<212> DNA
<213> Homo Sapiens

<400> 552
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aa 2162

<210> 553
<211> 403
<212> PRT
<213> Homo Sapiens

<400> 553
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20 25 30
Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
35 40 45
Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
50 55 60
Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
65 70 75 80
Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
85 90 95
Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
100 105 110
Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu
115 120 125
Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser
130 135 140
Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
145 150 155 160
Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
165 170 175
Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
180 185 190
Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
195 200 205
Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
210 215 220
Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
225 230 235 240
Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
245 250 255
Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys
260 265 270
Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile
275 280 285
Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu
290 295 300
Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln
305 310 315 320
Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu
325 330 335
Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu
340 345 350
Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu
355 360 365
Lys Phe Lys Lys Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu

370 375 380
Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg
385 390 395 400
Lys Pro Lys

<210> 554
<211> 1789
<212> DNA
<213> Homo Sapiens

<400> 554
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aaagagcaac taaagcataa agaatttctt ctggctgcta atacttgtaa ccgtgttggt 180
ggtctttgtt tgaaatgtgc tcagcatgaa gctgttcttt cccaaaccca tactaatgtt 240
catatgcaga ccatcgaaag actggttaaa gaaagagatg acttgatgtc tgcactagtt 300
tccgtaagga gcagcttggc agatacgcag caaagagaag caagtgctta tgaacaggtg 360
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tgtgaccagt tgaggaagga gctggagagg caggcggagc gacttgaaaa agaacttgca 480
tctcagcaag agaaaagggc cattgagaaa gacatgatga aaaaggaaat aacgaaagaa 540
agggagtaca tgggatcaaa gatgttgatc ttgtctcaga atattgccca actggaggcc 600
caggtggaaa aggttacaaa ggaaaagatt tcagctatta atcaactgga ggaaattcaa 660
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gatgaaagca aacaacactt ggaacaggag cagcagaagg cagccctggc cagagaggag 900
tgcctgagac taacagaact gctgggcgaa tctgagcacc aactgcacct caccagacag 960
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gaagaatgct gtacattagc caagaaactg gaacaaatct ctcaaaaaac cagatctgaa 1200
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gactcctggt gtatgttttc agaaatggct tgaagttatg tgtttaaatc tgctcattcg 1740
tatgctaggt tatacatatg attttcaata aatgaacttt ttaaagaaa 1789

<210> 555
<211> 493
<212> PRT
<213> Homo Sapiens

<400> 555
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Glu Ile Glu Glu Ser Gln Leu Lys Phe Leu Arg Asn Asp Leu Ala Glu
20 25 30
Tyr Gln Arg Thr Cys Glu Asp Leu Lys Glu Gln Leu Lys His Lys Glu
35 40 45

Phe Leu Leu Ala Ala Asn Thr Cys Asn Arg Val Gly Gly Leu Cys Leu
50 55 60
Lys Cys Ala Gln His Glu Ala Val Leu Ser Gln Thr His Thr Asn Val
65 70 75 80
His Met Gln Thr Ile Glu Arg Leu Val Lys Glu Arg Asp Asp Leu Met
85 90 95
Ser Ala Leu Val Ser Val Arg Ser Ser Leu Ala Asp Thr Gln Gln Arg
100 105 110
Glu Ala Ser Ala Tyr Glu Gln Val Lys Gln Val Leu Gln Ile Ser Glu
115 120 125
Glu Ala Asn Phe Glu Lys Thr Lys Ala Leu Ile Gln Cys Asp Gln Leu
130 135 140
Arg Lys Glu Leu Glu Arg Gln Ala Glu Arg Leu Glu Lys Glu Leu Ala
145 150 155 160
Ser Gln Gln Glu Lys Arg Ala Ile Glu Lys Asp Met Met Lys Lys Glu
165 170 175
Ile Thr Lys Glu Arg Glu Tyr Met Gly Ser Lys Met Leu Ile Leu Ser
180 185 190
Gln Asn Ile Ala Gln Leu Glu Ala Gln Val Glu Lys Val Thr Lys Glu
195 200 205
Lys Ile Ser Ala Ile Asn Gln Leu Glu Glu Ile Gln Ser Gln Leu Ala
210 215 220
Ser Arg Glu Met Asp Val Thr Lys Val Cys Gly Glu Met Arg Tyr Gln
225 230 235 240
Leu Asn Lys Thr Asn Met Glu Lys Asp Glu Ala Glu Lys Glu His Arg
245 250 255
Glu Phe Arg Ala Lys Thr Asn Arg Asp Leu Glu Ile Lys Asp Gln Glu
260 265 270
Ile Glu Lys Leu Arg Ile Glu Leu Asp Glu Ser Lys Gln His Leu Glu
275 280 285
Gln Glu Gln Gln Lys Ala Ala Leu Ala Arg Glu Glu Cys Leu Arg Leu
290 295 300
Thr Glu Leu Leu Gly Glu Ser Glu His Gln Leu His Leu Thr Arg Gln
305 310 315 320
Glu Lys Asp Ser Ile Gln Gln Ser Phe Ser Lys Glu Ala Lys Ala Gln
325 330 335
Ala Leu Gln Ala Gln Gln Arg Glu Gln Glu Leu Thr Gln Lys Ile Gln
340 345 350
Gln Met Glu Ala Gln His Asp Lys Thr Glu Asn Glu Gln Tyr Leu Leu
355 360 365
Leu Thr Ser Gln Asn Thr Phe Leu Thr Lys Leu Lys Glu Glu Cys Cys
370 375 380
Thr Leu Ala Lys Lys Leu Glu Gln Ile Ser Gln Lys Thr Arg Ser Glu
385 390 395 400
Ile Ala Gln Leu Ser Gln Glu Lys Arg Tyr Thr Tyr Asp Lys Leu Gly
405 410 415
Lys Leu Gln Arg Arg Asn Glu Glu Leu Glu Glu Gln Cys Val Gln His
420 425 430
Gly Arg Val His Glu Thr Met Lys Gln Arg Leu Arg Gln Leu Asp Lys
435 440 445
His Ser Gln Ala Thr Ala Gln Gln Leu Val Gln Leu Leu Ser Lys Gln
450 455 460
Asn Gln Leu Leu Leu Glu Arg Gln Ser Leu Ser Glu Glu Val Asp Arg
465 470 475 480
Leu Arg Thr Gln Leu Pro Ser Met Pro Gln Ser Asp Cys

485 490

<210> 556
<211> 1306
<212> DNA
<213> Homo Sapiens

<400> 556
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cggcaaagga gaaaagaaat tgcccagaag gcagcagagg aaaatgagag ataccggaag 240
gagatggaac agattgtaga ggaggaagag aagtttaaga agcaatggga agaagactgg 300
ggctcaaagg aacagctact cttgcctaaa accatcactg ctgaggtaca cccagtaccc 360
cttcgcaagc caaagtatga tcagggagtg gaacctgagc tcgagcccgc agatgacctg 420
gatggaggca cggaggagca gggagagcag gatttccgga aatatgagga aggctttgac 480
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<210> 557
<211> 328
<212> PRT
<213> Homo Sapiens

<400> 557
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20 25 30
Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu Lys Phe Lys Lys
35 40 45
Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu Leu Leu Pro Lys
50 55 60
Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg Lys Pro Lys Tyr
65 70 75 80
Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp Asp Leu Asp Gly
85 90 95
Gly Thr Glu Glu Gln Gly Glu Gln Asp Phe Arg Lys Tyr Glu Glu Gly
100 105 110
Phe Asp Pro Tyr Ser Met Phe Thr Pro Glu Gln Ile Met Gly Lys Asp
115 120 125
Val Arg Leu Leu Arg Ile Lys Lys Glu Gly Ser Leu Asp Leu Ala Leu
130 135 140

Glu Gly Gly Val Asp Ser Pro Ile Gly Lys Val Val Val Ser Ala Val
145 150 155 160
Tyr Glu Arg Gly Ala Ala Glu Arg His Gly Gly Ile Val Lys Gly Asp
165 170 175
Glu Ile Met Ala Ile Asn Gly Lys Ile Val Thr Asp Tyr Thr Leu Ala
180 185 190
Glu Ala Asp Ala Ala Leu Gln Lys Ala Trp Asn Gln Gly Gly Asp Trp
195 200 205
Ile Asp Leu Val Val Ala Val Cys Pro Pro Lys Glu Tyr Asp Asp Glu
210 215 220
Leu Thr Phe Leu Leu Lys Ser Lys Arg Gly Asn Gln Ile His Ala Leu
225 230 235 240
Gly Asn Ser Glu Leu Arg Pro His Leu Val Asn Thr Lys Pro Arg Thr
245 250 255
Ser Leu Glu Arg Gly His Met Thr His Thr Arg Trp His Pro Trp Asp
260 265 270
Leu Asn Leu Ser Pro Arg Asn Leu Lys Leu Pro Leu Ala Leu Asn Gln
275 280 285
Gly Gln Ile Arg Asn Ser Ser Gly His Phe Phe Glu Gly Gln Cys Gly
290 295 300
Gly Lys Gly Ala Ala Ser Arg Leu Gly Glu Asp Leu Lys Asp Pro Asp
305 310 315 320
Ser His Ser Phe Pro Leu Ala Gln
325

<210> 558
<211> 2289
<212> DNA
<213> Homo Sapiens

<400> 558
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gtgctgcgaa tgtaccacca gaccatggac gtggccgtgc tcgtgggaga cctgaagctg 240
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gaggtcatca acctcattcg aaccaagaaa actgtgtcca tcaaagtgag acacatcggc 600
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gaacctgagc tcgagcccgc agatgacctg gatggaggca cggaggagca gggagagcag 1380
ccacaggaga tgttgaagag gatggtggtt tatcaagaca gcattcaaga caagatttcc 1440

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gtgtggactc cccсattggg aaggtggtcg tttctgctgt gtatgagcgg ggagctgctg    1620
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cccacctcgt gaacacaaag cctcggacca gccttgagag aggccacatg acacacacca    1920
gatggcatcc ttgggacctg aatctatcac ccaggaatct caaactccct ttggccctga    1980
accagggcca gataaggaac agctcgggcc actttttttga aggccaatgt ggaggaaagg    2040
gagcagccag ccgtttggga gaagatctca aggatccaga ctctcattcc tttcctctgg    2100
cccagtgaat ttggtctctc ccagctttgg gggactcctt ccttgaaccc taataagacc    2160
ccactggagt ctctctctct ccatccctct cctctgccct ctgctctaat tgctgccagg    2220
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ttaaaaaaa                                                            2289
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<210> 559
<211> 481
<212> PRT
<213> Homo Sapiens

<400> 559

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            20                  25                  30
Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
        35                  40                  45
Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
    50                  55                  60
Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
65                  70                  75                  80
Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
                85                  90                  95
Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
            100                 105                 110
Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu
        115                 120                 125
Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser
    130                 135                 140
Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
145                 150                 155                 160
Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
                165                 170                 175
Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
            180                 185                 190
Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
        195                 200                 205
Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
    210                 215                 220
Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
225                 230                 235                 240
Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
                245                 250                 255
Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys
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260 265 270
Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile
275 280 285
Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu
290 295 300
Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln
305 310 315 320
Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu
325 330 335
Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu
340 345 350
Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu
355 360 365
Lys Phe Lys Lys Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu
370 375 380
Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg
385 390 395 400
Lys Pro Lys Tyr Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp
405 410 415
Asp Leu Asp Gly Gly Thr Glu Glu Gln Gly Glu Gln Pro Gln Glu Met
420 425 430
Leu Lys Arg Met Val Val Tyr Gln Asp Ser Ile Gln Asp Lys Ile Ser
435 440 445
Gly Asn Met Arg Lys Ala Leu Thr Pro Thr Leu Cys Ser Pro Gln Ser
450 455 460
Arg Ser Trp Gly Arg Met Ser Gly Ser Tyr Ala Ser Arg Arg Arg Asp
465 470 475 480
Pro

<210> 560
<211> 2409
<212> DNA
<213> Homo Sapiens

<400> 560
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ttccggcata aggtggattt tctgattgaa aatgatgcag agaaggacta tctctatgat 180
gtgctgcgaa tgtaccacca gaccatggac gtggccgtgc tcgtgggaga cctgaagctg 240
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aagcaccagg tggaatatga tcagctgacc ccccggcgct ccaggaagct gaaggaggtg 360
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ggctgtgggc tcttcatctc ccacctcatc aaaggcggtc aggcagacag cgtcgggctc 480
caggtagggg acgagatcgt ccggatcaat ggatattcca tctcctcctg tacccatgag 540
gaggtcatca acctcattcg aaccaagaaa actgtgtcca tcaaagtgag acacatcggc 600
ctgatccccg tgaaaagctc tcctgatgag cccctcactt ggcagtatgt ggatcagttt 660
gtgtcggaat ctgggggcgt gcgaggcagc ctgggctccc ctggaaatcg ggaaaacaag 720
gagaagaagg tcttcatcag cctggtaggc tcccgaggcc ttggctgcag catttccagc 780
ggccccatcc agaagcctgg catctttatc agccatgtga aacctggctc cctgtctgct 840
gaggtgggat tggagatagg ggaccagatt gtcgaagtca atggcgtcga cttctctaac 900
ctggatcaca aggaggctgt aaatgtgctg aaaaatagcc gcagcctgac catctccatt 960
gtagctgcag ctggccggga gctgttcatg acagaccggg agcggctggc agaggcgcgg 1020
cagcgtgagc tgcagcggca ggagcttctc atgcagaagc ggctggcgat ggagtccaac 1080
aagatcctcc aggagcagca ggagatggag cggcaaagga gaaaagaaat tgcccagaag 1140

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gcagcagagg aaaatgagag ataccggaag gagatggaac agattgtaga ggaggaagag    1200
aagtttaaga agcaatggga agaagactgg ggctcaaagg aacagctact cttgcctaaa    1260
accatcactg ctgaggtaca cccagtaccc cttcgcaagc caaagtatga tcagggagtg    1320
gaacctgagc tcgagcccgc agatgacctg gatggaggca cggaggagca gggagagcag    1380
acattttgcc caagcccaca gcctccacga ggccctggcg tgtccaccat ctccaaacct    1440
gtcatggtcc accaggagcc caatttcatc tacaggccag ctgtgaaatc tgaagttctg    1500
ccacaggaga tgttgaagag gatggtggtt tatcaagaca gcattcaaga caagatttcc    1560
ggaaatatga ggaaggcttt gacccctact ctatgttcac cccagagcag atcatgggga    1620
aggatgtccg gctcctacgc atcaagaagg agggatcctt agacctggcc ctggaaggcg    1680
gtgtggactc ccccattggg aaggtggtcg tttctgctgt gtatgagcgg ggagctgctg    1740
agcggcatgg tggcattgtg aaaggggacg agatcatggc aatcaacggc aagattgtga    1800
cagactacac cctggctgag gctgacgctg ccctgcagaa ggcctggaat cagggcgggg    1860
actggatcga ccttgtggtt gccgtctgcc ccccaaagga gtatgacgat gagctgacct    1920
tcttgctgaa gtccaaaagg ggaaaccaaa ttcacgcgtt aggaaacagt gagctccggc    1980
cccacctcgt gaacacaaag cctcggacca gccttgagag aggccacatg acacacacca    2040
gatggcatcc ttgggacctg aatctatcac ccaggaatct caaactccct ttggccctga    2100
accagggcca gataaggaac agctcgggcc actttttttga aggccaatgt ggaggaaagg    2160
gagcagccag ccgtttggga gaagatctca aggatccaga ctctcattcc tttcctctgg    2220
cccagtgaat ttggtctctc ccagctttgg gggactcctt ccttgaaccc taataagacc    2280
ccactggagt ctctctctct ccatccctct cctctgccct ctgctctaat tgctgccagg    2340
attgtcactc caaaccttac tctgagctca ttaataaaat aaacagattt attttccagc    2400
ttaaaaaaa                                                            2409
```

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<210> 561
<211> 521
<212> PRT
<213> Homo Sapiens

<400> 561
Met Asp Arg Lys Val Ala Arg Glu Phe Arg His Lys Val Asp Phe Leu
 1               5                  10                  15
Ile Glu Asn Asp Ala Glu Lys Asp Tyr Leu Tyr Asp Val Leu Arg Met
            20                  25                  30
Tyr His Gln Thr Met Asp Val Ala Val Leu Val Gly Asp Leu Lys Leu
        35                  40                  45
Val Ile Asn Glu Pro Ser Arg Leu Pro Leu Phe Asp Ala Ile Arg Pro
    50                  55                  60
Leu Ile Pro Leu Lys His Gln Val Glu Tyr Asp Gln Leu Thr Pro Arg
65                  70                  75                  80
Arg Ser Arg Lys Leu Lys Glu Val Arg Leu Asp Arg Leu His Pro Glu
                85                  90                  95
Gly Leu Gly Leu Ser Val Arg Gly Gly Leu Glu Phe Gly Cys Gly Leu
            100                 105                 110
Phe Ile Ser His Leu Ile Lys Gly Gly Gln Ala Asp Ser Val Gly Leu
        115                 120                 125
Gln Val Gly Asp Glu Ile Val Arg Ile Asn Gly Tyr Ser Ile Ser Ser
    130                 135                 140
Cys Thr His Glu Glu Val Ile Asn Leu Ile Arg Thr Lys Lys Thr Val
145                 150                 155                 160
Ser Ile Lys Val Arg His Ile Gly Leu Ile Pro Val Lys Ser Ser Pro
                165                 170                 175
Asp Glu Pro Leu Thr Trp Gln Tyr Val Asp Gln Phe Val Ser Glu Ser
            180                 185                 190
Gly Gly Val Arg Gly Ser Leu Gly Ser Pro Gly Asn Arg Glu Asn Lys
        195                 200                 205
```

Glu Lys Lys Val Phe Ile Ser Leu Val Gly Ser Arg Gly Leu Gly Cys
210 215 220
Ser Ile Ser Ser Gly Pro Ile Gln Lys Pro Gly Ile Phe Ile Ser His
225 230 235 240
Val Lys Pro Gly Ser Leu Ser Ala Glu Val Gly Leu Glu Ile Gly Asp
245 250 255
Gln Ile Val Glu Val Asn Gly Val Asp Phe Ser Asn Leu Asp His Lys
260 265 270
Glu Ala Val Asn Val Leu Lys Asn Ser Arg Ser Leu Thr Ile Ser Ile
275 280 285
Val Ala Ala Ala Gly Arg Glu Leu Phe Met Thr Asp Arg Glu Arg Leu
290 295 300
Ala Glu Ala Arg Gln Arg Glu Leu Gln Arg Gln Glu Leu Leu Met Gln
305 310 315 320
Lys Arg Leu Ala Met Glu Ser Asn Lys Ile Leu Gln Glu Gln Gln Glu
325 330 335
Met Glu Arg Gln Arg Arg Lys Glu Ile Ala Gln Lys Ala Ala Glu Glu
340 345 350
Asn Glu Arg Tyr Arg Lys Glu Met Glu Gln Ile Val Glu Glu Glu Glu
355 360 365
Lys Phe Lys Lys Gln Trp Glu Glu Asp Trp Gly Ser Lys Glu Gln Leu
370 375 380
Leu Leu Pro Lys Thr Ile Thr Ala Glu Val His Pro Val Pro Leu Arg
385 390 395 400
Lys Pro Lys Tyr Asp Gln Gly Val Glu Pro Glu Leu Glu Pro Ala Asp
405 410 415
Asp Leu Asp Gly Gly Thr Glu Glu Gln Gly Glu Gln Thr Phe Cys Pro
420 425 430
Ser Pro Gln Pro Pro Arg Gly Pro Gly Val Ser Thr Ile Ser Lys Pro
435 440 445
Val Met Val His Gln Glu Pro Asn Phe Ile Tyr Arg Pro Ala Val Lys
450 455 460
Ser Glu Val Leu Pro Gln Glu Met Leu Lys Arg Met Val Val Tyr Gln
465 470 475 480
Asp Ser Ile Gln Asp Lys Ile Ser Gly Asn Met Arg Lys Ala Leu Thr
485 490 495
Pro Thr Leu Cys Ser Pro Gln Ser Arg Ser Trp Gly Arg Met Ser Gly
500 505 510
Ser Tyr Ala Ser Arg Arg Arg Asp Pro
515 520

<210> 562
<211> 1445
<212> DNA
<213> Homo Sapiens

<400> 562
ctccggcagg gagtcctagc gcagactttg cggttcatgg agagtctctg ggagacaggc 60
acctgcggac gctgcagata agttacgacg cactgaaaga tgaaaattct aagctgagaa 120
gaaagctgaa tgaggttcag agcttctctg aagctcaaac agaaatggtg aggacgcttg 180
agcggaagtt agaagcaaaa atgatcaagg aggaaagcga ctaccacgac ctggagtcgg 240
tggttcagca ggtggagcag aacctggagc tgatgaccaa acgggctgta aaggcagaaa 300
accacgtcgt gaaactaaaa caggaaatca gtttgctcca ggcgcaggtc tccaacttcc 360
agcgagagaa tgaagccctg cggtgcggcc agggtgccag cctgaccgtg gtgaagcaga 420
acgccgacgt ggccctgcag aacctccggg tggtcatgaa cagtgcacag gcttccatca 480

agcaactggt ttccggagct gagacactga atcttgttgc cgaaatcctt aaatctatag 540
acagaatttc tgaagttaaa gacgaggagg aagactcttg aggacccctg ggtgttctca 600
gcatgaagct ccgtgtatac cctgaggtca ccaccgctcg atctaaatgt gcagttgtgt 660
ccttaaatat gcagtcttca cccagagtaa agtgttgatc gcaagagtcc agtgtcgtgc 720
cctcagccag ttcttggcca ccacaatggg agcagccctg gccgagttgt ctctgtggtt 780
tctatgcagc ccttcttggc gaaattcctg cgatcttata gattctaatg agctcttgga 840
agacattgtc ataaaagcca gtgattttaa gaaaaagagt ggttctggaa tcaatgtttt 900
ccagtcccat cccagaacat cagttgtaag ataagtacaa ttggttgtcc ttgatttcat 960
aagtagaaca aacactaaat gtgcctctga gatggccacc ccgggcaggg acctgtgcct 1020
tccgccgatg ctcagggctc cctctggctc ccgggtcact cttgtggccc cagtgggtgg 1080
tccctgcagt catggcctga gtgcgcaggg gccaccgcgt ggctgctgct gtcctcctcc 1140
ggggaccacg gggaacaag gtcacacctt ccgtgctgtg aagctgtcca gatgtgcctc 1200
tttggctggg ggttttggtg gacgtttcaa gtggcatttt gtacaatgca ggttagaatt 1260
caggaatttc aagtatgtgc ccgggtntgt caggtcccag ttgcctttnt gacggccccc 1320
ctcagaggga cggcgatgag cactaaatgc tttttgant attttcctat agattttttt 1380
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tcacc 1445

<210> 563
<211> 192
<212> PRT
<213> Homo Sapiens

<400> 563

Pro Ala Gly Ser Pro Ser Ala Asp Phe Ala Val His Gly Glu Ser Leu
1 5 10 15
Gly Asp Arg His Leu Arg Thr Leu Gln Ile Ser Tyr Asp Ala Leu Lys
20 25 30
Asp Glu Asn Ser Lys Leu Arg Arg Lys Leu Asn Glu Val Gln Ser Phe
35 40 45
Ser Glu Ala Gln Thr Glu Met Val Arg Thr Leu Glu Arg Lys Leu Glu
50 55 60
Ala Lys Met Ile Lys Glu Glu Ser Asp Tyr His Asp Leu Glu Ser Val
65 70 75 80
Val Gln Gln Val Glu Gln Asn Leu Glu Leu Met Thr Lys Arg Ala Val
85 90 95
Lys Ala Glu Asn His Val Val Lys Leu Lys Gln Glu Ile Ser Leu Leu
100 105 110
Gln Ala Gln Val Ser Asn Phe Gln Arg Glu Asn Glu Ala Leu Arg Cys
115 120 125
Gly Gln Gly Ala Ser Leu Thr Val Val Lys Gln Asn Ala Asp Val Ala
130 135 140
Leu Gln Asn Leu Arg Val Val Met Asn Ser Ala Gln Ala Ser Ile Lys
145 150 155 160
Gln Leu Val Ser Gly Ala Glu Thr Leu Asn Leu Val Ala Glu Ile Leu
165 170 175
Lys Ser Ile Asp Arg Ile Ser Glu Val Lys Asp Glu Glu Glu Asp Ser
180 185 190

<210> 564
<211> 1226
<212> DNA
<213> Homo Sapiens

<400> 564

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ctgggccgcg aggcgcggag cttgggagcg gagcccaggc cgtgccgcgc ggcgccatga      60
agggcaagga ggagaaggag ggcggcgcac ggctgggcgc tggcggcgga agccccgaga     120
agagcccgag cgcgcaggag ctcaaggagc agggcaatcg tctgttcgtg ggccgaaagt     180
acccggaggc ggcggcctgc tacggccgcg cgatcacccg gaacccgctg gtggccgtgt     240
attacaccaa ccgggccttg tgctacctga agatgcagca gcacgagcag gccctggccg     300
actgccggcg cgccctggag ctggacgggc agtctgtgaa ggcgcacttc ttcctggggc     360
agtgccagct ggagatggag agctatgatg aggccatcgc caatctgcag cgagcttaca     420
gcctggccaa ggagcagcgg ctgaacttcg gggacgacat ccccagcgct cttcgaatcg     480
cgaagaagaa gcgctggaac agcattgagg agcggcgcat ccaccaggag agcgagctgc     540
actcctacct ctccaggctc attgccgcgg agcgtgagag ggagctggaa gagtgccagc     600
gaaaccacga gggtgatgag gacgacagcc acgtccgggc ccagcaggcc tgcattgagg     660
ccaagcacga caagtacatg gcggacatgg acgagctttt ttctcaggtg gatgagaaga     720
ggaagaagcg agacatcccc gactacctgt gtggcaagat cagctttgag ctgatgcggg     780
agccgtgcat cacgcccagt ggcatcacct acgaccgcaa ggacatcgag gagcacctgc     840
agcgtgtggg tcattttgac ccggtgaccg ggagcccccct gacccaggaa cagttcatcc     900
ccaacttggc tatgaaggag gttattgacg cattcatctc tgagaatggc tgggtggagg     960
actactgagg ttccctgccc tacctggcgt cctggtccag gggagccctg ggcagaagcc    1020
cccggcccct aaacatagtt tatgtttttg gccaccccga ccgcttcccc caagttctgc    1080
tgttggactc tggactgttt cccctctcag catcgctttt gctgggccgt gattgtcccc    1140
tttgtgggct ggaaaagcag gtgagggtgg gctgggctga ggccattgcc gccactatct    1200
gtgtaataaa atccgtgagc acgaaa                                         1226
```

<210> 565
<211> 303
<212> PRT
<213> Homo Sapiens

<400> 565

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Met Lys Gly Lys Glu Glu Lys Glu Gly Gly Ala Arg Leu Gly Ala Gly
1               5                   10                  15
Gly Gly Ser Pro Glu Lys Ser Pro Ser Ala Gln Glu Leu Lys Glu Gln
            20                  25                  30
Gly Asn Arg Leu Phe Val Gly Arg Lys Tyr Pro Glu Ala Ala Ala Cys
        35                  40                  45
Tyr Gly Arg Ala Ile Thr Arg Asn Pro Leu Val Ala Val Tyr Tyr Thr
    50                  55                  60
Asn Arg Ala Leu Cys Tyr Leu Lys Met Gln Gln His Glu Gln Ala Leu
65                  70                  75                  80
Ala Asp Cys Arg Arg Ala Leu Glu Leu Asp Gly Gln Ser Val Lys Ala
                85                  90                  95
His Phe Phe Leu Gly Gln Cys Gln Leu Glu Met Glu Ser Tyr Asp Glu
            100                 105                 110
Ala Ile Ala Asn Leu Gln Arg Ala Tyr Ser Leu Ala Lys Glu Gln Arg
        115                 120                 125
Leu Asn Phe Gly Asp Asp Ile Pro Ser Ala Leu Arg Ile Ala Lys Lys
    130                 135                 140
Lys Arg Trp Asn Ser Ile Glu Glu Arg Arg Ile His Gln Glu Ser Glu
145                 150                 155                 160
Leu His Ser Tyr Leu Ser Arg Leu Ile Ala Ala Glu Arg Glu Arg Glu
                165                 170                 175
Leu Glu Glu Cys Gln Arg Asn His Glu Gly Asp Glu Asp Asp Ser His
            180                 185                 190
Val Arg Ala Gln Gln Ala Cys Ile Glu Ala Lys His Asp Lys Tyr Met
        195                 200                 205
Ala Asp Met Asp Glu Leu Phe Ser Gln Val Asp Glu Lys Arg Lys Lys
```

```
210                 215                 220
Arg Asp Ile Pro Asp Tyr Leu Cys Gly Lys Ile Ser Phe Glu Leu Met
225                 230                 235                 240
Arg Glu Pro Cys Ile Thr Pro Ser Gly Ile Thr Tyr Asp Arg Lys Asp
                245                 250                 255
Ile Glu Glu His Leu Gln Arg Val Gly His Phe Asp Pro Val Thr Gly
            260                 265                 270
Ser Pro Leu Thr Gln Glu Gln Phe Ile Pro Asn Leu Ala Met Lys Glu
        275                 280                 285
Val Ile Asp Ala Phe Ile Ser Glu Asn Gly Trp Val Glu Asp Tyr
    290                 295                 300
```

<210> 566
<211> 1857
<212> DNA
<213> Homo Sapiens

<400> 566

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aactgaagct ttcctgcacc actggactta aggaanagtg tactcgtagg cggacagctt     120
tagtggccgg ccggccgctc tcatccccg taaggagcag agtcctttgt actgaccaag     180
atgagcaaca tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca     240
gctggagata ttgacataga gttgtggtcc aaagaagctc ctaaagcttg cagaaatttt     300
atcccaactt tgtttggaag cttattatga caataccatt tttcatagag ttgtgcctgg     360
tttcatagtc caaggcggag atcctactgg cacagggagt ggtggagagt ctatctatgg     420
agcgccattc aaagatgaat ttcattcacg gttgcgtttt aatcggagag gactggttgc     480
catggcaaat gctggttctc atgataatgg cacccacttt ttcttcacac tgggtcgagc     540
agatgaactt aacaataagc ataccatctt tggaaaggtt acaggggata cagtatataa     600
catgttgcga ctgtcagaag tagacattga tgatgacgaa agacccacata atccacacaa     660
aataaaaagc tgtgaggttt tgtttaatcc ttttgatgac atcattccaa gggaaattaa     720
aaggctgaaa aaagagaaac cagaggagga agtaaagaaa ttgaaaccca aaggcacaaa     780
aaatttagt ttactttcat ttggagagga agctgaggaa gaagaagagg aagtaaatcg     840
agttagtcag agcatgaagg gcaaaagcaa aagtagtcat gacttgctta aggatgatcc     900
acatctcagt tctgttccag ttgtagaaag tgaaaaaggt gatgcaccag atttagttga     960
tgatggagaa gatgaaagtg cagagcatga tgaatatatt gatggtgatg aaaagaacct    1020
gatgagagaa agaattgcca aaaaattaaa aaaggacaca agtgcgaatg ttaaatcagc    1080
tggagaagga gaagtggaga agaaatcagt cagccgcagt gaagagctca gaaaagaagc    1140
aagacaatta aaacgggaac tcttagcagc aaaacaaaaa aaagtagaaa atgcagcaaa    1200
acaagcagaa aaaagaagtg aagaggaaga agcccctcca gatggtgctg ttgccgaata    1260
cagaagagaa aagcaaaagt atgaagcttt gaggaagcaa cagtcaaaga agggaacttc    1320
ccgggaagat cagacccttg cactgctgaa ccagtttaaa tctaaactca ctcaagcaat    1380
tgctgaaaca cctgaaaatg acattcctga aacagaagta gaagatgatg aaggatggat    1440
gtcacatgta cttcagtttg aggataaaag cagaaaagtg aaagatgcaa gcatgcaaga    1500
ctcagataca tttgaaatct atgatcctcg gaatccagtg aataaaagaa ggagggaaga    1560
aagcaaaaag ctgatgagag agaaaaaaga aagaagataa aatgagaata atgataacca    1620
gaacttgctg gaaatgtgcc tacaatggcc ttgtaacagc cattgttccc aacagcatca    1680
cttaggggtg tgaaaagaag tatttttgaa cctgttgtct ggttttgaaa aacaattatc    1740
ttgttttgca aattgtggaa tgatgtaagc aaatgctttt ggttactggt acatgtgttt    1800
tttcctagct gaccttttat attgctaaat ctgaaataaa ataactttcc ttccaaa       1857
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<210> 567
<211> 372
<212> PRT
<213> Homo Sapiens

<400> 567

Met Ala Asn Ala Gly Ser His Asp Asn Gly Thr His Phe Phe Phe Thr
1   5   10   15
Leu Gly Arg Ala Asp Glu Leu Asn Asn Lys His Thr Ile Phe Gly Lys
            20   25   30
Val Thr Gly Asp Thr Val Tyr Asn Met Leu Arg Leu Ser Glu Val Asp
        35   40   45
Ile Asp Asp Asp Glu Arg Pro His Asn Pro His Lys Ile Lys Ser Cys
    50   55   60
Glu Val Leu Phe Asn Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys
65   70   75   80
Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys Pro
                85   90   95
Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu Ala Glu
            100   105   110
Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met Lys Gly Lys
        115   120   125
Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro His Leu Ser Ser
    130   135   140
Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala Pro Asp Leu Val Asp
145   150   155   160
Asp Gly Glu Asp Glu Ser Ala Glu His Asp Glu Tyr Ile Asp Gly Asp
                165   170   175
Glu Lys Asn Leu Met Arg Glu Arg Ile Ala Lys Lys Leu Lys Lys Asp
            180   185   190
Thr Ser Ala Asn Val Lys Ser Ala Gly Glu Gly Glu Val Glu Lys Lys
        195   200   205
Ser Val Ser Arg Ser Glu Glu Leu Arg Lys Glu Ala Arg Gln Leu Lys
    210   215   220
Arg Glu Leu Leu Ala Ala Lys Gln Lys Lys Val Glu Asn Ala Ala Lys
225   230   235   240
Gln Ala Glu Lys Arg Ser Glu Glu Glu Glu Ala Pro Pro Asp Gly Ala
                245   250   255
Val Ala Glu Tyr Arg Arg Glu Lys Gln Lys Tyr Glu Ala Leu Arg Lys
            260   265   270
Gln Gln Ser Lys Lys Gly Thr Ser Arg Glu Asp Gln Thr Leu Ala Leu
        275   280   285
Leu Asn Gln Phe Lys Ser Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro
    290   295   300
Glu Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met
305   310   315   320
Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp Ala
                325   330   335
Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg Asn Pro
            340   345   350
Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met Arg Glu Lys
        355   360   365
Lys Glu Arg Arg
    370

<210> 568
<211> 1537
<212> DNA
<213> Homo Sapiens

<400> 568
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caccaaccag atccgcctaa ccaatgtggc cgtggtacgg atgaagcgtg ccgggaagcg 180
cttcgaaatc gcctgctaca aaaacaaggt cgtcggctgg cggagcggcg tggaaaaaga 240
cctcgatgaa gttctgcaga cccactcagt gtttgtaaat gtttctaaag gtcaggttgc 300
caaaaaggaa gatctcatca gtgcgtttgg aacagatgac caaactgaaa tctgtaagca 360
gattttgact aaaggagaag ttcaagtatc agataaagaa agacacacac aactggagca 420
gatgtttagg gacattgcaa ctattgtggc agacaaatgt gtgaatcctg aaacaaagag 480
accatacacc gtgatcctta ttgagagagc catgaaggac atccactatt cggtgaaaac 540
caacaagagt acaaaacagc aggctttgga agtgataaag cagttaaaag agaaaatgaa 600
gatagaacgt gctcacatga agcttcggtt catccttcca gtcaatgaag gcaagaactg 660
aaagaaaagc tcaagccact gatcaaggtc atagaaagtg aagattatgg ccaacagtta 720
gaaatcgtat gtctgattga cccgggctgc ttccgagaaa ttgatgagct aataaaaaag 780
gaaactaaag gcaaaggttc tttggaagta ctcaatctga aagatgtaga agaaggagat 840
gagaaatttg aatgacaccc atcaatctct tcacctctaa aacactaaag tgtttccgtt 900
tccgacggca ctgtttcatg tctgtggtct gccaaatact tgcttaaact atttgacatt 960
ttctatcttt gtgttaacag tggacacagc aaggctttcc tacataagta taataatgtg 1020
ggaatgattt ggttttaatt ataaactggg gtctaaatcc taaagcaaaa ttgaaactcc 1080
aagatgcaaa gtccagagtg gcattttgct actctgtctc atgccttgat agctttccaa 1140
aatgaaagtt acttgangca gctcttgtgg gtgaaaagtt atttgtacag tagagtaaga 1200
ttattagggg tatgtctata caacaaaagg gggggtcttt cctaaaaaag aaaacatatg 1260
atgcttcatt tctacttaat ggaacttgtg ttctgagggt cattatggta tcgtaatgta 1320
aagcttggat gatgttcctg attatttgag gaacagatat aggaaaattg tgccggaatt 1380
acctttcatt gaacatgctg ccataaatta ggttattttt ggttaaaaaa taaaagtcaa 1440
ttatttttaa tttttaaagt ttataatata tattaatata ggtaaaattg tatgtaatca 1500
ataaaaccaa ttttatgttt attaaactta aaaaaaa 1537

<210> 569
<211> 210
<212> PRT
<213> Homo Sapiens

<400> 569
Ala Ala Arg Arg Ser Val Val Thr Ala Arg Arg Trp Trp Pro Ser Gly
1 5 10 15
Trp Thr Ala Arg Val Ser Pro Gly Ser Pro Ala Ser Gly Ser Leu Asn
20 25 30
Ser Arg Asp Val Asp Leu His Pro His Gln Pro Asp Pro Pro Asn Gln
35 40 45
Cys Gly Arg Gly Thr Asp Glu Ala Cys Arg Glu Ala Leu Arg Asn Arg
50 55 60
Leu Leu Gln Lys Gln Val Val Gly Trp Arg Ser Gly Val Glu Lys Asp
65 70 75 80
Leu Asp Glu Val Leu Gln Thr His Ser Val Phe Val Asn Val Ser Lys
85 90 95
Gly Gln Val Ala Lys Lys Glu Asp Leu Ile Ser Ala Phe Gly Thr Asp
100 105 110
Asp Gln Thr Glu Ile Cys Lys Gln Ile Leu Thr Lys Gly Glu Val Gln
115 120 125
Val Ser Asp Lys Glu Arg His Thr Gln Leu Glu Gln Met Phe Arg Asp
130 135 140
Ile Ala Thr Ile Val Ala Asp Lys Cys Val Asn Pro Glu Thr Lys Arg
145 150 155 160
Pro Tyr Thr Val Ile Leu Ile Glu Arg Ala Met Lys Asp Ile His Tyr

165 170 175
Ser Val Lys Thr Asn Lys Ser Thr Lys Gln Gln Ala Leu Glu Val Ile
180 185 190
Lys Gln Leu Lys Glu Lys Met Lys Ile Glu Arg Ala His Met Lys Leu
195 200 205
Arg Phe
210

<210> 570
<211> 1211
<212> DNA
<213> Homo Sapiens

<400> 570
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agacattgat gatgacgaaa gaccacataa tccacacaaa ataaaaagct gtgaggtttt 120
gtttaatcct tttgatgaca tcattccaag ggaaattaaa aggctgaaaa aagagaaacc 180
agaggaggaa gtaaagaaat tgaaacccaa aggcacaaaa aatttagtt tactttcatt 240
tggagaggaa gctgaggaag aagaggagga agtaaatcga gttagtcaga gcatgaaggg 300
caaaagcaaa agtagtcatg acttgcttaa ggatgatcca catctcagtt ctgttccagt 360
tgtagaaagt gaaaaaggtg atgcagcaga tttagttgat gatggagaag atgaaagtgc 420
agagcatgat gaatatattg atggtgatga aaagaacctg atgagagaaa gaattgccaa 480
aaaattaaaa aaggacacaa gtgcgaatgt taaatcagct ggagaaggag aagtggagaa 540
gaaatcagtc agccgcagtg aagagctcag aaaagaagca agacaattaa aacgggaact 600
cttagcagca gaacaaaaaa aagtagaaaa tgcagcaaaa caagcagaaa aaagaagtga 660
agaggaagaa gcccctccag atggtgctgt tgccgaatac agaagagaaa agcaaaagta 720
tgaagctctg aggaagcaac agtcaaagaa gggaacttcc cgggaagatc agacccttgc 780
actgctgaac cagtttaaat ctaaactcac tcaagcaatt gctgaaacgc ctgaaaatga 840
cattcctgaa acagaagtag aagatgatga aggatggatg tcacatgtac ttcagtttga 900
ggataaaagc agaaaagtga aagatgcaag catgcaagac tcagatacat ttgaaatcta 960
tgatcctcgg aatccagtga ataaaagaag gagggaagaa agcaaaaagc tgatgagaga 1020
gaaaaaagaa agaagataaa atgagaataa tgataaccag aacttgctgg aaatgtgcct 1080
acaatggcct tgtaacagcc attgttccca acagcatcac ttaggggtgt gaaaagaagt 1140
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gatgtaagca a 1211

<210> 571
<211> 354
<212> PRT
<213> Homo Sapiens

<400> 571
Pro Ser Leu Glu Arg Leu Gln Gly Tyr Thr Val Tyr Asn Met Leu Arg
1 5 10 15
Leu Ser Glu Val Asp Ile Asp Asp Asp Glu Arg Pro His Asn Pro His
20 25 30
Lys Ile Lys Ser Cys Glu Val Leu Phe Asn Pro Phe Asp Asp Ile Ile
35 40 45
Pro Arg Glu Ile Lys Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val
50 55 60
Lys Lys Leu Lys Pro Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe
65 70 75 80
Gly Glu Glu Ala Glu Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln
85 90 95
Ser Met Lys Gly Lys Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp

```
                100                     105                     110
Pro His Leu Ser Ser Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala
            115                     120                     125
Ala Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp Glu
        130                     135                     140
Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile Ala Lys
145                     150                     155                     160
Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala Gly Glu Gly
                    165                     170                     175
Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu Leu Arg Lys Glu
                180                     185                     190
Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala Glu Gln Lys Lys Val
            195                     200                     205
Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg Ser Glu Glu Glu Glu Ala
        210                     215                     220
Pro Pro Asp Gly Ala Val Ala Glu Tyr Arg Arg Glu Lys Gln Lys Tyr
225                     230                     235                     240
Glu Ala Leu Arg Lys Gln Gln Ser Lys Lys Gly Thr Ser Arg Glu Asp
                    245                     250                     255
Gln Thr Leu Ala Leu Leu Asn Gln Phe Lys Ser Lys Leu Thr Gln Ala
                260                     265                     270
Ile Ala Glu Thr Pro Glu Asn Asp Ile Pro Glu Thr Glu Val Glu Asp
            275                     280                     285
Asp Glu Gly Trp Met Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg
        290                     295                     300
Lys Val Lys Asp Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr
305                     310                     315                     320
Asp Pro Arg Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys
                    325                     330                     335
Leu Met Arg Glu Lys Lys Glu Arg Arg Ile Leu Pro Val Asn Glu Gly
                340                     345                     350
Lys Asn
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<210> 572
<211> 604
<212> DNA
<213> Homo Sapiens

<400> 572

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tccctttagc aacagggccc ccaagaagct cccgttcatt cacccttacc ttggccccca     120
ggttggaccc ccaaaggctc ccttacccca aagtgggtgg ttgaataaat cttctcagtt     180
ccctggctcc caaggcccat tgaagaagat tgtacaaggc gtgcctcaag taccccgagt     240
ggaaacagaa gcacctgcct cacttcaagc cgtggctgca cccggagcag agcccgttgc     300
cgagcctggc gctgtcggag ctgtcggtgc agcatgcgga ctcactggag aacatcgacg     360
agagcgcggt ggccgagagc agagaggagc ggatgggcgg cgcgggcggc gagggcagcg     420
acgacgacac cttcacctga gcccgcaccg cttcagggac ggagacagga ccgggcgagc     480
cctggggcgg cggccgctcc tgcactttct cccctccccc acccggcacc tggtggcacc     540
gggccaggcc caggcgggtg ctgcagcctg gctggacaga gcccaataaa cggatcccac     600
agcc                                                                  604
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<210> 573
<211> 195
<212> PRT

<213> Homo Sapiens

<400> 573

Leu Arg Gln Lys Ile Leu Val Pro Thr Phe Cys Ser Ile Pro Lys Gly
1   5   10   15
Leu Thr Phe Ile Pro Phe Ser Asn Arg Ala Pro Lys Lys Leu Pro Phe
            20   25   30
Ile His Pro Tyr Leu Gly Pro Gln Val Gly Pro Pro Lys Ala Pro Leu
        35   40   45
Pro Gln Ser Gly Trp Leu Asn Lys Ser Ser Gln Phe Pro Gly Ser Gln
    50   55   60
Gly Pro Leu Lys Lys Ile Val Gln Gly Val Pro Gln Val Pro Arg Val
65   70   75   80
Glu Thr Glu Ala Pro Ala Ser Leu Gln Ala Val Ala Ala Pro Gly Ala
                85   90   95
Glu Pro Val Ala Glu Pro Gly Ala Val Gly Ala Val Gly Ala Ala Cys
            100   105   110
Gly Leu Thr Gly Glu His Arg Arg Glu Arg Gly Gly Arg Glu Gln Arg
        115   120   125
Gly Ala Asp Gly Arg Arg Gly Arg Arg Gly Gln Arg Arg Arg His Leu
    130   135   140
His Leu Ser Pro His Arg Phe Arg Asp Gly Asp Arg Thr Gly Arg Ala
145   150   155   160
Leu Gly Arg Arg Pro Leu Leu His Phe Leu Pro Ser Pro Thr Arg His
                165   170   175
Leu Val Ala Pro Gly Gln Ala Gln Ala Gly Ala Ala Ala Trp Leu Asp
            180   185   190
Arg Ala Gln
        195

<210> 574
<211> 742
<212> DNA
<213> Homo Sapiens

<400> 574

cccaccaggg ccccctcgat gcagagacag aggtcggtgc tgaccgctgc acgtcgactg 60
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ggctgccggc aatggggggg cctggccccg gcccctgtga ggaccccgcg ggtgctgggg 180
gagcaggtgc agggggctcc gagcccctgg tgactgtcac cgtgcagtgc gccttcacag 240
tggccctgag ggcaggaaga ggagccgacc tgtccagcct gcgggcactg ctgggccaag 300
ccttccttca ccaggcccag cttgggcaat tcagttacct agccccaggt gaggacgggc 360
actgggtccc catccccgag gaggagtcgc tgcagagggc ctggcaggac gcagctgcct 420
gccccagggg gctgcagctg cagtgcaggg gagccggggg tcggccggtc ctttaccagg 480
tggtggccca gcacagatac tccgcccagg ggccagagga cctgggcttc cgacaggggg 540
acacggtgga cgtcctgtgt gaagtggacc aggcatggct ggagggccac tgtgacggcc 600
gcatcggcat cttccccaag tgcttcgtgg tccccgccgg ccctcggatg tcaggagccc 660
ccggccgcct gccccgatcc cagcagggag atcagcccta atgatgctgt gtccatgatg 720
cttttaataa aaacaacccc ca 742

<210> 575
<211> 232
<212> PRT
<213> Homo Sapiens

<400> 575
His Gln Gly Pro Leu Asp Ala Glu Thr Glu Val Gly Ala Asp Arg Cys
1 5 10 15
Thr Ser Thr Ala Tyr Gln Glu Gln Arg Pro Gln Val Glu Gln Val Gly
20 25 30
Lys Val Ala Pro Leu Ser Pro Gly Leu Pro Ala Met Gly Gly Pro Gly
35 40 45
Pro Gly Pro Cys Glu Asp Pro Ala Gly Ala Gly Gly Ala Gly Ala Gly
50 55 60
Gly Ser Glu Pro Leu Val Thr Val Thr Val Gln Cys Ala Phe Thr Val
65 70 75 80
Ala Leu Arg Ala Gly Arg Gly Ala Asp Leu Ser Ser Leu Arg Ala Leu
85 90 95
Leu Gly Gln Ala Phe Leu His Gln Ala Gln Leu Gly Gln Phe Ser Tyr
100 105 110
Leu Ala Pro Gly Glu Asp Gly His Trp Val Pro Ile Pro Glu Glu Glu
115 120 125
Ser Leu Gln Arg Ala Trp Gln Asp Ala Ala Ala Cys Pro Arg Gly Leu
130 135 140
Gln Leu Gln Cys Arg Gly Ala Gly Gly Arg Pro Val Leu Tyr Gln Val
145 150 155 160
Val Ala Gln His Arg Tyr Ser Ala Gln Gly Pro Glu Asp Leu Gly Phe
165 170 175
Arg Gln Gly Asp Thr Val Asp Val Leu Cys Glu Val Asp Gln Ala Trp
180 185 190
Leu Glu Gly His Cys Asp Gly Arg Ile Gly Ile Phe Pro Lys Cys Phe
195 200 205
Val Val Pro Ala Gly Pro Arg Met Ser Gly Ala Pro Gly Arg Leu Pro
210 215 220
Arg Ser Gln Gln Gly Asp Gln Pro
225 230

<210> 576
<211> 1087
<212> DNA
<213> Homo Sapiens

<400> 576
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caaaataagg gtaaaccaga cttgaataca acattgccaa ttagacaaac agcatcaatt 120
ttcaaacaac cggtaaccaa agtcacaaat catcctagta ataaagtgaa atcagaccca 180
caacgaatga atgaacagcc acgtcagctt ttctgggaga agaggctaca aggacttagt 240
gcatcagatg taacagaaca aattataaaa accatggaac tacccaaagg tcttcaagga 300
gttggtccag gtagcaatga tgagaccctt ttatctgctg ttgccagtgc tttgcacaca 360
agctctgcgc caatcacagg gcaagtctcc gctgctgtgg aaaagaaccc tgctgtttgg 420
cttaacacat ctcaacccct ctgcaaagct tttattgtca cagatgaaga catcaggaaa 480
caggaagagc gagtacagca agtacgcaag aaattggaag aagcactgat ggcagacatc 540
ttgtcgcgag ctgctgatac agaagagatg gatattgaaa tggacagtgg agatgaagcc 600
taagaatatg atcaggtaac tttcgaccga ctttccccaa gagaaaattc ctagaaattg 660
aacaaaaatg tttccactgg cttttgcctg taagaaaaaa aatgtacccg agcacataga 720
gctttttaat agcactaacc aatgcctttt tagatgtatt tttgatgtat atatctatta 780
ttcaaaaaat catgtttatt ttgagtccta ggacttaaaa ttagtctttt gtaatatcaa 840
gcaggaccct aagatgaagc tgagcttttg atgccaggtg caatttactg gaaatgtagc 900
acttacgtaa aacatttgtt tcccccacag ttttaataag aacagatcag gaattctaaa 960
taaatttccc agttaaagat tattgtgact tcactgtata taaacatatt tttatacttt 1020

attgaaaggg gacacctgta cattcttcca tcgtcactgt aaagacaaat aaatgattat 1080
attcaca 1087

<210> 577
<211> 200
<212> PRT
<213> Homo Sapiens

<400> 577
Lys Met Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg Leu Arg Asn
1 5 10 15
Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn Thr Thr Leu
20 25 30
Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val Thr Lys Val
35 40 45
Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln Arg Met Asn
50 55 60
Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln Gly Leu Ser
65 70 75 80
Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu Leu Pro Lys
85 90 95
Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr Leu Leu Ser
100 105 110
Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile Thr Gly Gln
115 120 125
Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu Asn Thr Ser
130 135 140
Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp Ile Arg Lys
145 150 155 160
Gln Glu Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu Glu Ala Leu
165 170 175
Met Ala Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu Met Asp Ile
180 185 190
Glu Met Asp Ser Gly Asp Glu Ala
195 200

<210> 578
<211> 2569
<212> DNA
<213> Homo Sapiens

<400> 578
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tgtttctcat ataaatgacc tttcagactt ttatgttcaa ctaatagaag atgaagctga 180
aattagtcat ctttcagaga gattaaacag tgttaaaaca aggcccgaat attatgtagg 240
tccacctttg caaagaggag atatgatatg tgctgttttc ccagaagata atttatggta 300
tcgtgctgtg atcaaggagc aacaacccaa tgaccttctc tctgtgcagt ttatagatta 360
tggcaatgtt tctgtggttc atactaacaa aataggtagg cttgaccttg ttaatgcaat 420
attgccgggg ttgtgcattc attgctcctt gcagggattt gaggttcctg acaataaaaa 480
ttctaagaaa atgatgcatt acttttccca acggaccagc gaggctgcaa taagatgtga 540
atttgttaaa tttcaagaca gatgggaagt tattcttgct gatgaacatg ggatcatagc 600
agatgatatg attagcaggt atgctctcag tgaaaaatct caagtagaac tttctaccca 660
agtaattaaa agtgccagtt caaagtctgt taacaaatca gacattgaca cttcagtatt 720
tcttaactgg tataatccag aaaaaaaaat gataagagct tatgccactg tgatagatgg 780

acctgagtac ttttggtgtc agtttgctga tacggagaaa cttcagtgtt tagaagtaga 840
agtacagact gctggagaac aggtagcaga caggagaaat tgtatcccat gtccttatat 900
tggagatcct tgtatagtaa gatacagaga agatggacat tattataggg cacttatcac 960
taatatttgt gaagattatc ttgtatctgt caggcttgtg gactttggaa acattgaaga 1020
ctgtgtggac ccaaaagcac tctgggccat tccttctgaa cttctgtcgg ttcccatgca 1080
agcctttcca tgttgcctct cagggtttaa catttcagaa ggattatgtt ctcaagaggg 1140
aaatgactat ttctatgaaa taataacaga agatgtgttg gaaataacaa tactagaaat 1200
cagaagggat gtttgtgata tccctttagc aattgttgac ttgaaaagca aaggtaaaag 1260
tattaatgag aaaatggaga aatattctaa gactggtatt aaaagtgctc ttccctatga 1320
aaatattgac tcagagataa agcagactct tgggtcctac aatcttgatg taggacttaa 1380
gaaattaagt aataaagctg tacaaaataa aatatatatg gaacaacaga cagatgagct 1440
tgctgaaata actgaaaaag atgtaaacat tattggaacc aaaccaagta acttccgtga 1500
ccctaaaact gataacattt gtgaagggtt tgaaaacccc tgcaaagata aaattgatac 1560
tgaggaactg gaaggtgaat tagagtgcca tctggttgac aaagcagagt ttgatgataa 1620
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agaactgaat tcacttgagg tgccgctttc tcctgatgat gaatcaaaag aattcttaga 1740
actggaatct attgagttac agaattctct ggtggtggat gaagaaaaag gggagctaag 1800
cccggtgcca ccgaatgtgc cactctccca agagtgtgtc acaaaaggcg ccatggagct 1860
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tacagcccag ctgcctttag atgacaagat ggatcctttg tctttaggag ttagtcagaa 1980
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tgaaatgaat atatgtgaag aagaatttgt agagtataaa aacaggatg ccatttcggc 2160
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acagctgaag aaggnacaag ggttttgaac ctttcaaatg gtatggagga gatagtgaac 2400
cctgagaatg tctggaatgn nanacccaaa ttggataaga gtccacctga gaaaaggggt 2460
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ccntgaacaa gtggcatctt acgcagacca acagagtatt tgagaaaat 2569

<210> 579
<211> 752
<212> PRT
<213> Homo Sapiens

<400> 579

Arg Val Lys Ala Thr Leu Ser Glu Arg Lys Ile Gly Asp Ser Cys Asp
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Lys Asp Leu Pro Leu Lys Phe Cys Glu Phe Pro Gln Lys Thr Ile Met
20 25 30
Pro Gly Phe Lys Thr Thr Val Tyr Val Ser His Ile Asn Asp Leu Ser
35 40 45
Asp Phe Tyr Val Gln Leu Ile Glu Asp Glu Ala Glu Ile Ser His Leu
50 55 60
Ser Glu Arg Leu Asn Ser Val Lys Thr Arg Pro Glu Tyr Tyr Val Gly
65 70 75 80
Pro Pro Leu Gln Arg Gly Asp Met Ile Cys Ala Val Phe Pro Glu Asp
85 90 95
Asn Leu Trp Tyr Arg Ala Val Ile Lys Glu Gln Gln Pro Asn Asp Leu
100 105 110
Leu Ser Val Gln Phe Ile Asp Tyr Gly Asn Val Ser Val Val His Thr
115 120 125
Asn Lys Ile Gly Arg Leu Asp Leu Val Asn Ala Ile Leu Pro Gly Leu
130 135 140

Cys Ile His Cys Ser Leu Gln Gly Phe Glu Val Pro Asp Asn Lys Asn
145 150 155 160
Ser Lys Lys Met Met His Tyr Phe Ser Gln Arg Thr Ser Glu Ala Ala
165 170 175
Ile Arg Cys Glu Phe Val Lys Phe Gln Asp Arg Trp Glu Val Ile Leu
180 185 190
Ala Asp Glu His Gly Ile Ile Ala Asp Asp Met Ile Ser Arg Tyr Ala
195 200 205
Leu Ser Glu Lys Ser Gln Val Glu Leu Ser Thr Gln Val Ile Lys Ser
210 215 220
Ala Ser Ser Lys Ser Val Asn Lys Ser Asp Ile Asp Thr Ser Val Phe
225 230 235 240
Leu Asn Trp Tyr Asn Pro Glu Lys Lys Met Ile Arg Ala Tyr Ala Thr
245 250 255
Val Ile Asp Gly Pro Glu Tyr Phe Trp Cys Gln Phe Ala Asp Thr Glu
260 265 270
Lys Leu Gln Cys Leu Glu Val Glu Val Gln Thr Ala Gly Glu Gln Val
275 280 285
Ala Asp Arg Arg Asn Cys Ile Pro Cys Pro Tyr Ile Gly Asp Pro Cys
290 295 300
Ile Val Arg Tyr Arg Glu Asp Gly His Tyr Tyr Arg Ala Leu Ile Thr
305 310 315 320
Asn Ile Cys Glu Asp Tyr Leu Val Ser Val Arg Leu Val Asp Phe Gly
325 330 335
Asn Ile Glu Asp Cys Val Asp Pro Lys Ala Leu Trp Ala Ile Pro Ser
340 345 350
Glu Leu Leu Ser Val Pro Met Gln Ala Phe Pro Cys Cys Leu Ser Gly
355 360 365
Phe Asn Ile Ser Glu Gly Leu Cys Ser Gln Glu Gly Asn Asp Tyr Phe
370 375 380
Tyr Glu Ile Ile Thr Glu Asp Val Leu Glu Ile Thr Ile Leu Glu Ile
385 390 395 400
Arg Arg Asp Val Cys Asp Ile Pro Leu Ala Ile Val Asp Leu Lys Ser
405 410 415
Lys Gly Lys Ser Ile Asn Glu Lys Met Glu Lys Tyr Ser Lys Thr Gly
420 425 430
Ile Lys Ser Ala Leu Pro Tyr Glu Asn Ile Asp Ser Glu Ile Lys Gln
435 440 445
Thr Leu Gly Ser Tyr Asn Leu Asp Val Gly Leu Lys Lys Leu Ser Asn
450 455 460
Lys Ala Val Gln Asn Lys Ile Tyr Met Glu Gln Gln Thr Asp Glu Leu
465 470 475 480
Ala Glu Ile Thr Glu Lys Asp Val Asn Ile Ile Gly Thr Lys Pro Ser
485 490 495
Asn Phe Arg Asp Pro Lys Thr Asp Asn Ile Cys Glu Gly Phe Glu Asn
500 505 510
Pro Cys Lys Asp Lys Ile Asp Thr Glu Glu Leu Glu Gly Glu Leu Glu
515 520 525
Cys His Leu Val Asp Lys Ala Glu Phe Asp Asp Lys Tyr Leu Ile Thr
530 535 540
Gly Phe Asn Thr Leu Leu Pro His Ala Asn Glu Thr Lys Glu Ile Leu
545 550 555 560
Glu Leu Asn Ser Leu Glu Val Pro Leu Ser Pro Asp Asp Glu Ser Lys
565 570 575
Glu Phe Leu Glu Leu Glu Ser Ile Glu Leu Gln Asn Ser Leu Val Val

580 585 590
Asp Glu Glu Lys Gly Glu Leu Ser Pro Val Pro Pro Asn Val Pro Leu
595 600 605
Ser Gln Glu Cys Val Thr Lys Gly Ala Met Glu Leu Phe Thr Leu Gln
610 615 620
Leu Pro Leu Ser Cys Glu Ala Glu Lys Gln Pro Glu Leu Glu Leu Pro
625 630 635 640
Thr Ala Gln Leu Pro Leu Asp Asp Lys Met Asp Pro Leu Ser Leu Gly
645 650 655
Val Ser Gln Lys Ala Gln Glu Ser Met Cys Thr Glu Asp Met Arg Lys
660 665 670
Ser Ser Cys Val Glu Ser Phe Asp Asp Gln Arg Arg Met Ser Leu His
675 680 685
Leu His Gly Ala Asp Cys Asp Pro Lys Thr Gln Asn Glu Met Asn Ile
690 695 700
Cys Glu Glu Glu Phe Val Glu Tyr Lys Asn Arg Asp Ala Ile Ser Ala
705 710 715 720
Leu Met Pro Phe Ser Leu Arg Lys Lys Ala Val Met Glu Ala Ser Thr
725 730 735
Ile Met Val Tyr Gln Ile Ile Phe Gln Asn Tyr Arg Thr Pro Thr Leu
740 745 750

<210> 580
<211> 2077
<212> DNA
<213> Homo Sapiens

<400> 580
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gaggtgactc gagcagtgat gaggataaag aataacatga aactcctgtg gaagtagaac 180
tcatgactca ggttgaccaa gaggatatca ctcttcagag tggcagagat gaactaaatg 240
aggagctcat tcaggaagaa agctctgaag acgaaggaga atatgaagag gttagaaaag 300
atcaggattc tgttggtgaa atgaaggatg aaggggaaga gacttaaatt atcctgatac 360
taccattgac ttgtctcacc ttcaacccca aaggtccatc cagaaattgg cttcaaaaga 420
ggaatcttct aattctagtg acagtaaatc acagagccgg agacatttgt cagccaagga 480
aagaagggaa atgaaaaaga aaaaacttcc aagtgactca ggagatttag aagcgttaga 540
gggaaaggat aaagaaaaag aaagtactgt acacattgaa actcatcaga acacaagcaa 600
aaatgttgcg gctgtgcagc caatgaaacg aggacaaaag agtaaaatga aaaaaatgaa 660
agaaaaatac aaagaccagg atgaagaaga ccgtgaactt atcatgaagt tgctggggtc 720
tgcaggttca aacaaagaag aaaaagggaa gaaggggaag aaaggaaaaa caaaggacga 780
acctgtgaag aaacagcccc agaaacctag aggtggacag agggtctctg acaacattaa 840
gaaagaaact ccgttccttg aggttataac tcatgagtta caagactttg ctgtagatga 900
tccacatgat gacaaggaag agcaagatct ggatcaacag ggaaatgagg aaaacctatt 960
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tgccccttac accaccatga caaactacaa atataaagtg aaacttactc ctggagtgca 1080
gaaaaaggga aagctgcaa aacagcctt gaatagtttc atgcattcca aagaagcaac 1140
agcaagagaa aaagacttat tccgcagcgt aaaggacaca gatttatcaa gaaacattcc 1200
tggcaaagtg aaaagtgtct gcacccaatc ttctgaacgt aaaaaggaaa tagctgaaat 1260
gaaattctaa aatatttgag aagagccaat tttatagcct tttggaagtt caaagatgaa 1320
agcaccatgt atcaggattt ccgcattata aaaatgaact aaacattgcc ttgctatatt 1380
caccaaaagg acttaattct tgtttttttc ccagttttat atagaggaaa cactgtctat 1440
gataggattt ccaaaagtat ttgtggacag ttaaatgcta attatataca tctgtagtta 1500
ttctacattt tcttgaaatt tgggaggtta ataccaagta ttcatttcat gatgtaaaga 1560
aactgaacag tgaagtggct tgattgctta aactattgac ttggtaagtc tactgtatat 1620

aacatctaat atatatatta caggccaaat gaactaaaca ttgccttgct atattcacca 1680
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tcctaaagta tttgtggaca gttaaatgct aattatatac atctgtagtt attctacatt 1800
ttcttgaaat ttgagaggtt aataccaagt attcatttca tgatgtaaag aaactgaaca 1860
gtgaagtggc ttgattgctt aaactattga cttggtaagt ctactgtata taacatctaa 1920
tatatatata ttataggcca gctacaaggg gtttaaatat ttaggattgt gtcttgaaaa 1980
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<210> 581
<211> 312
<212> PRT
<213> Homo Sapiens

<400> 581
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35 40 45
Lys Glu Arg Arg Glu Met Lys Lys Lys Lys Leu Pro Ser Asp Ser Gly
50 55 60
Asp Leu Glu Ala Leu Glu Gly Lys Asp Lys Glu Lys Glu Ser Thr Val
65 70 75 80
His Ile Glu Thr His Gln Asn Thr Ser Lys Asn Val Ala Ala Val Gln
85 90 95
Pro Met Lys Arg Gly Gln Lys Ser Lys Met Lys Lys Met Lys Glu Lys
100 105 110
Tyr Lys Asp Gln Asp Glu Glu Asp Arg Glu Leu Ile Met Lys Leu Leu
115 120 125
Gly Ser Ala Gly Ser Asn Lys Glu Glu Lys Gly Lys Lys Gly Lys Lys
130 135 140
Gly Lys Thr Lys Asp Glu Pro Val Lys Lys Gln Pro Gln Lys Pro Arg
145 150 155 160
Gly Gly Gln Arg Val Ser Asp Asn Ile Lys Lys Glu Thr Pro Phe Leu
165 170 175
Glu Val Ile Thr His Glu Leu Gln Asp Phe Ala Val Asp Asp Pro His
180 185 190
Asp Asp Lys Glu Glu Gln Asp Leu Asp Gln Gln Gly Asn Glu Glu Asn
195 200 205
Leu Phe Asp Ser Leu Thr Gly Gln Pro His Pro Glu Asp Val Leu Leu
210 215 220
Phe Ala Ile Pro Ile Cys Ala Pro Tyr Thr Thr Met Thr Asn Tyr Lys
225 230 235 240
Tyr Lys Val Lys Leu Thr Pro Gly Val Gln Lys Lys Gly Lys Ala Ala
245 250 255
Lys Thr Ala Leu Asn Ser Phe Met His Ser Lys Glu Ala Thr Ala Arg
260 265 270
Glu Lys Asp Leu Phe Arg Ser Val Lys Asp Thr Asp Leu Ser Arg Asn
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Ile Pro Gly Lys Val Lys Ser Val Cys Thr Gln Ser Ser Glu Arg Lys
290 295 300
Lys Glu Ile Ala Glu Met Lys Phe
305 310

<210> 582
<211> 3309
<212> DNA
<213> Homo Sapiens

<400> 582
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gccaatgagt tcagcgaccg gtgcaccccg tcagtcatat catttggatc aaaaaataga 180
acaatcggag ttgcagccaa aaatcagcaa atcactcatg caaacaatac ggtgtctaac 240
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ttgagttacg atttggttcc attgaaaaat ggtggagttg gaataaaggt aatgtacatg 360
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tgtttaagac ttatgaatga catgacagct gttgctttga attacggaat ttataagcag 600
gatctcccaa gcctggatga gaaacctcgg atagtggttt ttgttgatat gggacattca 660
gcttttcaag tgtctgcttg tgcttttaac aagggaaaat tgaaggtact gggaacagct 720
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aatatcgaat gctttatgaa tgataaagat gtttccggaa agatgaacag gtcacaattt 960
gaagaactct gtgctgaact tctgcaaaag atagaagtac cccttattc actgttggaa 1020
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attccagctg tgaaggaaag aattgccaaa ttctttggaa aagatattag cacaacactc 1140
aatgcagatg aagcagtagc cagaggatgt gcattacagt gtgcaatact ttccccggca 1200
tttaaagtta gagaattttc cgtcacagat gcagttcctt ttccaatatc tctgatctgg 1260
aaccatgatt cagaagatac tgaaggtgtt catgaagtct ttagtcgaaa ccatgctgct 1320
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catggcattt tcaccatctc tacggcatct atggtggaga aagtcccaac tgaggagaat 1560
gaaatgtctt ctgaagctga catggagtgt ctgaatcaga gaccaccaga aaacccagac 1620
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gacaagctgt gtggaccata tgaaaaattt atatgtgagc aggatcatca aaattttttg 2040
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gccaagatag cagctgactt cagaaataag gatgagaaat acaaccatat tgatgagtct 2280
gaaatgaaaa aagtggagaa gtctgttaat gaagtgatgg aatggatgaa taatgtcatg 2340
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gatttagaag acaaaaacaa ttttggtgct gaacctccac atcagaatgg tgaatgttac 2580
cctaatgaga aaaattctgt taatatggac ttggactaga taaccttaaa ttggcctatt 2640
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ctttctctct cactatacag tatattgtca tgtgaaagtg tggaatggaa gaaatgtcga 3240
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gtcatttct 3309

<210> 583
<211> 872
<212> PRT
<213> Homo Sapiens

<400> 583

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Arg Ala Gly Gly Ile Glu Thr Ile Ala Asn Glu Phe Ser Asp Arg Cys
35 40 45
Thr Pro Ser Val Ile Ser Phe Gly Ser Lys Asn Arg Thr Ile Gly Val
50 55 60
Ala Ala Lys Asn Gln Gln Ile Thr His Ala Asn Asn Thr Val Ser Asn
65 70 75 80
Phe Lys Arg Phe His Gly Arg Ala Phe Asn Asp Pro Phe Ile Gln Lys
85 90 95
Glu Lys Glu Asn Leu Ser Tyr Asp Leu Val Pro Leu Lys Asn Gly Gly
100 105 110
Val Gly Ile Lys Val Met Tyr Met Gly Glu Glu His Leu Phe Ser Val
115 120 125
Glu Gln Ile Thr Ala Met Leu Leu Thr Lys Leu Lys Glu Thr Ala Glu
130 135 140
Asn Ser Leu Lys Lys Pro Val Thr Asp Cys Val Ile Ser Val Pro Ser
145 150 155 160
Phe Phe Thr Asp Ala Glu Arg Arg Ser Val Leu Asp Ala Ala Gln Ile
165 170 175
Val Gly Leu Asn Cys Leu Arg Leu Met Asn Asp Met Thr Ala Val Ala
180 185 190
Leu Asn Tyr Gly Ile Tyr Lys Gln Asp Leu Pro Ser Leu Asp Glu Lys
195 200 205
Pro Arg Ile Val Val Phe Val Asp Met Gly His Ser Ala Phe Gln Val
210 215 220
Ser Ala Cys Ala Phe Asn Lys Gly Lys Leu Lys Val Leu Gly Thr Ala
225 230 235 240
Phe Asp Pro Phe Leu Gly Gly Lys Asn Phe Asp Glu Lys Leu Val Glu
245 250 255
His Phe Cys Ala Glu Phe Lys Thr Lys Tyr Lys Leu Asp Ala Lys Ser
260 265 270
Lys Ile Arg Ala Leu Leu Arg Leu Tyr Gln Glu Cys Glu Lys Leu Lys
275 280 285
Lys Leu Met Ser Ser Asn Ser Thr Asp Leu Pro Leu Asn Ile Glu Cys
290 295 300
Phe Met Asn Asp Lys Asp Val Ser Gly Lys Met Asn Arg Ser Gln Phe
305 310 315 320
Glu Glu Leu Cys Ala Glu Leu Leu Gln Lys Ile Glu Val Pro Leu Tyr

325 330 335
Ser Leu Leu Glu Gln Thr His Leu Lys Val Glu Asp Val Ser Ala Val
340 345 350
Glu Ile Val Gly Gly Ala Thr Arg Ile Pro Ala Val Lys Glu Arg Ile
355 360 365
Ala Lys Phe Phe Gly Lys Asp Ile Ser Thr Thr Leu Asn Ala Asp Glu
370 375 380
Ala Val Ala Arg Gly Cys Ala Leu Gln Cys Ala Ile Leu Ser Pro Ala
385 390 395 400
Phe Lys Val Arg Glu Phe Ser Val Thr Asp Ala Val Pro Phe Pro Ile
405 410 415
Ser Leu Ile Trp Asn His Asp Ser Glu Asp Thr Glu Gly Val His Glu
420 425 430
Val Phe Ser Arg Asn His Ala Ala Pro Phe Ser Lys Val Leu Thr Phe
435 440 445
Leu Arg Arg Gly Pro Phe Glu Leu Glu Ala Phe Tyr Ser Asp Pro Gln
450 455 460
Gly Val Pro Tyr Pro Glu Ala Lys Ile Gly Arg Phe Val Val Gln Asn
465 470 475 480
Val Ser Ala Gln Lys Asp Gly Glu Lys Ser Arg Val Lys Val Lys Val
485 490 495
Arg Val Asn Thr His Gly Ile Phe Thr Ile Ser Thr Ala Ser Met Val
500 505 510
Glu Lys Val Pro Thr Glu Glu Asn Glu Met Ser Ser Glu Ala Asp Met
515 520 525
Glu Cys Leu Asn Gln Arg Pro Pro Glu Asn Pro Asp Thr Asp Lys Asn
530 535 540
Val Gln Gln Asp Asn Ser Glu Ala Gly Thr Gln Pro Gln Val Gln Thr
545 550 555 560
Asp Ala Gln Gln Thr Ser Gln Ser Pro Pro Ser Pro Glu Leu Thr Ser
565 570 575
Glu Glu Asn Lys Ile Pro Asp Ala Asp Lys Ala Asn Glu Lys Lys Val
580 585 590
Asp Gln Pro Pro Glu Ala Lys Lys Pro Lys Ile Lys Val Val Asn Val
595 600 605
Glu Leu Pro Ile Glu Ala Asn Leu Val Trp Gln Leu Gly Lys Asp Leu
610 615 620
Leu Asn Met Tyr Ile Glu Thr Glu Gly Lys Met Ile Met Gln Asp Lys
625 630 635 640
Leu Glu Lys Glu Arg Asn Asp Ala Lys Asn Ala Val Glu Glu Tyr Val
645 650 655
Tyr Glu Phe Arg Asp Lys Leu Cys Gly Pro Tyr Glu Lys Phe Ile Cys
660 665 670
Glu Gln Asp His Gln Asn Phe Leu Arg Leu Leu Thr Glu Thr Glu Asp
675 680 685
Trp Leu Tyr Glu Glu Gly Glu Asp Gln Ala Lys Gln Ala Tyr Val Asp
690 695 700
Lys Leu Glu Glu Leu Met Lys Ile Gly Thr Pro Val Lys Val Arg Phe
705 710 715 720
Gln Glu Ala Glu Glu Arg Pro Lys Met Phe Glu Glu Leu Gly Gln Arg
725 730 735
Leu Gln His Tyr Ala Lys Ile Ala Ala Asp Phe Arg Asn Lys Asp Glu
740 745 750
Lys Tyr Asn His Ile Asp Glu Ser Glu Met Lys Lys Val Glu Lys Ser
755 760 765

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Val Asn Glu Val Met Glu Trp Met Asn Asn Val Met Asn Ala Gln Ala
    770                 775                 780
Lys Lys Ser Leu Asp Gln Asp Pro Val Val Arg Ala Gln Glu Ile Lys
785                 790                 795                 800
Thr Lys Ile Lys Glu Leu Asn Asn Thr Cys Glu Pro Val Val Thr Gln
                805                 810                 815
Pro Lys Pro Lys Ile Glu Ser Pro Lys Leu Glu Arg Thr Pro Asn Gly
            820                 825                 830
Pro Asn Ile Asp Lys Lys Glu Glu Asp Leu Glu Asp Lys Asn Asn Phe
    835                 840                 845
Gly Ala Glu Pro Pro His Gln Asn Gly Glu Cys Tyr Pro Asn Glu Lys
    850                 855                 860
Asn Ser Val Asn Met Asp Leu Asp
865                 870
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<210> 584
<211> 2918
<212> DNA
<213> Homo Sapiens

<400> 584
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gctccctgat ggagatggag gggaaggagg atgcccttta aggtgctgaa gtgcatgtac    180
tgtggacact cctttgagtc cttgcaggac ctcagcgtcc acatgatcaa aaccaagcat    240
taccagaaag tgcctctgaa ggagccagtg ccagccatca ccaaactggt cccctccacc    300
aaaaagcggg cgcttcagga cctggcgccc ccctgctccc ctgagccagc aggaatggcc    360
gcagaggtgg ccctgagtga gtcagccaag gatcagaaag cagcgaaccc gtacgtcacg    420
cccaataacc gctatggcta ccagaatggc gccagctaca cctggcagtt tgaggcccgc    480
aaggcgcaga tcctcaagtg catggagtgt ggcagctccc acgacacgct gcagcagctc    540
accgcccaca tgatggtcac cgggcacttc ctgaaagtga ccacctcggc ttctaagaag    600
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cccaccaccc acacgcggct gccggcctcc agcatcaaaa agcagcccga ctctcccgcg    720
gggtccacga cttctgaaga aaagaaagag ccagagaagg agaagccgcc tgtggctggc    780
gacgcggaga agatcaagga ggagagtgag gacagcttgg agaaatttga gcccagcacc    840
ctgtacccgt acctgcgtga ggaggacctg gacgacagcc ccaagggagg gctggacatt    900
ctcaagtccc tggagaatac cgtctccacg gccattagca aagctcagaa tggtgcgccc    960
tcatggggtg gctaccccag catccatgca gcctaccagc tcccgggcac cgtgaagcca   1020
ctgccggcgg ccgtgcagag cgtgcaggtg cagccgtcct atgctggcgg cgtgaagtcg   1080
ctgtcttccg ccgagcacaa cgccctcctg cactccccag ggagcctcac gcccccaccg   1140
cacaagagca acgtgtctgc catggaggag ctggtggaga aggtcacggg caaggtcaac   1200
atcaagaagg aggagagacc ccctgagaag gagaagagct ccctggccaa ggctgcgtcc   1260
cccatagcaa aagagaataa agatttcccg aaaacggagg aagtcagcgg caaaccacag   1320
aagaagggcc ctgaggccga gacttgggaa gccaaaaagg agggaccgct ggacgttcac   1380
accccaaatg gcacagagcc tctcaaagca aaggtcacca acggctgtaa caacctgggg   1440
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atcatgaaca cccacctggg caaggtgtcc aagcccgtga gtccctcgct ggacccgctg   1560
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ttaaccaagt ccaagaacaa gccgctggtg tccagcgtgg ctgattcggt ggcatcacct   1740
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acgcccaagt cctccacgcc ctccacagtt tcagagaagt ccgatgctga tggcagcagc   1860
tttgaggagg cgttggacga gctgtcaccg gtccacaaga ggaagggccg gcagtccaac   1920
tggaacccgc agcaccttct catcctgcag gcccagttcg cctcgagctt gcgggagacc   1980
acagaaggca agtacatcat gtcggacttg ggcccgcagg agagggtgca catctcgaag   2040
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<210> 585
<211> 687
<212> PRT
<213> Homo Sapiens

<400> 585

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Ala Ser Tyr Thr Trp Gln Phe Glu Ala Arg Lys Ala Gln Ile Leu Lys
        35                  40                  45
Cys Met Glu Cys Gly Ser Ser His Asp Thr Leu Gln Gln Leu Thr Ala
    50                  55                  60
His Met Met Val Thr Gly His Phe Leu Lys Val Thr Thr Ser Ala Ser
65                  70                  75                  80
Lys Lys Gly Lys Gln Leu Val Leu Asp Pro Val Val Glu Glu Lys Ile
                85                  90                  95
Gln Ser Ile Pro Leu Pro Pro Thr Thr His Thr Arg Leu Pro Ala Ser
            100                 105                 110
Ser Ile Lys Lys Gln Pro Asp Ser Pro Ala Gly Ser Thr Thr Ser Glu
        115                 120                 125
Glu Lys Lys Glu Pro Glu Lys Glu Lys Pro Pro Val Ala Gly Asp Ala
    130                 135                 140
Glu Lys Ile Lys Glu Glu Ser Glu Asp Ser Leu Glu Lys Phe Glu Pro
145                 150                 155                 160
Ser Thr Leu Tyr Pro Tyr Leu Arg Glu Glu Asp Leu Asp Asp Ser Pro
                165                 170                 175
Lys Gly Gly Leu Asp Ile Leu Lys Ser Leu Glu Asn Thr Val Ser Thr
            180                 185                 190
Ala Ile Ser Lys Ala Gln Asn Gly Ala Pro Ser Trp Gly Gly Tyr Pro
        195                 200                 205
Ser Ile His Ala Ala Tyr Gln Leu Pro Gly Thr Val Lys Pro Leu Pro
    210                 215                 220
Ala Ala Val Gln Ser Val Gln Val Gln Pro Ser Tyr Ala Gly Gly Val
225                 230                 235                 240
Lys Ser Leu Ser Ser Ala Glu His Asn Ala Leu Leu His Ser Pro Gly
                245                 250                 255
Ser Leu Thr Pro Pro Pro His Lys Ser Asn Val Ser Ala Met Glu Glu
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            260                     265                     270
Leu Val Glu Lys Val Thr Gly Lys Val Asn Ile Lys Lys Glu Glu Arg
        275                     280                     285
Pro Pro Glu Lys Glu Lys Ser Ser Leu Ala Lys Ala Ala Ser Pro Ile
    290                     295                     300
Ala Lys Glu Asn Lys Asp Phe Pro Lys Thr Glu Glu Val Ser Gly Lys
305                     310                     315                     320
Pro Gln Lys Lys Gly Pro Glu Ala Glu Thr Trp Glu Ala Lys Lys Glu
                325                     330                     335
Gly Pro Leu Asp Val His Thr Pro Asn Gly Thr Glu Pro Leu Lys Ala
            340                     345                     350
Lys Val Thr Asn Gly Cys Asn Asn Leu Gly Ile Ile Met Asp His Ser
        355                     360                     365
Pro Glu Pro Ser Phe Ile Asn Pro Leu Ser Ala Leu Gln Ser Ile Met
    370                     375                     380
Asn Thr His Leu Gly Lys Val Ser Lys Pro Val Ser Pro Ser Leu Asp
385                     390                     395                     400
Pro Leu Ala Met Leu Tyr Lys Ile Ser Asn Ser Met Leu Asp Lys Pro
                405                     410                     415
Val Tyr Pro Ala Thr Pro Val Lys Gln Ala Asp Ala Ile Asp Arg Tyr
            420                     425                     430
Tyr Tyr Glu Asn Ser Asp Gln Pro Ile Asp Leu Thr Lys Ser Lys Asn
        435                     440                     445
Lys Pro Leu Val Ser Ser Val Ala Asp Ser Val Ala Ser Pro Leu Arg
    450                     455                     460
Glu Ser Ala Leu Met Asp Ile Ser Asp Met Val Lys Asn Leu Thr Gly
465                     470                     475                     480
Arg Leu Thr Pro Lys Ser Ser Thr Pro Ser Thr Val Ser Glu Lys Ser
                485                     490                     495
Asp Ala Asp Gly Ser Ser Phe Glu Glu Ala Leu Asp Glu Leu Ser Pro
            500                     505                     510
Val His Lys Arg Lys Gly Arg Gln Ser Asn Trp Asn Pro Gln His Leu
        515                     520                     525
Leu Ile Leu Gln Ala Gln Phe Ala Ser Ser Leu Arg Glu Thr Thr Glu
    530                     535                     540
Gly Lys Tyr Ile Met Ser Asp Leu Gly Pro Gln Glu Arg Val His Ile
545                     550                     555                     560
Ser Lys Phe Thr Gly Leu Ser Met Thr Thr Ile Ser His Trp Leu Ala
                565                     570                     575
Asn Val Lys Tyr Gln Leu Arg Arg Thr Gly Gly Thr Lys Phe Leu Lys
            580                     585                     590
Asn Leu Asp Thr Gly His Pro Val Phe Phe Cys Asn Asp Cys Ala Ser
        595                     600                     605
Gln Phe Arg Thr Ala Ser Thr Tyr Ile Ser His Leu Glu Thr His Leu
    610                     615                     620
Gly Phe Ser Leu Lys Asp Leu Ser Lys Leu Pro Leu Asn Gln Ile Gln
625                     630                     635                     640
Glu Gln Gln Asn Val Ser Lys Val Leu Thr Asn Lys Thr Leu Gly Pro
                645                     650                     655
Leu Gly Ala Thr Glu Glu Asp Leu Gly Ser Thr Phe Gln Cys Lys Leu
            660                     665                     670
Cys Asn Arg Thr Phe Ala Lys Gln Ala Arg Ser Gln Thr Ala Pro
        675                     680                     685
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<210> 586

<211> 1898
<212> DNA
<213> Homo Sapiens

<400> 586

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tggagtcgga tggggaaggg ccgcccccca gggtgggctt tgtggacagc accatcaaga     180
gcctggacga naagctgcgg actctgctct accaggagca cgtgcccacc tcctcagcct     240
cagctgggac ccctgtggag gtgggcgaca ganacttcac cctggagccc ctgagagggg     300
accagccccg ctcanaggtc tgcggggggg acctggccct gcccccagtg cctaaggagg     360
cggtctcagg gcgtgtccag ctgccccagc ccttggtgga gaagtcagaa ctggccccca     420
ctcgaggggc cgtgatggag cagggcacgt cctcgtcaat gacagagtcg tctcccagga     480
gtatgctagg ctatgacaga gatggaaggc aggtggcctc agactcccat gtggtcccca     540
gcgtccccca ggatgtacct gcttttgtga gacctgcacg tgtggancc acanacaggg      600
atggtggana agctgganaa agctcggcan agcccccgcc gagtgacatg ggcanngtgg     660
ggggccaggc tagccacccc cagacactcg gcnctcgagc tttggggtcc cctcggaanc     720
gtccagatca ccaggatgtc agctcaccag ccaagactgt gggccgtttc tcggtggtca     780
gcactcagga cgagtggacc ctggcctccc cccacagcct gagatactct gccccacccg     840
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<210> 587
<211> 399
<212> PRT
<213> Homo Sapiens

<400> 587

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Pro Pro Gln Pro Pro Ser Ala Leu Glu Ser Asp Gly Glu Gly Pro Pro
        35                  40                  45
Pro Arg Val Gly Phe Val Asp Ser Thr Ile Lys Ser Leu Asp Lys Leu
    50                  55                  60
Arg Thr Leu Leu Tyr Gln Glu His Val Pro Thr Ser Ser Ala Ser Ala
65                  70                  75                  80
Gly Thr Pro Val Glu Val Gly Asp Arg Phe Thr Leu Glu Pro Leu Arg
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Gly Asp Gln Pro Arg Ser Val Cys Gly Gly Asp Leu Ala Leu Pro Pro
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Val Pro Lys Glu Ala Val Ser Gly Arg Val Gln Leu Pro Gln Pro Leu
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Val Glu Lys Ser Glu Leu Ala Pro Thr Arg Gly Ala Val Met Glu Gln
        130                     135                     140
Gly Thr Ser Ser Ser Met Thr Glu Ser Ser Pro Arg Ser Met Leu Gly
145                     150                     155                     160
Tyr Asp Arg Asp Gly Arg Gln Val Ala Ser Asp Ser His Val Val Pro
                    165                     170                     175
Ser Val Pro Gln Asp Val Pro Ala Phe Val Arg Pro Ala Arg Val Pro
                180                     185                     190
Thr Arg Asp Gly Gly Ala Gly Ser Ser Ala Pro Pro Pro Ser Asp Met
            195                     200                     205
Gly Val Gly Gly Gln Ala Ser His Pro Gln Thr Leu Gly Arg Ala Leu
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Gly Ser Pro Arg Arg Pro Asp His Gln Asp Val Ser Ser Pro Ala Lys
225                     230                     235                     240
Thr Val Gly Arg Phe Ser Val Val Ser Thr Gln Asp Glu Trp Thr Leu
                    245                     250                     255
Ala Ser Pro His Ser Leu Arg Tyr Ser Ala Pro Pro Asp Val Tyr Leu
                260                     265                     270
Asp Glu Ala Pro Ser Ser Pro Asp Val Lys Leu Ala Val Arg Arg Ala
            275                     280                     285
Gln Thr Ala Ser Ser Ile Glu Val Gly Val Gly Glu Pro Val Ser Ser
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Asp Ser Gly Asp Glu Gly Pro Arg Ala Arg Pro Pro Val Gln Lys Gln
305                     310                     315                     320
Ala Ser Leu Pro Val Ser Gly Ser Val Ala Gly Asp Phe Val Lys Lys
                    325                     330                     335
Ala Thr Ala Ser Cys Arg Gly Leu Leu Gly Pro Ala Ser Leu Gly Pro
                340                     345                     350
Glu Thr Pro Ser Arg Val Gly Met Lys Val Pro Thr Ile Ser Val Thr
            355                     360                     365
Ser Phe His Ser Gln Ser Ser Tyr Ile Ser Ser Asp Asn Asp Ser Glu
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Leu Glu Asp Ala Asp Ile Lys Lys Glu Leu Ser Leu Arg Glu Lys
385                     390                     395
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<210> 588
<211> 707
<212> DNA
<213> Homo Sapiens

<400> 588

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caaaagttgc acagaagtca tatggaaatg aaanaaggtt tttttgccca cctccttgtg     180
tatatcttat gggcantgga tggaagaaaa aaaangaaca aatggaacgc gatggttgtt     240
ctgaacaaaa gtctcaaccg tgtgcattta ttgggatagg aaatagtgac caaaaaatgc     300
agcagctana cttggaagga aagaactatt gcacagccaa aacattgtat atatctgact     360
cagacaagcg aaagcacttc atgttgtctg taaagatgtt ctatggcaac agtgatgaca     420
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attgaaaaat gctgacttat gcattgcctc angaacaaag gtggctctgt ttaatcgact     540
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acnatcccan acagttagta ccagatactt gcatgttana aggaggtnat tttcatgcca 600
gttcacagcn gtggggagcc ttttttattc anctcttgga tgatgatgan tccnaaggag 660
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<210> 589
<211> 551
<212> DNA
<213> Homo Sapiens

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aaggctggtg gaataaatga ttccaccatt tcggaccaaa gttactggaa cctggactgg 420
ttgccggacc catctccaac cttctcggaa tgcanaaatg tctgggacga cacagaacat 480
acctctccac acctgtacat aatttcagct tctacatccc caaaccacac tcgtaaattt 540
ggantnaaaa t 551

<210> 590
<211> 478
<212> DNA
<213> Homo Sapiens

<400> 590
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gattgctcct gctgcactgc aatgtggccg cgggcctgnt tcttatntgt tgtaaangtn 360
aggntggtgg aataaatgat tccatcatnt cgganccgaag ttgctgggaa ctgggannng 420
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<210> 591
<211> 707
<212> DNA
<213> Homo Sapiens

<400> 591
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tcattaaatg tnatactccg ccttatcngt cctaaangaa tgtncaa 707

<210> 592
<211> 541
<212> DNA
<213> Homo Sapiens

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attaaaatcc tntcctgtaa ttccaagcat ggctacttcc ccaccgccat tcaactnaag 480
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<210> 593
<211> 605
<212> DNA
<213> Homo Sapiens

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gaaag 605

<210> 594
<211> 666
<212> DNA
<213> Homo Sapiens

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<210> 595

<211> 600
<212> DNA
<213> Homo Sapiens

<400> 595
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<210> 596
<211> 835
<212> DNA
<213> Homo Sapiens

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<211> 443
<212> DNA
<213> Homo Sapiens

<400> 597
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aaattcangc tatngctgtt tgt 443

<210> 598
<211> 491
<212> DNA

<213> Homo Sapiens

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<210> 599
<211> 802
<212> DNA
<213> Homo Sapiens

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aactcngcaa aagaaaaaaa gc 802

<210> 600
<211> 523
<212> DNA
<213> Homo Sapiens

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<211> 530
<212> DNA
<213> Homo Sapiens

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<211> 311
<212> DNA
<213> Homo Sapiens

<400> 602
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acgtgnaggg c 311

<210> 603
<211> 289
<212> DNA
<213> Homo Sapiens

<400> 603
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<210> 604
<211> 356
<212> DNA
<213> Homo Sapiens

<400> 604
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<210> 605
<211> 290
<212> DNA
<213> Homo Sapiens

<400> 605

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<210> 606
<211> 714
<212> DNA
<213> Homo Sapiens

<400> 606
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<210> 607
<211> 687
<212> DNA
<213> Homo Sapiens

<400> 607
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<211> 843
<212> DNA
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aattngaant naaattatan ttngaaancg gcnncngaaa ccaancttna tggtccaatt 240
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<212> DNA
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<210> 611

<211> 663
<212> DNA
<213> Homo Sapiens

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<210> 612
<211> 621
<212> DNA
<213> Homo Sapiens

<400> 612
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gacaaacaac tttcaaacaa aactggatta gtaggatttc ttgcctgctt aactaacatg 240
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<211> 637
<212> DNA
<213> Homo Sapiens

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<210> 614

<211> 673
<212> DNA
<213> Homo Sapiens

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<211> 714
<212> DNA
<213> Homo Sapiens

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<210> 616
<211> 688
<212> DNA
<213> Homo Sapiens

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<210> 617
<211> 721
<212> DNA
<213> Homo Sapiens

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<211> 461
<212> DNA
<213> Homo Sapiens

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<210> 619
<211> 751
<212> DNA
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<211> 556
<212> DNA
<213> Homo Sapiens

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<210> 621
<211> 708
<212> DNA
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<211> 675
<212> DNA
<213> Homo Sapiens

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<210> 623
<211> 713
<212> DNA
<213> Homo Sapiens

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<210> 624
<211> 554
<212> DNA
<213> Homo Sapiens

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acctaaggga cagc 554

<210> 625
<211> 551
<212> DNA
<213> Homo Sapiens

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<210> 626
<211> 680

<212> DNA
<213> Homo Sapiens

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cgcanaaatg caaagacgcc tgagttatac aacttgcaat tattattttc tanacagaag 180
tgccaactgt tgtgctttcc agtgtatcag tggttgctac attctccttc ttgtcttcgg 240
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gttcttcaaa aanctgccgc tgccgcatgg gatcattcag ctcagtatac gcattgcata 480
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tttaaccnaa gggccattat ctgtgggtga tcacagatga atgtnggatt gatgcaagtc 600
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catccacanc ttttgccccc 680

<210> 627
<211> 753
<212> DNA
<213> Homo Sapiens

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cagatggcag cccagcacaa tatggtggat gatggttctg gccaagtgga aatttggcgt 660
gtncaaaaca atggtaggat ccaagttgac cnnaactcct atggtgactc ccatggtggt 720
gactgctact tcatactcta cacctatccc tga 753

<210> 628
<211> 675
<212> DNA
<213> Homo Sapiens

<400> 628
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gttaaancca ccttaacata aaccttatng caattntaca cntcttttga acncaatcta 180
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tctnactaat ggctaatgca ttataaaatt ncctatctna caaatcttnc taaattatgc 300
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cagntgaaaa aaaattncaa nccaaaacta accnttaaaa aataggcntt nggttnaggt 480
taattttttt ttttttttt ttgnaaanaa antcnctntt gcccagnctg gattgtggtg 540
gcnccaatcc tggctcactg caacctcagc ctcctgggtt caagcaattt ncctgtctca 600
gccttccaan ttccngggaa tacaggggtn cnccaccacn cccagctaaa tttttttgt 660
tttttttant aaaag 675

<210> 629
<211> 677
<212> DNA
<213> Homo Sapiens

<400> 629
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tataccacga agagttcgcc cgggcgggca agcaggcggg gctgcaggtc tggaggattg 120
agaagctgga gctggtgccc gtgccccaga gcgctcacgg cgacttctac gtcggggatg 180
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atgactttgt tagctatttc aaaggcggtc tgaaatacaa ggctggaggc gtggcatctg 420
gattaaatca tgttcttacg aacgacctga cagccaagan gctcctacat gtgaagggtc 480
gtanagtggt gagagccaca gaattcccct tagctgggac agtttcaaca agggtgactg 540
cttcatcatt gaccttggca ccgaaattta tcanttggtg tggttcctcn tgcaacaaat 600
atgaacgtct gaaggcaaac cangtancta ctggcattcg gtncaatgaa aggaaaggaa 660
ggtctgaact aattgtc 677

<210> 630
<211> 665
<212> DNA
<213> Homo Sapiens

<400> 630
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ggcgtgcacc accacgcgca gctaattttt ttgtattttt agtaaaggcg aggtttcgcc 180
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aagtgctggg attacaggtg tgagccaccg cgcccagcct taattttcaa aagacaaata 300
agcaaaaagc ttttcccgtt cctctcccaa aacagcaatg agataactgc cttgtaatgt 360
ttgtttgctt tttacaaata ccaatttacc acttgctgga atcccagccc aggaaccagc 420
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cttcattagc atctttgcca atccaaataa atatctgttc ccaagcatct agtaacatga 600
catcatcttc agctaaatca tcctgggtga actctccctg gaatctcttc aataacaaat 660
ctccc 665

<210> 631
<211> 698
<212> DNA
<213> Homo Sapiens

<400> 631
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tgatgttact ggtcaatggc agtaatcctg aaggtgaaga tcctgagagg gaacctgtan 180
aaaatgaaga ttatagagaa aagtcttcag atgatgatga aatggattct tccttggtct 240
ctcagcagcc tcccgataac caggaaaagg aacgactaaa tacatccatt ccacaaaaaa 300
ggaaaatgag aaatctgtta gttaccattg agaatgatac tcctctagag gaactctcaa 360
aatatgtaga catcantatt attgccctta ctcgaaatcg gaggacaagg agatggtaca 420
cttgtccact gtgtgggaaa cagtttaatg aaagttctta cctcatttcc caccagagga 480
cccacactgg agaaaaaccc tatgactgtn ntcactgtgg gaaaagcttc aatcatnaaa 540
caaacctcaa taaacatgag cgaattcnta caggagagaa accttattcc tgttctcagt 600
gtggaaaaaa cttccgtcng aattctcatc ggagtcgtcc tgaaggaatc catntaacgg 660

agaagatatt aagtgtccan aatgtgggaa aacctccc 698

<210> 632
<211> 466
<212> DNA
<213> Homo Sapiens

<400> 632
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tctgacattc aactgttttc ctatattcca aagtaaacaa ttcctttcaa cactcaagac 120
ttaaacaggt attcttagag ggttatatga attgctatca gaagctgttg gctaacaagc 180
cagtaatttg gttctttcac canaacacag ttccagataa gcatctttgc actatttctc 240
aantatgaat ccccatgtgg ggggaaaacg gatatacttt caatagacac aagtcactct 300
ttgccttcca agtaagcana ctccagattc atcttcaaag tgttgggaaa ngggatctgt 360
gacctgtnca ttatcatata acttcaaaaa ggaaagctcc ttantccaaa aagcctanat 420
gctgaggtat agcccttgaa atgttttctt ccctgtnaat ttccta 466

<210> 633
<211> 734
<212> DNA
<213> Homo Sapiens

<400> 633
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gtttatataa actctacatt ctcttaaagg ttttcgtttt gttttcactg gagattttta 120
gcctccaagt gaacttaaca tattgcctat gcatctgatt ctttatanac ttttanattt 180
taaaactaaa tttganaaac catgcatact gtatacctta tttaataatc caaanaattg 240
tttgcacttt caaaaaagtt acaaaaaggc tgaacacaag ttaaataacc tatatgatgt 300
aaatttttcca tttctgaata ctttttcagt attatatatt gcttgctgtc taataagtta 360
gattgtcaga nacgcttcag taaattatct ctactttaaa attatatctg aatccccttt 420
ctctganatg aacttgccaa tattaaacat tgtgccatat gcagtattan cccaaaagct 480
taaataagaa ccaaacttgt agactgaata ttttaacctt aaaattatat acctatatat 540
ncacctatgg tatgctgcat attaaattta acatttcaag taacatatat atagcaaaca 600
ttcagccaaa tactctttca tgaaaagata ctgtccttaa aataaaaagt tantgaaaag 660
cttatttaga ccnaatgtct aaatataant nctaagccta tgaaacttga anctaaagtc 720
tgctgtncta ttta 734

<210> 634
<211> 822
<212> DNA
<213> Homo Sapiens

<400> 634
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tgtaaatatt gtacttttca aactccagat ctaaatatgt ttacttttca tgtggattcg 180
gaacatccca atgtagtgct aaattcatcc tatgtttgtg tcgaatgcaa ttttcttacc 240
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aagttgacta tggtgaaacg taataaccag acaatctttg aacaaacaat aaatgatctg 360
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tctaatacaa gtacttccat tgtaaacaga atacatccaa gtactgccag cacggtagtg 660
acccagcagc agttcctccc tggattgggc ccaggtgata actgctgtnt ctgctccgcc 720

agaattctaa tttgattccc naagtcttaa tccctgttna tancatcccc cctacaatgc 780
tgcnttggat aacaaccccc tttttactta acccctacan cc 822

<210> 635
<211> 819
<212> DNA
<213> Homo Sapiens

<400> 635
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ctcaaagaat agaggcaata tatagcccat cttactagac atacagtatt aaactggact 120
gaatatgagg acaagctcta gtggtcatta aaccccctca gaaagtctaa gattcagaat 180
gtctccatca tattagaaga aaaatgtact gtattaaaat ttaaattgca tttttacaag 240
ttgtttttta attagtgttc tatttacatt gcanaacttc caccaactgc agtagtttaa 300
ctttggcaca acattaagtt ccatttcttt tgggtattgg atcctgcttt ttgagtgtgt 360
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cttgagttga agaattgatt ctccttcaac gttttaggca gatttcagtc atctgattta 480
gacagcttcc gtttcacatg tcgtggaagt cccaagtgtc actatcatct gtttcttctt 540
catcctcttc ctggtcatca ataacttcat cttcctcctc attttcctca aataattcta 600
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tatgtgattt gttaacaaat tcatcaaggt cttgctcatt aaaaaacttg tgcttcaggt 720
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cccagttgtt aattcctttt ggctcctcca aggcgcccca 819

<210> 636
<211> 704
<212> DNA
<213> Homo Sapiens

<400> 636
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aaaggaaaaa aatattttcc aaantccatg tgaaattgtc tcccattttt tggcttttgg 180
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<210> 637
<211> 693
<212> DNA
<213> Homo Sapiens

<400> 637
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agccaccttc aaatgaatct tcaaattgga aaatactgct tcaccacctg ttggggataa 180
nttgcaaatg gaataattta gtatggtttg tagctatttt gatnaccacc tcgcctgnat 240
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cctctaaatc cccactgttg ctgttgctga tattgtncct tcgacatggc tacttttatt 360

tcacatttac taaaaccaac attgtggtat ttcttttcca ttatcttctt cactggttct 420
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gtatctggan aaaggccacc ancnaaaatt ttttaaccgg ctcttttgtt tccatggctt 600
tgggcctttt angatcaatc accttcccca ttcaatttat gttcttttg gatccatgaa 660
cctttntcta cnccctcccg aattccttaa ata 693

<210> 638
<211> 619
<212> DNA
<213> Homo Sapiens

<400> 638
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aagaatcgga gagtgtanat aaggtcatgg atcaaaaaga acataaattg aatgggaagg 120
tgattgatcc taaaagggcc aaagccatga aaacaaaaga gccggttaaa aaatttttgt 180
tggtggcctt tctccagata cacctgaaga gaaaataagg gagtactttg gtggttttgg 240
tgaggtggaa tccatagagc tccccatgga caacaagacc aataagaggc gtgggttctg 300
ctttattacc tttaaggaag aagaaccagt gaagaagata atggaaaaga aataccacaa 360
tgttggtctt agtaaatgtg aaataaaagt agccatgtcg aaggaacaat atcagcaaca 420
gcaacagtgg ggatctanag gaggatttgc angaagagct cgtggaagan gtggtggccc 480
cactcaaaac tggaaccang gatatantna ctattggaat cnaggctatg gcaactatgg 540
atatnacagc ccaggttacc gtggttntgg aagatatgac tncactggtt acnacaacta 600
ctatggatat ggtgattat 619

<210> 639
<211> 694
<212> DNA
<213> Homo Sapiens

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ttagtgcagc gggagagagc gggagtgtgc gccgcgcgag agtgggaggc gaagggggca 120
ngccagggan aggcgcagga gcctttgcag ccacgcgcgc gccttccctg tcttgtgtgc 180
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cgcggcagcg gcgggtgtat tctcggcggc agcggcggag acactatcac tatgtcggag 300
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gaccgggacc gggggcggaa ccgcntctgg angctccnaa gggggcnncg ccnaatccga 480
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ttgttaaact gccctcttga aattttnatn ctatcccngg ggcnatcaaa ggggtttttg 660
gctttttcc tattttaaac aaatcccgaa aaat 694

<210> 640
<211> 728
<212> DNA
<213> Homo Sapiens

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cagatggggt tccttcagat tccgtggaag ctgctaaaaa tgcaagtaac acagaaaagc 120
tcacagatca ggtgatgcag aatcctcgag ttctggcagc tttacaggag cgacttgaca 180
atgtccctca cacccttcc agctacatcg aaactttacc taaagcagta aaaagaagaa 240
ttaatgcatt gaaacaactt caggtgagat gtgctcacat agaagccaag ttctatgaag 300

aggtacatga cttggaaaga aagtatgcag cgctatacca gcctctcttt gacaagagaa 360
gagaatttat caccggcgat gctgaaccaa cagatgcgga atcggaatgg cacagtgaaa 420
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acacctgcag gatnttaaag ttgaaatttt ctgaccctgg acagcctatg tcttttgtgt 660
tagaattcca ctttgaaccc cacgactact ttaccaactc agtcctgaca aaaaccttac 720
cagatgaa 728

<210> 641
<211> 732
<212> DNA
<213> Homo Sapiens

<400> 641
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gcataagtcc actgtcaata aatgtttgtt gtggccagac ctccataaaa gagatattcc 120
ctgtgttcac aagttccctg aagcttaggt tttgagagaa tattgttgag tcactaggca 180
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gcgggactat ccgctcacgg aaaaagtgtc caatttcaaa atcagaagct aatgtgaatt 540
caaaatcttc atccagtgat ctccatcccc ggatgctttc caatggattg aagaaattga 600
aaaaggactc attgggtact gtttcgtaat tgttctaaca gtgcctcaac cttatgcttc 660
tgctttncnt ggaaggtntt gaaagtaaca ttcttncctt cttccaantc aattattnac 720
ccccgttcac aa 732

<210> 642
<211> 582
<212> DNA
<213> Homo Sapiens

<400> 642
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tctcagcctc ttgttccatc ctctggagct ctgcatctgg atctggatgc ccttctgcca 120
naaggcgctg cctgatttcc tcaagctcct ccttctctct cttcctatct cgttcatctg 180
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<210> 643
<211> 784
<212> DNA
<213> Homo Sapiens

<400> 643
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ataatgagga tgcaacagat aaagttaata aagttggtga gatccatgtg aagacattag 120
aagaaattct tcttgaaaga gccagtcaga aacgtggaga attgcaaact aaactcaaga 180

cagaaggacc ttcaaaaact gatgattcta cttcagggag caagaagctc ctccactatc 240
cgtatcaaaa ccttctctga ggtcctggct gaaaaaaaac atcggcagca gggaagcaga 300
gagacnaaaa agcnaaaagg gatacaactt gcatcaagct aaagattgat agtgaaatta 360
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gaaganoctt ccgggaaggg aatgaagttg attctcagag cngtattaga acngaagcta 660
aagangctcc gggtgagaac nccggggttg acctccctaa aattccagtc cagagatgtn 720
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<210> 644
<211> 749
<212> DNA
<213> Homo Sapiens

<400> 644
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tattttttaa aaaagcaaaa naataaagaa tatatacaaa agggacctgn aatctgtaag 180
gtgattccaa aaacnaaata antagaaaat ccatggtgaa acctgaacat tctacctctg 240
ctttggagaa gggctatcat acaacattca gtcagctgaa natggattgg tanaggtgtg 300
tctatacata aacttcagtc atttttgctt gtgcanaatc atcccaatct tcccaanact 360
gaatgggcag tcctgtggct ttcttccttt tccatattcc caacaaggct acgtgaagtt 420
caactcttga tgagccgctt acaacagcag ttccttaggg agccaacatg acaggtgggt 480
canatttccc tatgagaaac aaaactggcc acctacagca aaatatcaaa atgggtaagt 540
ccttccttcc tcttcctcct gattatatac aacatatctc ctttcaagac tattatttcc 600
atcatgctta ttccttcaca aatctaaacc ttgaggtgat atgaaggaaa ccancntcaa 660
aaaaaagaaa actcaattcc gaaatgaana aaactgggcn nggtatncaa tacnccccan 720
aacatctcca tatccctggc ccagttacc 749

<210> 645
<211> 751
<212> DNA
<213> Homo Sapiens

<400> 645
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acaaaattat tttttaaaaa agcaaaagaa taaagaatat atacaaaagg gacctggaat 180
ctgtaaggtg attccaaaaa cgaaataagt agaaaatcca tggtgaaacc tgaacattct 240
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aggtgtgtct atacataaac ttcagtcatt tttgcttgtg cagaatcatc ccaatcttcc 360
caanactgaa tgggcagtcc tgtggctttc ttccttttcc atattcccaa caaggctacg 420
tgaagttcaa ctcttgatga gccgcttaca acagcagttc cttaggancc caacatgaca 480
ggtgggtcag atttccctat gagaaacaaa actggncacc tacagcaaaa tntcaaaatg 540
ggtaagtcct tccttcctct tcctcctgat tatntacaac atatctcctt tcaagantat 600
tatttccatc atgcttattc cttcccaaat ctaaaccttg aaggtgattt gaagggaaac 660
cnccatccnn aaaaagaaaa acccattccc aaattgaaaa aaaactnggc agggtataca 720
atacaccccc canaaactcn ccaattttcc c 751

<210> 646
<211> 760
<212> DNA

<213> Homo Sapiens

<400> 646
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tcaaataatg cggaacacga aacattgact aatacaagtg ctttaaatat gaaacaaaat 120
tatttttaa aaaagcaaaa gaataaagaa tatatacaaa agggacctgg aatctgtaag 180
gtgattccaa aaacnaaata agtagaaaat ccatggtgaa acctgaacat tctacctctg 240
ctttggagaa gggctatcat acaacattca gtcagctgaa natggattgg tagaggtgtg 300
tctatacata aacttcagtc atttttgctt gtgcanaatc atcccaatct tcccaanact 360
gaatgggcag tcctgtggct ttcttccttt tccatattcc caacaaggct acgtgaagtt 420
caactcttga tgagccgctt acaacagcag ttccttagga gccaacatga caggtgggtc 480
aaatttccct atganaaaca aaactggcca cctacagcaa aatatcaaaa tgggtaantc 540
cttccttcct cttcctcctg attatataca acatatctcc tttcaagact attattccat 600
catgcttatt ccttcacaaa tctaaacctt gaagtgatat gaangaaacc nccntccaga 660
aaagaaaact cnantcanaa atgaaaaaaa ctggcaggta tncaatacac cccaaaacnt 720
ctcaatntcc tggcacanta caatccattg ttctgctaca 760

<210> 647
<211> 1041
<212> DNA
<213> Homo Sapiens

<400> 647
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cacattatgg caagaagggc gctgttttcg acaggtgtgc aggtttcggc acatggagat 120
tgataaaaaa cgcagtgaaa ttccttgtta ttgggaaaat cagccaacag gatgtcaaaa 180
attaaactgc gctttccatc acaatagagg acgatatgtt gatggccttt tcctacctcc 240
gagcaaaact gtgttgccca ctgtgcctga gtcaccagaa gaggaagtga aggctagcca 300
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cgttatgaaa gtagaaagtt ccgaaaatgt tcctagcccc acgcatccac cagttgtaat 420
taatgctgca gatgatgatg aagatgatga tgatcagttt tctgaggaag gtgatgaaac 480
caaaacacct accctgcaac caactcctga agttcacaat ggattacgag tgacttctgt 540
ccggaaacct gcagtcaata taaagcaagg tgaatgtttg aattttggaa taaaaactct 600
tgaggaaatt aagtcaaaga aaatgaagga aaaatctaag aagcaaggtg agggttcttc 660
aggagtttcc aagtctttta ctccaccctg agcccgttcc aagtcctgaa aaagaaaatg 720
tcaggactgt ggtgaaggac agtaactctc tccaacaaac aanggagaaa gaanccttgg 780
gtagattgag tcctactgan agacgggga aacgaaaant tcagcaagcg gtgacaagtg 840
atcctccaat aaagcgttac cctgcacaaa ggctagggaa aaaaanttaa ancccanaaa 900
actaacattg acaaaaccac caaagaaagc tcaagnttcc aagtccccta agggaccgan 960
taagcatgtc aaccggatca anataatgng gntgcaacag ttaaagntta aaaaattggg 1020
gaaattcagt taaaacattt g 1041

<210> 648
<211> 810
<212> DNA
<213> Homo Sapiens

<400> 648
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ttcaaataat gcggaacacn aaacattgac taatacaant gctttaaata tgaaacaaaa 120
ttattttta aaaaagcaaa agaataaana atatatacaa aagggacctg naatctgtaa 180
gctgattcca aaaacnaaat aantanaaaa tccatggtga aacctgaaca ttctacctct 240
gctttggana agggctatca tacaacattc antcagctga aaatggattg gtaaaggtgt 300
gtctatacat aaacttcant cattttgct tgtgcaaaat catcccaatc ttcccaaaac 360
tgaatgggca gtcctgtggc tttcttcctt ttccatattc ccaacaaggc tacntgaant 420

tcaactcttg atnagccgct tacaacagca gttccttagg agccaacatg acaggtgggt 480
caaatttccc tatgaanaaa caaaactggc cacctacagc aaaatatcaa aatgggtaag 540
tccttccttc ctcttcctcc tgattatata caacatatct cctttcaaga ctattatttc 600
catcatgctt attccttcac aaatctaaac cttgaggtga tatgaaggaa accancatca 660
agaaaagaaa accaattcan aaatgaanaa aactggcagg tntacaatac accccananc 720
atctcaatat ccctggcaca gttacaattc agtgttctgc tacagcccat aaaataaata 780
ttggcagctt gaataancnc atttttccc 810

<210> 649
<211> 656
<212> DNA
<213> Homo Sapiens

<400> 649
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ttcaaataat gcgnaacaca aaacnttgac taatacaatt gctttaaata tnaaacaaaa 120
ttattttttta aaaancaaa aaaataaaaa atatntacaa aagggacctg aaatctgtaa 180
nctnatncca aaaacaaaat aattaaaaaa tccatggtna aacctnaacn tnctacctct 240
gcttnggaaa agggctatca tacaacntnc antcanctna aaatggatng gtaaaggtnt 300
ntctatacat aaacttcant cattttngct tgtgcaaaat cancccaatc tncccaaaac 360
tnaatgggca ntcctgtggc ttnctncctt tnccatatnc ccaacaaggc tacttnaatt 420
tcaactcttn ataanccgct tacaacagca ntnccttagn anccaacatn acaggtgggt 480
caaattcccc tataaaaaac aaaactggcc ncctacanca aaatatcaaa atgggtaatt 540
ccttcctncc tctnccncct nattatatac aacatttctc ctttcaaaac tattattncc 600
atcatgcttn ttcctncaca aatctaaacc ttgangtgat ttgaaggaac cacctc 656

<210> 650
<211> 645
<212> DNA
<213> Homo Sapiens

<400> 650
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aantggtnca aatantgcgn aacncaaaac tttnactaat acaattgctt taaatntaaa 120
ncaaanttat tttttaaaaa accaaaaaaa taaaaaatnt ttccaaangg gacctgaaan 180
ctntaaccta atcccaaaaa caaaataatt aaaaannccn nggtnaancc tnaacntnct 240
nccnctnctt tgnaaaaggg ctatcanaca acntncattc ncctaaaaat gnatnggtaa 300
aggtttttct anacataaac ttcattcatt ttggcttntn caaaancacc ccaanctncc 360
caaaactnaa tgggcnncct ntggcttnct ccctttccca tntncccaac aaggctactt 420
naattncaac ncttnataac cccttacaa caccattncc ttagnaccaa cataacaggt 480
gggtcaaatt ncccnataaa aaacaaanct ggcccctncc ccaaaatncc caaatgggta 540
ttcctncctn ccctcccccc ngnatatata caacatntcc cctttcanaa atatattccc 600
ccacgcttat tccncccaaa nntaanccttt gaagttattt aagga 645

<210> 651
<211> 780
<212> DNA
<213> Homo Sapiens

<400> 651
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ctcttttctc cgacattttt atgtttctaa cattgaactc taaggaagct ggtgaacaaa 120
cacgccatat gtatgcagaa cacttaacag aattatgcta tgttgtctgt ttttgtttgt 180
atttcttgtc cttgctgaag attgacttga aatcttaaac taagttctcc ctctttatag 240
gcggtgacag tgatcctcca ttaaagcgta gcctggcaca gaggctaggg aagaaagttg 300

aagctccaga aactaacatt gacaaaacac caaagaaagc tcaagtttcc aagtctctta 360
aggagcgatt aggcatgtca gctgatccag ataatgagga tgcaacagat aaagttaata 420
aagttggtga gatccatgtg aagacattag aagaaattct tcttgaaaga gccagtcaga 480
aacgtggaga attgcaaact aaactcaaga cagaaggacc ttcaaaaact gatgattcta 540
cttcaggagc aagaagctcc tccactatcc gtatcaaaac cttctctgag gtcctggctg 600
aaaaaaaaca tcngcagcag ggaactgaag agacaaaaaa gccnaaagga tacaacttgc 660
atcaagctaa agattgatag tgaaattaaa aaaaacagta attttngcca cccattgttg 720
ccngcagaag acaatcanaa gaacctgcag gtaaaacaaa ntctatgcag ggaggtgccc 780

<210> 652
<211> 518
<212> DNA
<213> Homo Sapiens

<400> 652
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aaatggttca aataatgcgg aacacaaaac nttnactaat acaattgctt taaatntnaa 120
acaaaattat tttttaaaaa ancaaaaaaa taaaaaatnt ttncaaangg gacctgaaat 180
ctntaanctn atnccaaaaa caaaataatt naaaaatcca nggtgaaacc tnaacntnct 240
nccnctgctt tggaaaaggg ctntcataca acnttcattc ncctaaaaat ggattggtaa 300
angtttttnt atacataaac tncattcatt tttgcttntg caaaatcanc ccaanctncc 360
caaaactnaa tgggcantcc tntggctttc tncctttccc anatncccaa caaggctact 420
tnaatttcaa cncttnataa nccgcttaca acancatttc cttaggancc aacatnacgg 480
tgggtcaaat cccctataaa aaacaaaact ggccncct 518

<210> 653
<211> 490
<212> DNA
<213> Homo Sapiens

<400> 653
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agtcagaaac gtggagaatt gcaaactaaa ctcaagacag aaggaccttc aaaaactgat 120
gattctactt caggagcaag aagctcctcc actatccgta tcaaaacctt ctctgaggtc 180
ctggctgaaa aaaaacatcg gcagcaggaa gcagagagac aaaaaagcaa aaaggataca 240
acttgcatca agctaaagat tgatagtgaa attaaaaaaa cagtagtttt gccacccatt 300
gttgccagca gaggacaatc agaggagcct gcaggtaaaa caaagtctat gcagggaggt 360
gcacatcaag acgctggaag aaattaaact ggagaaggca ctgagggtgc agcagagctc 420
tgagagcagc accagctccc cgtctcaaca cnaggccact ccaagggcaa ggcggctgct 480
gcnaatcccc 490

<210> 654
<211> 359
<212> DNA
<213> Homo Sapiens

<400> 654
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tccaattatn ncgaacncca aaccttnaan natnccaatt ncttaaatnt taaaccaaat 120
tnnttttttta aaaagccaaa naattaagaa ttttttccaa agggaacnng aatccnttag 180
ggtaatccca aaaccaaatt agttaaaaat ccctggntaa acccnaacnt tccnccnccn 240
ccttggaaaa agggnnnccn ncnaccttcc atncncntaa aaatgaatgg ntaaagnttt 300
ttcnnncctt aacntccatc ctttttgnct nttccaaanc ctccccancc tccccaaaa 359

<210> 655

<211> 611
<212> DNA
<213> Homo Sapiens

<400> 655
tgaaaaaaaa catcggcagc aggaancaga aagacnaaaa agcaaaaagg atactacttg 60
catcangcta angattgata gtgaaattaa aaaaacagta tttttgccac ccattgttgc 120
cancagagga caatcanagg agcctgcagg taaaannaag tctatgcagg aggtgcacat 180
caagacgctg gaagaaatta aactggagaa ggcactgagg gtgcagcana gctctgagag 240
cagcaccagc tccccgtctc aacacnaagc cactccatgg gcnangcggc tgctgcgant 300
cnccnaaaga ncagggatga angaagagaa gaaccttcag gaaggaaatg aatttgattc 360
tcagancatt attataactg aagctnnana ngcttcnggt gagaccacng ganttgacat 420
cactaaaatt ccagtcaaga gatgtgagac catgagagag aagcacatgc acaaaacanc 480
nngagaggga aaaatcagtc ttgacacctc ttcggggaga tgtagcatct tgcggnaccc 540
aantggcaga gaaaccagtg ctcactgctg tgccaggaat cacncggcac ctgaccaagc 600
ggcttcccac a 611

<210> 656
<211> 634
<212> DNA
<213> Homo Sapiens

<400> 656
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tcaaataatg cggaacacna aacattgact aatacaantn ctttaaatat gaaacaaaat 120
tattttttaa aaaancnaaa naataaagaa tatntncaaa agggacctgg aatctgtnag 180
ctgattccaa aaacnaaata anttnaaaat ccntggtgaa acctgaacat tctacctctg 240
ctttggaaaa gggntatcat acaacattca gtcngctgaa aatggattgg taaaagtntn 300
tctatacata aacttcagtc atttttgctt gtncaaaatc atcccaatct tcccaaaant 360
gaatgggcag tcctgtggct ttcttccttt tccatattcc caacaaggnt acntnaantt 420
caactcttga nnanccgctt acaacagcag ttccttagga nccccatgac aggtgggtcn 480
aatttcccta tnaaaaacaa aactgggccc tacagcaaaa tatccaaatg ggtnagtcct 540
tccttcctct tcccctgant atatacacat atctcctttc aanaatanta tttccccatg 600
cttattcctt cccnaatcta aaccttgaag tgat 634

<210> 657
<211> 958
<212> DNA
<213> Homo Sapiens

<400> 657
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tgaaattcta ccctctaaga aaatgaaagt ttctaacaac aaaaagaagc cagaggaaga 120
aggcagtgct catcaagata ctgctgaaaa gaatgcatct tccccagaga aagccaaggg 180
tagacatact gtgccttgta tgccacctgc aaagcagaag tttctaaaaa gtactgagga 240
gcaagagctg gagaagagta tgaaaatgca gcaagaggtg gtggagatgc ggaaaaagaa 300
tgaagaattc aagaaacttg ctctggctgg aatagggcaa cctgtgaaga aatcagtgag 360
ccaggtcacc aaatcagttg acttccactt ccgcacagat gagcgaatca aacaacatcc 420
taagaaccag gaggaatata aggaagtgaa ctttacatct gaactacgaa agcatccttc 480
atctcctgcc cgagtgacta agggatgtac cattgttaag cctttcaacc tgtcccaagg 540
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cctgttaccc tccaaatctt ctgtgaccaa gatttgcaga gacccacagg actcctgtac 720
tgcaaacaan acaccgtgca cgggctgtga cctgcaaaaa gtacagcaga gctggaggct 780
gaggagctnc gagaaattgc aaccantaca anttccaaag cacgtngaac cttgattccc 840

agaataactt gangggtggg cccaaccttg cccaagaaaa ccaccngtga aancaancca 900
acggagccct antnggcttt gatttgggaa tttgggaaan gaatncaagg gaggngag 958

<210> 658
<211> 816
<212> DNA
<213> Homo Sapiens

<400> 658
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tccctgttgt tatcagcacc agtaaggaaa gaacgtgcct taacggcagc cccacccaga 120
gcctgctgcg tggctgctgt gaggctcccc atgaatccac gcagtcttct tcctcactgg 180
tgcagttggt gaggttttct accctcacag caaagggatc cttaactata aattcacggt 240
atgcagagaa gaggacagaa tctgatttac tgattgttcc tcatttaaac catgacttaa 300
tctctatctt aggatttaac tatctttatt ttctggttaa aatttttaaa aaaagtgggg 360
agagggtgag agtcgtaagg ggcaatagca atagagatta cactgtgctg acacagagac 420
taaattctag tcagagtgaa gaccatataa aaggccggct gatggtttaa aggaagtaac 480
tacatggagt ctaatcgaga cattcatgan ttacatctca ttattagcct tagtaatgta 540
agaaaacaat tctcaacaaa actgggagtc cacagttgtc aagtatgctt tctcangcac 600
gggtaggtaa aagtctggan aaatgggttc tctccatgcc caatgacaaa gcaagacggt 660
cctaggtttg aagttaaaaa caggtcccaa ttgcccgggc ggtatccgcc agctcacagc 720
tgaatttaan catggaaatc caatggaaaa attgggagnat acnggcacat tcanaaggct 780
ggtcctttga cttatctcca naacccgggt actggc 816

<210> 659
<211> 726
<212> DNA
<213> Homo Sapiens

<400> 659
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gtcacaagtt aaaagctctt attcctatga tgccccctcg gatttcatca atttttcatc 120
cttggatgat gaaggagata ctcaaaacat agattcatgg tttgaggaga aggccaattt 180
ggagaataag ttactgggga agaatggaac tggagggctt tttcagggca aaactccttt 240
gagaaaggct aatcttcagc aagctattgt cacacctttg aaaccagttg acaacactta 300
ctacaaagag gcagaaaaag aaaatcttgt ggaacaatcc attccgtcaa atgcttgttc 360
ttccctggaa gttgaggcag ccatatcaag aaaaactcca gcccagcctc agagaagatc 420
tcttaggctt tctgctcaga aggatttgga acagaaagaa aagcatcatg taaaaatgaa 480
agccaagaga tgtgccactc ctgtaatcat cgatgaaatt ctaccctcta agaaaatgaa 540
agtttctaac ancacaaaga agccagagga agaaggcagt gctcatcaag atactgctga 600
aaagaatgca tcttccccaa gagaaagcca agggtagaca tactgtgcct tgtatgccac 660
ctgcanagca gaagtttcna aaangtactg angagcaang aatctggaga agagtatgaa 720
aaatgc 726

<210> 660
<211> 824
<212> DNA
<213> Homo Sapiens

<400> 660
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agtcgtaagg ggcaatagca atagagatta cactgtgctg acacagagac taaattctag 120
tcagagtgaa nacccatata aaaggccggc tgatggttta aaggaagtaa ctacatggag 180
tctaatcgag acattcatga gttacatctc attattagcc ttagtaatgt aagaaaacaa 240
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aagtctggan aaatgggttc tctccatgcc caatgacaaa gcaagacggt cctaggtttg 360
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ggaatcgagt ggagaatttg gggagataca ggcncagtca gaggctggtc acttgacttt 480
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ctgatttcnt ctctttcttg gggaaccaag ggcccctgaa aaaanaaacg gtgtttggaa 780
caaaccntga aacaagcngc ctccttctgc ctgtcccaat tcct 824

<210> 661
<211> 399
<212> DNA
<213> Homo Sapiens

<400> 661
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nggtcccctn tntttttcnc ccccattaag gaaaaaactt gcntnancgg nagccccccc 120
caaaacctnc tgcttggctg ctttaaggnc cccataannc cccccatnnt cctcccccac 180
tggtncattg gtnaggtttc ctcccccccn ccaaaggnnt ccttacntat aaatcccngg 240
tttncaaaaa aaaananaaa accaatttcn gatnntcccc cttnaancca gnacttaatc 300
cctntctnag gattnaacaa ccttttttttn cgggttaaaa tttttaaaaa aattngggaa 360
anggttaaat ccttaggggg aatnccnata aaaattacc 399

<210> 662
<211> 826
<212> DNA
<213> Homo Sapiens

<400> 662
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gcctcagaga agatctctta ggctttctgc tcagaaggat ttggaacaga aagaaaagca 120
tcatgtaaaa atgaaagcca agagatgtgc cactcctgta atcatcgatg aaattctacc 180
ctctaagaaa atgaaagttt ctaacaacaa aaagaagcca gaggaagaag gcagtgctca 240
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gccttgtatg ccacctgcaa agcagaagtt tctaaaaagt actgaggagc aagagctgga 360
gaagagtatg aaaatgcagc aagaggtggt ggagatgcgg aaaaagaatg aagaattcaa 420
gaaacttgct ctggctggaa tagggcaacc tgtgaagaaa tcagtgagcc aggtcaccaa 480
atcagttgac ttccacttcc gcacagatga gcgaatcnaa caacatccta ngaaccagga 540
ggaatataag ggaagtgaac tttacatctg aactacgaaa gcatccttca tctcctgccc 600
gaantgacta aggggatgtt ccattgttaa gcctttcaac ctgtcccngg gaaagaanag 660
aacntttgat gaaacagttt ctacatatgt gccccttgcc cngcaagttg aagacttccn 720
taancgaacc ctnactgatt tcttttgang aaccagaang gntgattttn ccctgtttcc 780
ctccaatctt ctgtgaacaa gatttggccg aanacccccg aacccc 826

<210> 663
<211> 770
<212> DNA
<213> Homo Sapiens

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gtttgaagtt aaaaacangt cccattgccg gcggtatccg cagctcacag ctgaatttac 720
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<210> 664
<211> 593
<212> DNA
<213> Homo Sapiens

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<210> 665
<211> 1024
<212> DNA
<213> Homo Sapiens

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<210> 666
<211> 734
<212> DNA

<213> Homo Sapiens

<400> 666

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caccatgccc agctaatttt tattttggta nanacaaggt ttcaccatgt tgcctaggta    180
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caggttctta aggggtctct tccaccaatg tgctagggaa gggctgccat cacctctgtt    660
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<210> 667
<211> 592
<212> DNA
<213> Homo Sapiens

<400> 667

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acagctgtnt ataataagct tcgctatgaa catacatttc tcaagtcaga atttgaacac    240
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ngcaaactg gaggaagatn aagaagaact acgtanccag ctgcttaatg tngatctcac     360
anaagacagc aaacgagtgg aacaacttgc tcgagaaaaa gtctatttgt gtccaaaatt    420
aagangttta gaggctgaag taccngaatt aaaggctgaa naggagaatt ctgangctca    480
ggtggaaaat gcccaaanaa tacacgtgcg gcagttggct gagatgcacg ctacagtcag    540
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<210> 668
<211> 373
<212> DNA
<213> Homo Sapiens

<400> 668

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acaaagtaaa aattttaaaa cttgactcta actagttcct ttttgtttta cattctcaaa    300
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<210> 669
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<212> DNA
<213> Homo Sapiens

<400> 669

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<210> 670
<211> 401
<212> DNA
<213> Homo Sapiens

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<210> 671
<211> 1347
<212> DNA
<213> Homo Sapiens

<400> 671
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<210> 672
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<212> DNA
<213> Homo Sapiens

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<211> 1016
<212> DNA
<213> Homo Sapiens

<400> 673
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<212> DNA
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<210> 675
<211> 1067
<212> DNA
<213> Homo Sapiens

<400> 675
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<212> DNA
<213> Homo Sapiens

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<210> 677
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<212> DNA
<213> Homo Sapiens

<400> 677

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<400> 678

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<212> DNA
<213> Homo Sapiens

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<213> Homo Sapiens

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<212> DNA
<213> Homo Sapiens

<400> 681

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<212> DNA
<213> Homo Sapiens

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<210> 683
<211> 3127
<212> DNA
<213> Homo Sapiens

<400> 683

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acaaatttga gtatttcaac aggagtcacc aaacttaaga aaacagaaga aaagaaacac    2160
aggactctgc acacagaaga actaacatcc aaagaagcag acttaacaga ggaaacagaa    2220
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ggttcaagtc ttgagattgt cagtgcttgt cgagtaccta gtaaaattga tgaaaagaga    2640
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<211> 803
<212> PRT
<213> Homo Sapiens

<400> 684
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Lys Ala Thr Ile Pro Glu Val Lys Asn Ser Glu Asn Ser Ser Ser Arg
35 40 45
Gln Val Ser Ala Asn Asn Gln Phe Ser Ile Thr Lys Asn Arg Asp Gly
50 55 60
Arg Glu Asn Arg Arg Arg Asn Ser Lys Ile Gly Asp Asp Asn Glu Asn
65 70 75 80
Leu Thr Phe Lys Leu Glu Val Asn Glu Leu Ser Gly Lys Leu Asp Asn
85 90 95
Thr Asn Glu Tyr Asn Ser Asn Asp Gly Lys Lys Leu Pro Gln Gly Glu
100 105 110
Ser Arg Ser Tyr Glu Val Met Gly Ser Met Glu Glu Thr Leu Cys Asn
115 120 125
Ile Asp Asp Arg Asp Gly Asn Arg Asn Val His Leu Glu Phe Thr Glu
130 135 140
Arg Glu Ser Arg Lys Asp Gly Glu Asp Glu Phe Val Lys Glu Met Arg
145 150 155 160
Glu Glu Arg Lys Phe Gln Lys Leu Lys Asn Lys Glu Glu Val Leu Lys
165 170 175
Ala Ser Arg Glu Glu Lys Val Leu Met Asp Glu Gly Ala Val Leu Thr
180 185 190
Leu Ala Ala Asp Leu Ser Ser Ala Thr Leu Asp Ile Ser Lys Gln Trp
195 200 205
Ser Asn Val Phe Asn Ile Leu Arg Glu Asn Asp Phe Glu Pro Lys Phe
210 215 220
Leu Cys Glu Val Lys Leu Ala Phe Lys Cys Asp Gly Glu Ile Lys Thr
225 230 235 240
Phe Ser Asp Leu Gln Ser Leu Arg Lys Phe Ala Ser Gln Lys Ser Ser
245 250 255
Met Xaa Xaa Leu Leu Xaa Asp Val Leu Pro Gln Lys Glu Glu Ile Asn
260 265 270
Gln Gly Gly Arg Lys Tyr Gly Ile Gln Glu Lys Arg Asp Lys Thr Leu
275 280 285
Ile Asp Ser Xaa His Arg Ala Gly Glu Ile Thr Ser Asp Gly Leu Ser
290 295 300
Phe Leu Phe Leu Lys Glu Val Lys Val Ala Lys Pro Glu Glu Met Lys
305 310 315 320
Asn Leu Glu Thr Gln Glu Glu Glu Phe Ser Glu Leu Glu Glu Leu Asp
325 330 335
Glu Glu Ala Ser Gly Met Glu Asp Asp Glu Asp Thr Ser Gly Leu Glu
340 345 350
Glu Glu Glu Glu Glu Glu Ala Ser Gly Leu Glu Glu Asp Xaa Ser Ser
355 360 365
Xaa Leu Glu Glu Glu Glu Glu Gln Thr Ser Glu Gln Asp Ser Thr Phe
370 375 380
Xaa Gly His Thr Leu Val Asp Ala Lys His Glu Val Glu Ile Thr Ser

385 390 395 400
Xaa Gly Met Glu Thr Thr Phe Ile Asp Ser Val Glu Asp Ser Glu Ser
405 410 415
Glu Glu Glu Glu Glu Gly Lys Ser Ser Glu Thr Gly Lys Val Lys Thr
420 425 430
Thr Ser Leu Thr Glu Lys Lys Ala Ser Arg Arg Gln Lys Glu Ile Pro
435 440 445
Phe Ser Tyr Leu Val Gly Asp Ser Gly Lys Lys Lys Leu Val Lys His
450 455 460
Gln Val Val His Lys Thr Gln Glu Glu Glu Glu Thr Ala Val Pro Thr
465 470 475 480
Ser Gln Gly Thr Gly Thr Thr Cys Leu Thr Leu Cys Leu Ala Ser Pro
485 490 495
Ser Lys Ser Leu Glu Met Ser His Asp Glu His Lys Lys His Ser His
500 505 510
Thr Asn Leu Ser Ile Ser Thr Gly Val Thr Lys Leu Lys Lys Thr Glu
515 520 525
Glu Lys Lys His Arg Thr Leu His Thr Glu Glu Leu Thr Ser Lys Glu
530 535 540
Ala Asp Leu Thr Glu Glu Thr Glu Glu Asn Leu Arg Ser Ser Val Ile
545 550 555 560
Asn Ser Ile Arg Glu Ile Lys Glu Glu Ile Gly Asn Leu Lys Ser Ser
565 570 575
His Ser Gly Val Leu Glu Ile Glu Asn Ser Val Asp Asp Leu Ser Ser
580 585 590
Arg Met Asp Ile Leu Glu Glu Arg Ile Asp Ser Leu Glu Asp Gln Ile
595 600 605
Glu Glu Phe Ser Lys Asp Thr Met Gln Met Thr Lys Gln Ile Ile Ser
610 615 620
Lys Glu Gly Pro Arg Asp Ile Glu Glu Arg Ser Arg Ser Cys Asn Ile
625 630 635 640
Arg Leu Ile Gly Ile Pro Glu Lys Glu Ser Tyr Glu Asn Arg Ala Glu
645 650 655
Asp Ile Ile Lys Glu Ile Ile Asp Glu Asn Phe Ala Glu Leu Lys Lys
660 665 670
Gly Ser Ser Leu Glu Ile Val Ser Ala Cys Arg Val Pro Ser Lys Ile
675 680 685
Asp Glu Lys Arg Leu Thr Pro Arg His Ile Leu Val Lys Phe Trp Asn
690 695 700
Ser Ser Asp Lys Glu Lys Ile Ile Arg Pro Ser Arg Glu Arg Arg Glu
705 710 715 720
Ile Thr Tyr Gln Gly Thr Arg Ile Arg Leu Thr Ala Asp Leu Ser Leu
725 730 735
Asp Thr Leu Asp Ala Arg Ser Lys Trp Ser Asn Val Phe Lys Val Leu
740 745 750
Leu Glu Lys Gly Phe Asn Pro Arg Thr Leu Tyr Pro Ala Lys Met Ala
755 760 765
Phe Asp Phe Arg Gly Lys Thr Lys Val Phe Leu Ser Ile Glu Glu Phe
770 775 780
Arg Asp Tyr Val Leu His Met Pro Thr Leu Arg Glu Leu Leu Gly Asn
785 790 795 800
Asn Ile Pro

<210> 685

<211> 947
<212> PRT
<213> Homo Sapiens

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Gln Tyr Leu Gln Lys Val Val Leu Lys Asp Leu Trp Lys His Ser Phe
35 40 45
Ser Trp Pro Phe Gln Arg Pro Val Asp Ala Val Lys Leu Lys Leu Pro
50 55 60
Asp Tyr Tyr Thr Ile Ile Lys Asn Pro Met Asp Leu Asn Thr Ile Lys
65 70 75 80
Lys Arg Leu Glu Asn Lys Tyr Tyr Ala Lys Ala Ser Glu Cys Ile Glu
85 90 95
Asp Phe Asn Thr Met Phe Ser Asn Cys Tyr Leu Tyr Asn Lys Pro Gly
100 105 110
Asp Asp Ile Val Leu Met Ala Gln Ala Leu Glu Lys Leu Phe Met Gln
115 120 125
Lys Leu Ser Gln Met Pro Gln Glu Glu Gln Val Val Gly Val Lys Glu
130 135 140
Arg Ile Lys Lys Gly Thr Gln Gln Asn Ile Ala Val Ser Ser Ala Lys
145 150 155 160
Glu Lys Ser Ser Pro Ser Ala Thr Glu Lys Val Phe Lys Gln Gln Glu
165 170 175
Ile Pro Ser Val Phe Pro Lys Thr Ser Ile Ser Pro Leu Asn Val Val
180 185 190
Gln Gly Ala Ser Val Asn Ser Ser Ser Gln Thr Ala Ala Gln Val Thr
195 200 205
Lys Gly Val Lys Arg Lys Ala Asp Thr Thr Thr Pro Ala Thr Ser Ala
210 215 220
Val Lys Ala Ser Ser Glu Phe Ser Pro Thr Phe Thr Glu Lys Ser Val
225 230 235 240
Ala Leu Pro Pro Ile Lys Glu Asn Met Pro Lys Asn Val Leu Pro Asp
245 250 255
Ser Gln Gln Gln Tyr Asn Val Val Glu Thr Val Lys Val Thr Glu Gln
260 265 270
Leu Arg His Cys Ser Glu Ile Leu Lys Glu Met Leu Ala Lys Lys His
275 280 285
Phe Ser Tyr Ala Trp Pro Phe Tyr Asn Pro Val Asp Val Asn Ala Leu
290 295 300
Gly Leu His Asn Tyr Tyr Asp Val Val Lys Asn Pro Met Asp Leu Gly
305 310 315 320
Thr Ile Lys Glu Lys Met Asp Asn Gln Glu Tyr Lys Asp Ala Tyr Ser
325 330 335
Phe Ala Ala Asp Val Arg Leu Met Phe Met Asn Cys Tyr Lys Tyr Asn
340 345 350
Pro Pro Asp His Glu Val Val Thr Met Ala Arg Met Leu Gln Asp Val
355 360 365
Phe Glu Thr His Phe Ser Lys Ile Pro Ile Glu Pro Val Glu Ser Met
370 375 380
Pro Leu Cys Tyr Ile Lys Thr Asp Ile Thr Glu Thr Thr Gly Arg Glu
385 390 395 400

Asn Thr Asn Glu Ala Ser Ser Glu Gly Asn Ser Ser Asp Asp Ser Glu
405 410 415

Asp Glu Arg Val Lys Arg Leu Ala Lys Leu Gln Glu Gln Leu Lys Ala
420 425 430

Val His Gln Gln Leu Gln Val Leu Ser Gln Val Pro Phe Arg Lys Leu
435 440 445

Asn Lys Lys Lys Glu Lys Ser Lys Lys Glu Lys Lys Lys Glu Lys Val
450 455 460

Asn Asn Ser Asn Glu Asn Pro Arg Lys Met Cys Glu Gln Met Arg Leu
465 470 475 480

Lys Glu Lys Ser Lys Arg Asn Gln Pro Lys Lys Arg Lys Gln Gln Phe
485 490 495

Ile Gly Leu Lys Ser Glu Asp Glu Asp Asn Ala Lys Pro Met Asn Tyr
500 505 510

Asp Glu Lys Arg Gln Leu Ser Leu Asn Ile Asn Lys Leu Pro Gly Asp
515 520 525

Lys Leu Gly Arg Val Val His Ile Ile Gln Ser Arg Glu Pro Ser Leu
530 535 540

Ser Asn Ser Asn Pro Asp Glu Ile Glu Ile Asp Phe Glu Thr Leu Lys
545 550 555 560

Ala Ser Thr Leu Arg Glu Leu Glu Lys Tyr Val Ser Ala Cys Leu Arg
565 570 575

Lys Arg Pro Leu Lys Pro Pro Ala Lys Lys Ile Met Met Ser Lys Glu
580 585 590

Glu Leu His Ser Gln Lys Lys Gln Glu Leu Glu Lys Arg Leu Leu Asp
595 600 605

Val Asn Asn Gln Leu Asn Ser Arg Lys Arg Gln Thr Lys Ser Asp Lys
610 615 620

Thr Gln Pro Ser Lys Ala Val Glu Asn Val Ser Arg Leu Ser Glu Ser
625 630 635 640

Ser Ser Ser Ser Ser Ser Ser Ser Glu Ser Glu Ser Ser Ser Ser Asp
645 650 655

Leu Ser Ser Ser Asp Ser Ser Asp Ser Glu Ser Glu Met Phe Pro Lys
660 665 670

Phe Thr Glu Val Lys Pro Asn Asp Ser Pro Ser Lys Glu His Val Lys
675 680 685

Lys Met Lys Asn Glu Cys Ile Leu Pro Glu Gly Arg Thr Gly Val Thr
690 695 700

Gln Ile Gly Tyr Cys Val Gln Asp Thr Thr Ser Ala Asn Thr Thr Leu
705 710 715 720

Val His Gln Thr Thr Pro Ser His Val Met Pro Pro Asn His His Gln
725 730 735

Leu Ala Phe Asn Tyr Gln Glu Leu Glu His Leu Gln Thr Val Lys Asn
740 745 750

Ile Ser Pro Leu Gln Ile Leu Pro Pro Ser Gly Asp Ser Glu Gln Leu
755 760 765

Ser Asn Gly Ile Thr Val Met His Pro Ser Gly Asp Ser Asp Thr Thr
770 775 780

Met Leu Glu Ser Glu Cys Gln Ala Pro Val Gln Lys Asp Ile Lys Ile
785 790 795 800

Lys Asn Ala Asp Ser Trp Lys Ser Leu Gly Lys Pro Val Lys Pro Ser
805 810 815

Gly Val Met Lys Ser Ser Asp Glu Leu Phe Asn Gln Phe Arg Lys Ala
820 825 830

Ala Ile Glu Lys Glu Val Lys Ala Arg Thr Gln Glu Leu Ile Arg Lys

835 840 845
His Leu Glu Gln Asn Thr Lys Glu Leu Lys Ala Ser Gln Glu Asn Gln
850 855 860
Arg Asp Leu Gly Asn Gly Leu Thr Val Glu Ser Phe Ser Asn Lys Ile
865 870 875 880
Gln Asn Lys Cys Ser Gly Glu Glu Gln Lys Glu His Pro Gln Ser Ser
885 890 895
Glu Ala Gln Asp Lys Ser Lys Leu Trp Leu Leu Lys Asp Arg Asp Leu
900 905 910
Ala Arg Pro Lys Glu Gln Glu Arg Arg Arg Arg Glu Ala Met Val Gly
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Asn Phe Asp
945

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<211> 3106
<212> DNA
<213> Homo Sapiens

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<211> 1759
<212> DNA
<213> Homo Sapiens

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<210> 688
<211> 207
<212> PRT
<213> Homo Sapiens

<400> 688

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            20                  25                  30
Ile Ser Ala Ser Arg Lys Val Pro Asn Leu Ser Val Ser Lys Leu Ile
        35                  40                  45
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    50                  55                  60
Ala Leu Lys Lys Ala Leu Ala Ala Ala Gly Tyr Asp Val Glu Lys Asn
65                  70                  75                  80
Asn Ser Arg Ile Lys Leu Ser Leu Lys Ser Leu Val Asn Lys Gly Ile
                85                  90                  95
Leu Val Gln Thr Arg Gly Thr Gly Ala Ser Gly Ser Phe Lys Leu Ser
            100                 105                 110
Lys Lys Val Ile Pro Lys Ser Thr Arg Ser Lys Ala Lys Lys Ser Val
        115                 120                 125
Ser Ala Lys Thr Lys Lys Leu Val Leu Ser Arg Asp Ser Lys Ser Pro
    130                 135                 140
Lys Thr Ala Lys Thr Asn Lys Arg Ala Lys Lys Pro Arg Ala Thr Thr
145                 150                 155                 160
Pro Lys Thr Val Arg Ser Gly Arg Lys Ala Lys Gly Ala Lys Gly Lys
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<210> 689
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<212> DNA
<213> Homo Sapiens

<400> 689

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aagaggaggc cgcctcctcg gggctccagg ctggcttgcc cgcgctcttt cttccctcgt 1380
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caaataaaca gctatttaag gggg 1464

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<211> 363
<212> PRT
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20 25 30
Asp Glu Ser Thr Gly Ser Ile Ala Lys Arg Leu Gln Ser Ile Gly Thr
35 40 45
Glu Asn Thr Glu Glu Asn Arg Arg Phe Tyr Arg Gln Leu Leu Leu Thr
50 55 60
Ala Asp Asp Arg Val Asn Pro Cys Ile Gly Gly Val Ile Leu Phe His
65 70 75 80
Glu Thr Leu Tyr Gln Lys Ala Asp Asp Gly Arg Pro Phe Pro Gln Val
85 90 95
Ile Lys Ser Lys Gly Gly Val Val Gly Ile Lys Val Asp Lys Gly Val
100 105 110
Val Pro Leu Ala Gly Thr Asn Gly Glu Thr Thr Thr Gln Gly Leu Asp
115 120 125
Gly Leu Ser Glu Arg Cys Ala Gln Tyr Lys Lys Asp Gly Ala Asp Phe
130 135 140
Ala Lys Trp Arg Cys Val Leu Lys Ile Gly Glu His Thr Pro Ser Ala
145 150 155 160
Leu Ala Ile Met Glu Asn Ala Asn Val Leu Ala Arg Tyr Ala Ser Ile
165 170 175
Cys Gln Gln Asn Gly Ile Val Pro Ile Val Glu Pro Glu Ile Leu Pro
180 185 190
Asp Gly Asp His Asp Leu Lys Arg Cys Gln Tyr Val Thr Glu Lys Val
195 200 205
Leu Ala Ala Val Tyr Lys Ala Leu Ser Asp His His Ile Tyr Leu Glu
210 215 220
Gly Thr Leu Leu Lys Pro Asn Met Val Thr Pro Gly His Ala Cys Thr
225 230 235 240
Gln Lys Phe Ser His Glu Glu Ile Ala Met Ala Thr Val Thr Ala Leu
245 250 255
Arg Arg Thr Val Pro Pro Ala Val Thr Gly Ile Thr Phe Leu Ser Gly
260 265 270
Gly Gln Ser Glu Glu Glu Ala Ser Ile Asn Leu Asn Ala Ile Asn Lys
275 280 285
Cys Pro Leu Leu Lys Pro Trp Ala Leu Thr Phe Ser Tyr Gly Arg Ala

290 295 300
Leu Gln Ala Ser Ala Leu Lys Ala Trp Gly Gly Lys Lys Glu Asn Leu
305 310 315 320
Lys Ala Ala Gln Glu Glu Tyr Val Lys Arg Ala Leu Ala Asn Ser Leu
325 330 335
Ala Cys Gln Gly Lys Tyr Thr Pro Ser Gly Gln Ala Gly Ala Ala Ala
340 345 350
Ser Glu Ser Leu Phe Val Ser Asn His Ala Tyr
355 360

<210> 691
<211> 1216
<212> DNA
<213> Homo Sapiens

<400> 691
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ctggcagtcc agctctccaa ggggcgtgag agtgttctga tcatctccac agacccagca 180
cacaacatct cagatgcttt tgaccagaag ttctcaaagg tgcctaccaa ggtcaaaggc 240
tatgacaacc tctttgctat ggagattgac cccagcctgg gcgtggcgga cgtgcctgac 300
gagttcttcg aggaggacaa catgctgagc atgggcaaga agatgatgca ggaggccatg 360
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ggcatgaact tctcggtggt ggtatttgac acggcaccca cgggccacac cctgaggctg 480
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atcagccctt tcatctcaca gatgtgcaac atgctgggcc tgggggacat gaacgcagac 600
cagctggcct ccaagctgga ggagacgctg cccgtcatcc gctcagtcag cgaacagttc 660
aaggaccctg agcagacaac tttcatctgc gtatgcattg ctgagttcct gtccctgtat 720
gagacagaga ggctgatcca ggagctggcc aagtgcaaga ttgacacaca caatataatt 780
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aagctgccgc tgttacccca tgaggtgcgg ggggcagaca aggtcaacac cttctcggcc 960
ctcctcctgg agccctacaa gcccccagt gcccagtagc acagctgcca gcccaaccg 1020
ctgccatttc acactcaccc tccaccctcc ccaccccctc ggggcagagt ttgcacaaag 1080
tcccccccat aatacagggg gagccacttg ggcaggaggc agggaggggt ccattccccc 1140
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aaatgatctt aaactg 1216

<210> 692
<211> 1958
<212> DNA
<213> Homo Sapiens

<400> 692
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tcccgcccac gtcccatttc gcccctcgcg tccggagtcc ccgtggccag atctaaccat 180
gagctaccct ggctatcccc cgccccagg tggctaccca ccagctgcac caggtggtgg 240
tccctgggga ggtgctgcct accctcctcc gcccagcatg ccccccatcg ggctggataa 300
cgtggccacc tatgcggggc agttcaacca ggactatctc tcgggaatgg cggccaacat 360
gtctgggaca tttggaggag ccaacatgcc caacctgtac cctggggccc ctggggctgg 420
ctacccacca gtgccccctg gcggctttgg gcagcccccc tctgcccagc agcctgttcc 480
tccctatggg atgtatccac ccccaggagg aaacccaccc tccaggatgc cctcatatcc 540
gccataccca ggggcccctg tgccgggcca gcccatgcca ccccccggac agcagccccc 600
aggggcctac cctgggcagc caccagtgac ctaccctggt cagcctccag tgccactccc 660

tgggcagcag cagccagtgc cgagctaccc aggatacccg gggtctggga ctgtcacccc 720
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ccccctgcga gatgccgagg tcctgcggaa ggccatgaaa ggcttcggga cggatgagca 840
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ccgcagcaat gagcacatcc gagaattaaa cagagcctac aaagcagaat tcaaaaagac 1140
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cagcgagacc gacctcctgg acatcagatc agagtataag cggatgtacg gcaagtcgct 1620
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tcaccgtcct agagcttagg cctgtcttcc acccctcctg acccgtatag tgtgccacag 1860
gacctgggtc ggtctagaac tctctcagga tgcctttttct accccatccc tcacagcctc 1920
ttgctgctaa aatagatgtt tcattttctt gaaaaaaa 1958

<210> 693
<211> 505
<212> PRT
<213> Homo Sapiens

<400> 693
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Ala Pro Gly Gly Gly Pro Trp Gly Gly Ala Ala Tyr Pro Pro Pro Pro
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Ser Met Pro Pro Ile Gly Leu Asp Asn Val Ala Thr Tyr Ala Gly Gln
35 40 45
Phe Asn Gln Asp Tyr Leu Ser Gly Met Ala Ala Asn Met Ser Gly Thr
50 55 60
Phe Gly Gly Ala Asn Met Pro Asn Leu Tyr Pro Gly Ala Pro Gly Ala
65 70 75 80
Gly Tyr Pro Pro Val Pro Pro Gly Gly Phe Gly Gln Pro Pro Ser Ala
85 90 95
Gln Gln Pro Val Pro Pro Tyr Gly Met Tyr Pro Pro Pro Gly Gly Asn
100 105 110
Pro Pro Ser Arg Met Pro Ser Tyr Pro Pro Tyr Pro Gly Ala Pro Val
115 120 125
Pro Gly Gln Pro Met Pro Pro Pro Gly Gln Gln Pro Pro Gly Ala Tyr
130 135 140
Pro Gly Gln Pro Pro Val Thr Tyr Pro Gly Gln Pro Pro Val Pro Leu
145 150 155 160
Pro Gly Gln Gln Gln Pro Val Pro Ser Tyr Pro Gly Tyr Pro Gly Ser
165 170 175
Gly Thr Val Thr Pro Ala Val Pro Pro Thr Gln Phe Gly Ser Arg Gly
180 185 190
Thr Ile Thr Asp Ala Pro Gly Phe Asp Pro Leu Arg Asp Ala Glu Val
195 200 205

Leu Arg Lys Ala Met Lys Gly Phe Gly Thr Asp Glu Gln Ala Ile Ile
210 215 220
Asp Cys Leu Gly Ser Arg Ser Asn Lys Gln Arg Gln Gln Ile Leu Leu
225 230 235 240
Ser Phe Lys Thr Ala Tyr Gly Lys Asp Leu Ile Lys Asp Leu Lys Ser
245 250 255
Glu Leu Ser Gly Asn Phe Glu Lys Thr Ile Leu Ala Leu Met Lys Thr
260 265 270
Pro Val Leu Phe Asp Ile Tyr Glu Ile Lys Glu Ala Ile Lys Gly Val
275 280 285
Gly Thr Asp Glu Ala Cys Leu Ile Glu Ile Leu Ala Ser Arg Ser Asn
290 295 300
Glu His Ile Arg Glu Leu Asn Arg Ala Tyr Lys Ala Glu Phe Lys Lys
305 310 315 320
Thr Leu Glu Glu Ala Ile Arg Ser Asp Thr Ser Gly His Phe Gln Arg
325 330 335
Leu Leu Ile Ser Leu Ser Gln Gly Asn Arg Asp Glu Ser Thr Asn Val
340 345 350
Asp Met Ser Leu Ala Gln Arg Asp Ala Gln Glu Leu Tyr Ala Ala Gly
355 360 365
Glu Asn Arg Leu Gly Thr Asp Glu Ser Lys Phe Asn Ala Val Leu Cys
370 375 380
Ser Arg Ser Arg Ala His Leu Val Ala Val Phe Asn Glu Tyr Gln Arg
385 390 395 400
Met Thr Gly Arg Asp Ile Glu Lys Ser Ile Cys Arg Glu Met Ser Gly
405 410 415
Asp Leu Glu Glu Gly Met Leu Ala Val Val Lys Cys Leu Lys Asn Thr
420 425 430
Pro Ala Phe Phe Ala Glu Arg Leu Asn Lys Ala Met Arg Gly Ala Gly
435 440 445
Thr Lys Asp Arg Thr Leu Ile Arg Ile Met Val Ser Arg Ser Glu Thr
450 455 460
Asp Leu Leu Asp Ile Arg Ser Glu Tyr Lys Arg Met Tyr Gly Lys Ser
465 470 475 480
Leu Tyr His Asp Ile Ser Gly Asp Thr Ser Gly Asp Tyr Arg Lys Ile
485 490 495
Leu Leu Lys Ile Cys Gly Gly Asn Asp
500 505

<210> 694
<211> 1141
<212> DNA
<213> Homo Sapiens

<400> 694
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gaatttcgta accagaagcc gaagccggag aaccaagatg aatcagaact ccttacggtt 120
cctgatggtt ggaaggaacc agcttttttcc aaagaggaca atcccagagg acttttggag 180
gagagcagtt tcgcaacttt gttcccaaaa tacagggaag cttacttgaa agagtgttgg 240
ccattggtgc agaaagcctt aaatgaacat catgttaatg caaccctgga cctgatcgaa 300
ggcagcatga ctgtttgtac tacaaagaag acttttgatc catatatcat cattagggcc 360
agagatctga taaaactgtt agcaaggagt gtttcatttg aacaggcagt acgaattctt 420
caggatgatg ttgcatgtga catcattaaa ataggttctt tagtaaggaa taaagagaga 480
tttgtaaaac gaagacaacg gcttattggt cccaaaggat ctacattgaa ggcattggaa 540
ctcttaacta attgttacat tatggttcag ggaaacacag tttcagccat tggacctttt 600

agtggcttaa aagaggttag aaaagtagtc cttgatacta tgaagaatat tcatccaatt 660
tataacatta aaagcttaat gattaagaga gagttggcaa aagattctga attacgatca 720
caaagttggg agagattttt gccacagttc aaacacaaaa atgtgaataa acgcaaggaa 780
ccaaagaaaa aaactgttaa gaaagatata cgccattccc accaccacaa ccagaaagtc 840
agatcgataa agaattggct agtggtgaat actttttgaa ggcaaatcag aagaagcggc 900
agaaaatgaa gcaataaagg ctaaacaagc agaagccatc agtaagagac aagaggaaag 960
aaacaaagca tttattccac ctaaggaaaa accaattgtg aaacctaagg aagcttctac 1020
tgaaactaaa attgatgtgg ccagcatcaa ggaaaaggtt aagaaagcaa agaataagaa 1080
actgggagct cttacagctg aagaaattgc acttaagatg gaggcagatg aaaaaaaaaa 1140
a 1141

<210> 695
<211> 288
<212> PRT
<213> Homo Sapiens

<400> 695
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Glu Phe Arg Asn Gln Lys Pro Lys Pro Glu Asn Gln Asp Glu Ser Glu
20 25 30
Leu Leu Thr Val Pro Asp Gly Trp Lys Glu Pro Ala Phe Ser Lys Glu
35 40 45
Asp Asn Pro Arg Gly Leu Leu Glu Glu Ser Ser Phe Ala Thr Leu Phe
50 55 60
Pro Lys Tyr Arg Glu Ala Tyr Leu Lys Glu Cys Trp Pro Leu Val Gln
65 70 75 80
Lys Ala Leu Asn Glu His His Val Asn Ala Thr Leu Asp Leu Ile Glu
85 90 95
Gly Ser Met Thr Val Cys Thr Thr Lys Lys Thr Phe Asp Pro Tyr Ile
100 105 110
Ile Ile Arg Ala Arg Asp Leu Ile Lys Leu Leu Ala Arg Ser Val Ser
115 120 125
Phe Glu Gln Ala Val Arg Ile Leu Gln Asp Asp Val Ala Cys Asp Ile
130 135 140
Ile Lys Ile Gly Ser Leu Val Arg Asn Lys Glu Arg Phe Val Lys Arg
145 150 155 160
Arg Gln Arg Leu Ile Gly Pro Lys Gly Ser Thr Leu Lys Ala Leu Glu
165 170 175
Leu Leu Thr Asn Cys Tyr Ile Met Val Gln Gly Asn Thr Val Ser Ala
180 185 190
Ile Gly Pro Phe Ser Gly Leu Lys Glu Val Arg Lys Val Val Leu Asp
195 200 205
Thr Met Lys Asn Ile His Pro Ile Tyr Asn Ile Lys Ser Leu Met Ile
210 215 220
Lys Arg Glu Leu Ala Lys Asp Ser Glu Leu Arg Ser Gln Ser Trp Glu
225 230 235 240
Arg Phe Leu Pro Gln Phe Lys His Lys Asn Val Asn Lys Arg Lys Glu
245 250 255
Pro Lys Lys Lys Thr Val Lys Lys Asp Ile Arg His Ser His His His
260 265 270
Asn Gln Lys Val Arg Ser Ile Lys Asn Trp Leu Val Val Asn Thr Phe
275 280 285

<210> 696

<211> 1008
<212> DNA
<213> Homo Sapiens

<400> 696
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atactacagt gaagaaacct gaatcaaaga aggaacagac cccagagcat gggaagaaaa 120
aacgtggcag aggaaaagcc caagttaaag caacaaatga atccgaagac gaaatcccac 180
agctggtacc aataggaaag aagactccag ctaatgaaaa agtagagatt caaaaacatg 240
ccacagggaa gaagtctcca gcaaagagtc ctaatcccag cacacctcgt gggaagaaaa 300
agaaaggctt tgccagcatc tgagacccca aaagctgcag agtctgagac cccagggaaa 360
agcccagaga agaagcctaa aatcaaagaa gaggcagtga aggaaaaaag tccttcgctg 420
gggaaaaaag atgcgagaca gactcccaaa aaagccagag gccaagtttt tcaccattcc 480
tagtaaatct gtgagaaaag cttcccacac ccccaaaaaa tggcccaaaa aacccaaagt 540
accccagtcg acctaaagtc agtgattcaa ctggaaggaa acctcaatgc tgcctccaga 600
gctttttgga aatactcaga tcctggccgc ctttgtaacc ttctctaaac gtcaggcctg 660
gacttaaaag atttttaaa acctccataa gtagtccagg ggcggtggct cacgcctgta 720
atcccagcac tttgggaggc cgaggcaggc ggatcacaag gtcaacgaga tcgagaccat 780
cctggccaac atggtgaaac cctgtctgta ccaaaaatac aaaaattaat tgggcatggt 840
ggtggacacc tgtaatccca gctactaggg aggctgaggc aggagaattg cttgaacctg 900
ggaggcggag gttgcagtga gccactgcac tccagcctga tgacagagca agactcagtc 960
tcaaaaataa ataaaaataa taaaacctcc ataagtaatc ctgaaaaa 1008

<210> 697
<211> 685
<212> DNA
<213> Homo Sapiens

<400> 697
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aaaaaanaaa aagaaaaaag anaatgccca gcgcggtggc taatgcctgt aaccctagtg 120
agacagccaa gtaaaaacgg ctcccaagac aatctacaag cactgggagg atggggtgca 180
gcaccaaaat gttcacacca tttgcagagg ggaacagcct ggcccctgct gttccaggat 240
agtaaccagg aattcagttg gtgagatgga cagcctgtta gcaggactcc atctcacttt 300
gctgtgttgt tctttttccc ttttgcccaa taaattngta acccctcacc tttcaaagtg 360
tctgcgtgcc taatctttcc ctgccatgtg accagaaccc ggttttgttt acaacaccag 420
cactttggga ggcgaagatg ggctgattgc ttgagctcag ggtttaaga acagcctggg 480
caacatagtg aaaccctagt ttttaccaaa aatacgaaaa ttaaccaggc atgcctgtta 540
tcccagctga ggcacaagaa tcccttgaac ccaggaggcn gaannctaat tnnaacccga 600
aaatttgcnc ccactggccc ccccaggcgg aagctagtga gccgagattg cgccactgca 660
cccctgagac gctgtntcaa aaaaa 685

<210> 698
<211> 1205
<212> DNA
<213> Homo Sapiens

<400> 698
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ggatgtgctt ttacatggaa ctcctgacca aaaacgaaaa ctcatcagag aatgtcttac 180
cggagaaagt gaatcatcta gtgaagatga atttgaaaag gagatggaag ctgaattaaa 240
ttctaccatg aaaacaatgg aggacaagtt atcctctctg ggaactggat cttcctcagg 300
aaatggaaaa gttgcaacag ctccgacaag gtactacgat gatatatatt ttgattctga 360
ttccgaggat gaagacagag cagtacaggt gaccaagaaa aaaaagaaga aacaacacaa 420

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gattccaaca aatgacgaat tactgtntga tcctgaaaaa gataacagag atcaggcctg     480
ggttgatgca cagagaaggg gttaccatgg tttgggacca cagagatcac gtcaacaaca     540
gcctgttcca aatagtgatg ctgtcttgan ttgtcctgcc tgcatgacca cactttgcct     600
tgattgccaa aggcatgant catacaaaac tcaatataga gcaatgtttg taatgaattg     660
ttctattaac aaagaggagg ttctaagata taaagcctca gagaacagga agaaaaggcg     720
ggtccataag aagatgaggt ctaaccggga agatgctgcc gagaaggcag agacagatgt     780
ggaagaaatc tatcacccag tcatgtgcac tgaatgttcc actgaagtgg cagtctacga     840
caaggatgaa gtctttcatt ttttcaatgt tttagcaagc cattcctaaa cagcccaact     900
ggcatttaat tacccaatac tgtatataag gcaaatatgg acagttactt tcctcttgcc     960
tgttcatatc cttcagtgac attgaggaag cagtgtttct ctttttaaag gagaatagtt    1020
gtcaaccttc attcatctct tacatctctc accctctcct tttttttttc tttgattttc    1080
ccccttattg atgggactga tattcattct gtttttgatg aacatttgga aactgtcggg    1140
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aaaaa                                                                1205
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<210> 699
<211> 1427
<212> DNA
<213> Homo Sapiens

<400> 699

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gatgttgcca caagctgcat tggagactca ttgcagtaat atttccaatg tgccacctac     180
aagagagata cttcaagtct ttcttactga tgtacacatg aaggaagtaa ttcagcagtt     240
cattgatgtc ctgagtgtag cagtcaagaa acgtgtcttg tgtttaccta gggatgaaaa     300
cctgacagca aatgaagttt tgaaaacgtg tgataggaaa gcaaatgttg caatcctgtt     360
ttctgggggc attgattcca tggttattgc aacccttgct gaccgtcata ttcctttaga     420
tgaaccaatt gatcttctta atgtagcttt catagctgaa gaaaagacca tgccaactac     480
ctttaacaga gaagggaata aacagaaaaa taaatgtgaa ataccttcag aagaattctc     540
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ttttgttgaa attaatgttt ctatggaaga actgcagaaa ttaagaagaa ctcgaatatg     720
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tgcttctaga ggaattggtt ggttagtggc ccaggaagga gtgaaatcct atcagagcaa     840
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agaagcaaga tttcctttcc tggatgaaaa tgttgtctcc tttctaaatt ctctgccgat    1080
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tggatcaaga attgcaaaaa tggaaaaaat taatgaaaag gcatctgata aatgtggacg    1260
gctccaaatc atgtccttag aaaatctttc tattgaaaag gagactaaat tgtaatgtga    1320
ttcacaatgt aacaatataa aaataagttt ttatataatt atataaaagt aagatactct    1380
gctgctttac tattgtataa tatagtagtt ttaaagttca aaaaaaa                  1427
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<210> 700
<211> 1967
<212> DNA
<213> Homo Sapiens

<400> 700

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ggcacgaggg aaagaggtac gaaatgatga aggaaaagta attcggttcc attgtaaatt      60
atgcgagtgc agctttaatg atcccaatgc taaggagatg cacttaaaag ggcgaagaca     120
cagacttcaa tataaaaaaa aagtaaatcc agatttgcaa gtagaagtaa agcctagtat     180
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tcgagcaaga aagattcaag aagagaaaat gaggaagcaa atgcagaagg aggagtactg 240
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gtactggagg agaatggagg aagaacaaca tcattgggat gatcgccgcc gaatgccaga 360
tggaggttat cctcatggtc ctccaggccc attaggcctt ctgggagtcc gaccaggcat 420
gcctcctcag cctcaggggc ctgcaccctt acgtcgtcct gactcatctg atgaccgttt 480
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gactcatctg atgaccgtta tgtaatgaca aaacatgcca ccatttatcc aactgaagag 600
gagttacagg cagttcagaa aattgtttct attactgaac gtgctttaaa actcgtttca 660
gacagtttgt ctgaacatga gaagaacaag aacaaagagg gagatgataa gaaagaggga 720
ggtaaagaca gagctttgaa aggagttttg cgagtgggag tatttgcaaa agggattact 780
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<213> Homo Sapiens

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<400> 708

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Phe Ala Asn Val Glu Glu His Ser Phe Ser Tyr Gly Ala Arg Asp Gly
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Pro His Gly Asp Tyr Arg Gly Gly Glu Gly Pro Gly His Asp Phe Arg
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Glu Gly Pro Pro Met Asp Tyr Arg Gly Gly Asp Gly Thr Ser Met Asp
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Tyr Arg Gly Arg Glu Ala Pro His Met Asn Tyr Arg Asp Arg Asp Ala
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His Ala Val Asp Phe Arg Gly Arg Asp Ala Pro Pro Ser Asp Phe Arg
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Gly Arg Gly Thr Tyr Asp Leu Asp Phe Arg Gly Arg Asp Gly Ser His
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Ala Asp Phe Arg Gly Arg Asp Leu Ser Asp Leu Asp Phe Arg Ala Arg
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Glu Gln Ser Arg Ser Asp Phe Arg Asn Arg Asp Val Ser Asp Leu Asp
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Gly Thr Thr Asp Leu Asp Phe Arg Asp Arg Asp Thr Pro His Ser Asp
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Phe Arg Gly Arg His Arg Ser Arg Thr Asp Gln Asp Phe Arg Gly Arg
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Glu Met Gly Ser Cys Met Glu Phe Lys Asp Arg Glu Met Pro Pro Val
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Asp Pro Asn Ile Leu Asp Tyr Ile Gln Pro Ser Thr Gln Asp Arg Glu
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His Ser Gly Met Asn Val Asn Arg Arg Glu Glu Ser Thr His Asp His
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Ser Glu Thr Arg Glu Gly Glu Thr Gln Gly Val Ala Phe Glu His Glu
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Ser Pro Ala Asp Phe Gln Asn Ser Gln Ser Pro Val Gln Asp Gln Asp
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Lys Ser Gln Leu Ser Gly Arg Glu Glu Gln Ser Ser Asp Ala Gly Leu
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Phe Lys Glu Glu Gly Gly Leu Asp Phe Leu Gly Arg Gln Asp Thr Asp
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Tyr Arg Ser Met Glu Tyr Arg Asp Val Asp His Arg Leu Pro Gly Ser
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Gln Met Phe Gly Tyr Gly Gln Ser Lys Ser Phe Pro Glu Gly Lys Thr
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Ala Arg Asp Ala Gln Arg Asp Leu Gln Asp Gln Asp Tyr Arg Thr Gly
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Glu Asp Ala Thr Lys Glu Glu Ile Leu Asn Ala Phe Arg Thr Pro Asp
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Asp Tyr Gly Tyr Val Cys Val Glu Phe Ser Leu Leu Glu Asp Ala Ile
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Gly Cys Met Glu Ala Asn Gln Gly Thr Leu Met Ile Gln Asp Lys Glu
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Val Thr Leu Glu Tyr Val Ser Ser Leu Asp Phe Trp Tyr Cys Lys Arg
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Asn Pro Arg Glu Val Thr Glu Ala Lys Gln Glu Leu Ile Thr Tyr Pro
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Gln Pro Gln Lys Thr Ser Ile Pro Ala Pro Leu Glu Lys Gln Pro Asn
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Gln Pro Leu Arg Pro Ala Asp Lys Glu Pro Glu Pro Arg Lys Arg Glu
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Glu Gly Gln Glu Ser Arg Leu Gly His Gln Lys Arg Glu Ala Glu Arg
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Tyr Leu Pro Pro Ser Arg Arg Glu Gly Pro Thr Phe Arg Arg Asp Arg
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Glu Arg Glu Ser Trp Ser Gly Glu Thr Arg Gln Asp Gly Glu Ser Lys
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Thr Ile Met Leu Lys Arg Ile Tyr Arg Ser Thr Pro Pro Glu Val Ile
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Val Glu Val Leu Glu Pro Tyr Val Arg Leu Thr Thr Ala Asn Val Arg
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Ile Ile Lys Asn Arg Thr Gly Pro Met Gly His Thr Tyr Gly Phe Ile

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His Ser Gly Asn Phe Pro Gly Arg Asp Ser Leu Pro Phe Asp Phe Gln
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Pro Gly His Asp Phe Arg Gly Gly Asp Phe Ser Ser Ser Asp Phe Gln
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Ser Arg Asp Ser Ser Gln Leu Asp Phe Arg Gly Arg Asp Ile His Ser
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Asp Gly Thr Ser Met Asp Tyr Arg Gly Arg Glu Ala Pro His Met Asn
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Tyr Arg Asp Arg Asp Ala His Ala Val Asp Phe Arg Gly Arg Asp Ala
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Pro Pro Ser Asp Phe Arg Gly Arg Gly Thr Tyr Asp Leu Asp Phe Arg
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Lys Gly Glu Phe Glu His Ser Glu Thr Arg Glu Gly Glu Thr Gln Gly
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<210> 800
<211> 364
<212> PRT
<213> Homo Sapiens

<400> 800
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20 25 30
Ala Asp Glu Ser Thr Gly Ser Ile Ala Lys Arg Leu Gln Ser Ile Gly
35 40 45
Thr Glu Asn Thr Glu Glu Asn Arg Arg Phe Tyr Arg Gln Leu Leu Leu
50 55 60
Thr Ala Asp Asp Arg Val Asn Pro Cys Ile Gly Gly Val Ile Leu Phe
65 70 75 80
His Glu Thr Leu Tyr Gln Lys Ala Asp Asp Gly Arg Pro Phe Pro Gln
85 90 95
Val Ile Lys Ser Lys Gly Gly Val Val Gly Ile Lys Val Asp Lys Gly
100 105 110
Val Val Pro Leu Ala Gly Thr Asn Gly Glu Thr Thr Thr Gln Gly Leu
115 120 125
Asp Gly Leu Ser Glu Arg Cys Ala Gln Tyr Lys Lys Asp Gly Ala Asp
130 135 140
Phe Ala Lys Trp Arg Cys Val Leu Lys Ile Gly Glu His Thr Pro Ser
145 150 155 160
Ala Leu Ala Ile Met Glu Asn Ala Asn Val Leu Ala Arg Tyr Ala Ser
165 170 175
Ile Cys Gln Gln Asn Gly Ile Val Pro Ile Val Glu Pro Glu Ile Leu
180 185 190
Pro Asp Gly Asp His Asp Leu Lys Arg Cys Gln Tyr Val Thr Glu Lys
195 200 205
Val Leu Ala Ala Val Tyr Lys Ala Leu Ser Asp His His Ile Tyr Leu
210 215 220
Glu Gly Thr Leu Leu Lys Pro Asn Met Val Thr Pro Gly His Ala Cys
225 230 235 240

Thr Gln Lys Phe Ser His Glu Glu Ile Ala Met Ala Thr Val Thr Ala
245 250 255
Leu Arg Arg Thr Val Pro Pro Ala Val Thr Gly Ile Thr Phe Leu Ser
260 265 270
Gly Gly Gln Ser Glu Glu Glu Ala Ser Ile Asn Leu Asn Ala Ile Asn
275 280 285
Lys Cys Pro Leu Leu Lys Pro Trp Ala Leu Thr Phe Ser Tyr Gly Arg
290 295 300
Ala Leu Gln Ala Ser Ala Leu Lys Ala Trp Gly Gly Lys Lys Glu Asn
305 310 315 320
Leu Lys Ala Ala Gln Glu Glu Tyr Val Lys Arg Ala Leu Ala Asn Ser
325 330 335
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Ala Ser Glu Ser Leu Phe Val Ser Asn His Ala Tyr
355 360

<210> 801
<211> 3504
<212> DNA
<213> Homo Sapiens

<400> 801
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cacctgagaa tagtgacatt ggtacaggaa agaaagagaa agaaaagaaa aatagaaagg 720
gcaaggacaa ggaaaatggc tctgtatcca ccagtgagac accaccacct ccaccaccaa 780
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tgacctgtgt gtcctatggt ttaagagcaa attttgaaac ttggagttgt ggtttttcag    2160
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<210> 802
<211> 429
<212> PRT
<213> Homo Sapiens

<400> 802

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            20                  25                  30
Lys Thr Val Ile Val Asn Met Val Asp Val Ala Lys Ala Leu Asn Arg
        35                  40                  45
Pro Pro Thr Tyr Pro Thr Lys Tyr Phe Gly Cys Glu Leu Gly Ala Gln
    50                  55                  60
Thr Gln Phe Asp Val Lys Asn Asp Arg Tyr Ile Val Asn Gly Ser His
65                  70                  75                  80
Glu Ala Asn Lys Leu Gln Asp Met Leu Asp Gly Phe Ile Lys Lys Phe
                85                  90                  95
Val Leu Cys Pro Glu Cys Glu Asn Pro Glu Thr Asp Leu His Val Asn
            100                 105                 110
Pro Lys Lys Gln Thr Ile Gly Asn Ser Cys Lys Ala Cys Gly Tyr Arg
        115                 120                 125
Gly Met Leu Asp Thr His His Lys Leu Cys Thr Phe Ile Leu Lys Asn
    130                 135                 140
Pro Pro Glu Asn Ser Asp Ile Gly Thr Gly Lys Lys Glu Lys Glu Lys
145                 150                 155                 160
Lys Asn Arg Lys Gly Lys Asp Lys Glu Asn Gly Ser Val Ser Thr Ser
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165 170 175
Glu Thr Pro Pro Pro Pro Pro Pro Asn Glu Ile Ser Pro Pro His Ala
180 185 190
Val Glu Glu Glu Glu Asp Asp Asp Trp Gly Glu Asp Thr Thr Glu Glu
195 200 205
Ala Gln Arg Arg Arg Met Asp Glu Ile Ser Asp His Ala Lys Gly Leu
210 215 220
Thr Leu Ser Asp Asp Leu Glu Arg Thr Val Glu Glu Arg Val Asn Ile
225 230 235 240
Leu Phe Asp Phe Val Lys Lys Lys Lys Glu Glu Gly Ile Ile Asp Ser
245 250 255
Ser Asp Lys Asp Ile Val Ala Glu Ala Glu Arg Leu Asp Val Lys Ala
260 265 270
Met Gly Pro Leu Val Leu Thr Glu Val Leu Phe Asp Glu Lys Ile Arg
275 280 285
Glu Gln Ile Lys Lys Tyr Arg Arg His Phe Leu Arg Phe Cys His Asn
290 295 300
Asn Lys Lys Ala Gln Arg Tyr Leu Leu His Gly Leu Glu Cys Val Val
305 310 315 320
Ala Met His Gln Ala Gln Leu Ile Ser Lys Ile Pro His Ile Leu Lys
325 330 335
Glu Met Tyr Asp Ala Asp Leu Leu Glu Glu Glu Val Ile Ile Ser Trp
340 345 350
Ser Glu Lys Ala Ser Lys Lys Tyr Val Ser Lys Glu Leu Ala Lys Glu
355 360 365
Ile Arg Val Lys Ala Glu Pro Phe Ile Lys Trp Leu Lys Glu Ala Glu
370 375 380
Glu Glu Ser Ser Gly Gly Glu Glu Glu Asp Glu Asp Glu Asn Ile Glu
385 390 395 400
Val Val Tyr Ser Lys Thr Ala Ser Val Pro Lys Val Glu Thr Val Lys
405 410 415
Ser Asp Asn Lys Asp Asp Asp Ile Asp Ile Asp Ala Ile
420 425

<210> 803
<211> 2251
<212> DNA
<213> Homo Sapiens

<400> 803
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gcttattcca ggggtgtgtt tcgtcgagat gcacacaaga gtgaggttgc tcatcggttt 180
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tccaagttag tgacagatct taccaaagtc cacacggaat gctgccatgg agatctgctt 900

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<210> 804
<211> 609
<212> PRT
<213> Homo Sapiens

<400> 804

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Tyr Ser Arg Gly Val Phe Arg Arg Asp Ala His Lys Ser Glu Val Ala
            20                  25                  30
His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu
        35                  40                  45
Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His Val
    50                  55                  60
Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala Asp
65                  70                  75                  80
Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly Asp
                85                  90                  95
Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met Ala
            100                 105                 110
Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu Gln
        115                 120                 125
His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu Val
    130                 135                 140
Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu Lys
145                 150                 155                 160
Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala Pro
                165                 170                 175
Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu Cys
            180                 185                 190
Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu Pro Lys Leu Asp Glu
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195 200 205
Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys Gln Arg Leu Lys Cys
210 215 220
Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe Lys Ala Trp Ala Val
225 230 235 240
Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu Phe Ala Glu Val Ser
245 250 255
Lys Leu Val Thr Asp Leu Thr Lys Val His Thr Glu Cys Cys His Gly
260 265 270
Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp Leu Ala Lys Tyr Ile
275 280 285
Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu Lys Glu Cys Cys Glu
290 295 300
Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala Glu Val Glu Asn Asp
305 310 315 320
Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala Asp Phe Val Glu Ser
325 330 335
Lys Asp Val Cys Lys Asn Tyr Ala Glu Ala Lys Asp Val Phe Leu Gly
340 345 350
Met Phe Leu Tyr Glu Tyr Ala Arg Arg His Pro Asp Tyr Ser Val Val
355 360 365
Leu Leu Leu Arg Leu Ala Lys Thr Tyr Glu Thr Thr Leu Glu Lys Cys
370 375 380
Cys Ala Ala Ala Asp Pro His Glu Cys Tyr Ala Lys Val Phe Asp Glu
385 390 395 400
Phe Lys Pro Leu Val Glu Glu Pro Gln Asn Leu Ile Lys Gln Asn Cys
405 410 415
Glu Leu Phe Lys Gln Leu Gly Glu Tyr Lys Phe Gln Asn Ala Leu Leu
420 425 430
Val Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Leu Val
435 440 445
Glu Val Ser Arg Asn Leu Gly Lys Val Gly Ser Lys Cys Cys Lys His
450 455 460
Pro Glu Ala Lys Arg Met Pro Cys Ala Glu Asp Tyr Leu Ser Val Val
465 470 475 480
Leu Asn Gln Leu Cys Val Leu His Glu Lys Thr Pro Val Ser Asp Arg
485 490 495
Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys Phe
500 505 510
Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn Ala
515 520 525
Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys Glu
530 535 540
Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His Lys
545 550 555 560
Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe Ala
565 570 575
Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys Phe
580 585 590
Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu Gly
595 600 605
Leu

<210> 805

<211> 1356
<212> DNA
<213> Homo Sapiens

<400> 805
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aagcttcaag gaacaataaa tagtaacctg gtaatg 1356

<210> 806
<211> 299
<212> PRT
<213> Homo Sapiens

<400> 806
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Gly Glu Ser Pro Val Trp Glu Glu Val Ser Asn Ser Leu Leu Phe Val
20 25 30
Asp Ile Pro Ala Lys Lys Val Cys Arg Trp Asp Ser Phe Thr Lys Gln
35 40 45
Val Gln Arg Val Thr Met Asp Ala Pro Val Ser Ser Val Ala Leu Arg
50 55 60
Gln Ser Gly Gly Tyr Val Ala Thr Ile Gly Thr Lys Phe Cys Ala Leu
65 70 75 80
Asn Trp Lys Glu Gln Ser Ala Val Val Leu Ala Thr Val Asp Asn Asp
85 90 95
Lys Lys Asn Asn Arg Phe Asn Asp Gly Lys Val Asp Pro Ala Gly Arg
100 105 110
Tyr Phe Ala Gly Thr Met Ala Glu Glu Thr Ala Pro Ala Val Leu Glu
115 120 125
Arg His Gln Gly Ala Leu Tyr Ser Leu Phe Pro Asp His His Val Lys
130 135 140
Lys Tyr Phe Asp Gln Val Asp Ile Ser Asn Gly Leu Asp Trp Ser Leu
145 150 155 160

Asp His Lys Ile Phe Tyr Tyr Ile Asp Ser Leu Ser Tyr Ser Val Asp
165 170 175

Ala Phe Asp Tyr Asp Leu Gln Thr Gly Gln Ile Ser Asn Arg Arg Ser
180 185 190

Val Tyr Lys Leu Glu Lys Glu Glu Gln Ile Pro Asp Gly Met Cys Ile
195 200 205

Asp Ala Glu Gly Lys Leu Trp Val Ala Cys Tyr Asn Gly Gly Arg Val
210 215 220

Ile Arg Leu Asp Pro Val Thr Gly Lys Arg Leu Gln Thr Val Lys Leu
225 230 235 240

Pro Val Asp Lys Thr Thr Ser Cys Cys Phe Gly Gly Lys Asn Tyr Ser
245 250 255

Glu Met Tyr Val Thr Cys Ala Arg Asp Gly Met Asp Pro Glu Gly Leu
260 265 270

Leu Arg Gln Pro Glu Ala Gly Gly Ile Phe Lys Ile Thr Gly Leu Gly
275 280 285

Val Lys Gly Ile Ala Pro Tyr Ser Tyr Ala Gly
290 295

<210> 807
<211> 1980
<212> DNA
<213> Homo Sapiens

<400> 807

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atgaaagccg cggagagggg agatgtagaa aaagtttcct caatccttgc taaaaagggc 180
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<210> 808
<211> 659
<212> PRT
<213> Homo Sapiens

<400> 808
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35 40 45
Val Glu Lys Val Ser Ser Ile Leu Ala Lys Lys Gly Ile Asn Pro Gly
50 55 60
Lys Leu Asp Val Glu Gly Arg Ser Ala Phe His Val Val Ala Ser Lys
65 70 75 80
Gly Asn Leu Glu Cys Leu Asn Ala Ile Leu Ile His Gly Val Asp Ile
85 90 95
Thr Thr Ser Asp Thr Ala Gly Arg Asn Ala Leu His Leu Ala Ala Lys
100 105 110
Tyr Gly His Ala Leu Cys Leu Gln Lys Leu Leu Gln Tyr Asn Cys Pro
115 120 125
Thr Glu His Ala Asp Leu Gln Gly Arg Thr Ala Leu His Asp Ala Ala
130 135 140
Met Ala Asp Cys Pro Ser Ser Ile Gln Leu Leu Cys Asp His Gly Ala
145 150 155 160
Ser Val Asn Ala Lys Asp Val Asp Gly Arg Thr Pro Leu Val Leu Ala
165 170 175
Thr Gln Met Cys Arg Pro Ala Ile Cys Gln Leu Leu Ile Asp Arg Gly
180 185 190
Ala Glu Ile Asn Ser Arg Asp Lys Gln Asn Arg Thr Ala Leu Met Leu
195 200 205
Gly Cys Glu Tyr Gly Cys Lys Asp Ala Val Glu Val Leu Leu Lys Asn
210 215 220
Gly Ala Asp Val Ser Leu Leu Asp Ala Leu Gly His Asp Ser Ser Tyr
225 230 235 240
Tyr Ala Arg Ile Gly Asp Asn Leu Asp Ile Leu Thr Leu Leu Lys Thr
245 250 255
Ala Ser Glu Asn Thr Asn Lys Gly Arg Glu Leu Trp Lys Lys Gly Pro
260 265 270
Ser Leu Gln Gln Arg Asn Leu Pro Tyr Met Leu Asp Glu Val Asn Val
275 280 285
Lys Ser Ser Gln Arg Glu His Arg Asn Ile Gln Glu Leu Glu Ile Glu
290 295 300
Asn Glu Asp Leu Lys Asp Arg Leu Arg Lys Ile Gln Gln Glu Gln Arg
305 310 315 320
Ile Leu Leu Asp Lys Val Asn Gly Leu Gln Leu Gln Leu Asn Glu Glu
325 330 335
Val Met Val Ala Asp Asp Leu Glu Ser Glu Lys Glu Lys Leu Lys Ser
340 345 350
Leu Leu Val Ala Lys Glu Lys Gln His Glu Glu Ser Leu Arg Thr Ile

355 360 365
Glu Ser Leu Lys Asn Arg Phe Lys Tyr Phe Glu Cys Thr Ser Pro Gly
370 375 380
Val Pro Ala His Met Gln Ser Arg Ser Met Leu Arg Pro Leu Glu Leu
385 390 395 400
Ser Leu Pro Asn Gln Thr Ser Tyr Ser Glu Asn Asp Leu Leu Lys Lys
405 410 415
Glu Leu Glu Ala Met Arg Thr Phe Cys Glu Ser Ala Lys Gln Asp Arg
420 425 430
Leu Lys Leu Gln Asn Gly Val Ala His Lys Val Ala Glu Cys Lys Ala
435 440 445
Leu Gly Leu Glu Cys Glu Arg Ile Lys Glu Asp Ser Asp Glu Gln Ile
450 455 460
Lys Gln Leu Glu Asp Ala Leu Lys Asp Val Gln Lys Arg Met Tyr Glu
465 470 475 480
Ser Glu Gly Lys Val Lys Gln Met Gln Thr His Phe Leu Ala Leu Lys
485 490 495
Glu His Leu Thr Ser Glu Ala Ala Ile Gly Asn His Arg Leu Met Glu
500 505 510
Glu Leu Lys Asp Gln Leu Lys Asp Met Lys Ala Lys Tyr Glu Gly Ala
515 520 525
Ser Ala Glu Val Gly Lys Leu Arg Asn Gln Ile Lys Gln Asn Glu Leu
530 535 540
Leu Val Glu Gln Phe Arg Arg Asp Glu Gly Lys Leu Val Glu Glu Asn
545 550 555 560
Lys Arg Leu Gln Lys Glu Leu Ser Met Cys Glu Thr Glu Arg Asp Lys
565 570 575
Lys Gly Arg Arg Val Ala Glu Val Glu Gly Gln Val Lys Glu Leu Leu
580 585 590
Ala Lys Leu Thr Leu Ser Val Pro Thr Glu Lys Phe Glu Ser Met Lys
595 600 605
Ser Leu Leu Ser Ser Glu Val Asn Glu Lys Val Lys Lys Ile Gly Glu
610 615 620
Thr Glu Arg Glu Tyr Glu Lys Ser Leu Thr Glu Ile Arg Gln Leu Arg
625 630 635 640
Arg Glu Leu Glu Asn Cys Lys Arg Gln Thr Ser Ser Ala Cys Gln Ala
645 650 655
Arg Gly Ala

<210> 809
<211> 1725
<212> DNA
<213> Homo Sapiens

<400> 809
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<210> 810
<211> 355
<212> PRT
<213> Homo Sapiens

<400> 810
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35 40 45
Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro
50 55 60
Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly
65 70 75 80
Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly
85 90 95
Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val
100 105 110
Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe
115 120 125
His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr
130 135 140
Ile Ser Phe Gln Asn Pro Arg Thr Val Pro Val Gln Pro Ala Phe Ser
145 150 155 160
Thr Val Pro Phe Ser Gln Pro Val Cys Phe Pro Pro Arg Pro Arg Gly
165 170 175
Arg Arg Gln Lys Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile
180 185 190
Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe
195 200 205
Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro
210 215 220

Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser
225 230 235 240
Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile
245 250 255
Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe
260 265 270
Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly
275 280 285
Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln
290 295 300
Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala
305 310 315 320
Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu
325 330 335
Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His
340 345 350
Val Gln Thr
355

<210> 811
<211> 1022
<212> DNA
<213> Homo Sapiens

<400> 811
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ca 1022

<210> 812
<211> 317
<212> PRT
<213> Homo Sapiens

<400> 812
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20 25 30
Thr Glu Glu Gln Glu Ala Ala Val Ser Ser Ser Ser Pro Leu Val Leu

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Gly Thr Leu Glu Lys Val Pro Ala Ala Glu Ser Ala Asp Pro Pro Gln
    50                  55                  60
Ser Pro Gln Gly Ala Ser Ala Leu Pro Thr Thr Ile Ser Phe Thr Cys
65                  70                  75                  80
Trp Arg Gln Pro Asn Glu Gly Ser Ser Ser Gln Glu Glu Glu Glu Ala
                85                  90                  95
Ser Thr Ser Pro Asp Ala Glu Ser Leu Phe Arg Glu Ala Leu Ser Asn
            100                 105                 110
Lys Val Asp Glu Leu Ala His Phe Leu Leu Arg Lys Tyr Arg Ala Lys
        115                 120                 125
Glu Leu Val Thr Lys Ala Glu Met Leu Glu Arg Val Ile Lys Asn Tyr
    130                 135                 140
Lys Arg Cys Phe Pro Val Ile Phe Gly Lys Ala Ser Glu Ser Leu Lys
145                 150                 155                 160
Met Ile Phe Gly Ile Asp Val Lys Glu Val Asp Pro Ala Ser Asn Thr
                165                 170                 175
Tyr Thr Leu Val Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly
            180                 185                 190
Asn Asn Gln Ile Phe Pro Lys Thr Gly Leu Leu Ile Ile Val Leu Gly
        195                 200                 205
Thr Ile Ala Met Glu Gly Asp Ser Ala Ser Glu Glu Glu Ile Trp Glu
    210                 215                 220
Glu Leu Gly Val Met Gly Val Tyr Asp Gly Arg Glu His Thr Val Tyr
225                 230                 235                 240
Gly Glu Pro Arg Lys Leu Leu Thr Gln Asp Trp Val Gln Glu Asn Tyr
                245                 250                 255
Leu Glu Tyr Arg Gln Val Pro Gly Ser Asn Pro Ala Arg Tyr Glu Phe
            260                 265                 270
Leu Trp Gly Pro Arg Ala Leu Ala Glu Thr Ser Tyr Val Lys Val Leu
        275                 280                 285
Glu His Val Val Arg Val Asn Ala Arg Val Arg Ile Ala Tyr Pro Ser
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Leu Arg Glu Ala Ala Leu Leu Glu Glu Glu Gly Val
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<210> 813
<211> 5175
<212> DNA
<213> Homo Sapiens

<400> 813

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(57) Abstract

Tumor cell-specific antigens from melanoma cells have previously been identified using autologous cytolytic T cells clones from the patient, but the same approach did not work well with other tumour types. Here, screening of such antigens was successfully performed using antisera from the patient. Provided are several tumor cell-specific antigens, nucleic acids encoding them, antibodies and CTL's directed against these antigens, antigenic fragments diagnostic kits, etc.

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PCT/ ⌐ 98/14679

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C07K14/705 C12Q1/68 G01N33/53 C07K16/28 A61K38/17 A61K31/70 A61K39/00 A61K35/12 A61K39/395 A61K48/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K A61K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 97 17470 A (HOLLAND JAMES F) 15 May 1997 Also against claims 82-84,116,117see whole document, particularly the claims -/--	1,2, 4-10,18, 21-23, 27,28, 31,32, 40,42, 44,45, 48-51, 58-60, 67-70, 76-79

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

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Date of the actual completion of the international search	Date of mailing of the international search report
3 June 1999	29. 06. 1999
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Authorized officer Smalt, R

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GB 2 273 099 A (ASTA MEDICA AG) 8 June 1994 Also against claims 108,109,116,117. See whole document, particularly the claims and examples. ---	1,2, 4-10,31, 32,40, 42,43, 49,50, 58-60, 67,69, 71,72, 74-79, 82-84, 99-104
X	WO 97 17441 A (KISHIMURA MASAAKI ;OSAKADA FUMIO (JP); OSAKI SHOICHI (JP); NAKAO K) 15 May 1997 see the whole document -& EP 0 869 176 A (KANEKA CORPORATION, OSAKA, JAPAN) 7 October 1998 Also against claims 68-72,74,76,77,82,116,117 see claims 10,12; examples 2,5 ---	1,2,4-8, 13,18, 21,22, 24, 27-29, 31,32, 35,40, 42,44, 45, 47-50, 54,59, 60,63,67
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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	VAUGHAN, J.H. ET AL.: "Epstein-Barr virus-induced autoimmune responses." JOURNAL OF CLINICAL INVESTIGANTION, vol. 95, no. 3, March 1995, pages 1306-15, XP002103180	1,2,18, 21,22, 24, 27-29, 31,35, 40,44, 45, 47-50, 54,59, 60,63, 67-72, 74-80,82
	see the whole document -& DATABASE EMBL - EMHUM1 Entry HSIGGAUA, Acc.no. L38696, 17 February 1995 VAUGHAN, J.H. ET AL.: "Homo sapiens autoantigen p542 mRNA, complete cds." XP002103198 see the whole document ---	
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Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
X	ZWIJSEN, A. ET AL.: "Characterization of a rat C6 glioma-secreted follistatin-related protein (FRP); cloning and sequencing of the human homologue." EUROPEAN JOURNAL OF BIOCHEMISTRY, vol. 225, no. 3, November 1994, pages 937-46, XP002103181 see page 945, right-hand column, paragraph 2-4; figure 3	18,21, 22,24, 27,28, 44,45, 47-50, 54,59, 60,63, 67-72, 74-80,82
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Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
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X	JIN, Y-J. ET AL.: "Molecular cloning of a 25-kDa high affinity rapamycin binding protein, FKBP25." JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 267, no. 16, 5 June 1992, pages 10942-5, XP002104550 see figure 3 ---	44, 47-50, 54,59, 60,63, 67-72, 75,83,84
X	MACLEOD, A.R. ET AL.: "A muscle-type tropomycin in human fibroblasts: evidence for expression by an alternative RNA splicing mechanism." PROC.NAT'L.ACAD.SCI.USA, vol. 82, December 1985, pages 7835-9, XP002103179 see figures 2,3 ---	44,59, 60,63, 67-70
X	DATABASE EMBL - EMEST20 Entry/Acc.no. T09468, 8 August 1993 ADAMS, M.D. ET AL.: "EST07361 Homo sapiens cDNA clone HIBBU63 5' end." XP002103195 see the whole document -& ADAMS, M.D. ET AL.: "Rapid DNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library." NATURE GENETICS, vol. 4, 1993, pages 373-380, XP000574910 see the whole document ---	44,45, 67,70
X	DATABASE EMBL - EMEST17 Entry HSZZ32361, Acc.no. AA327309, 18 April 1997 ADAMS, M.D. ET AL.: "EST30621 Colon I Homo sapiens cDNA 5' end." XP002103199 see the whole document -& ADAMS, M.D. ET AL.: "Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence." NATURE, vol. 377, 1995, pages 3-17, XP002042918 see the whole document ---	44,45, 60,62, 67,70
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Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	DATABASE EMBL - EMEST11 Entry HS1282878, Acc.no. AA487071, 28 June 1997 HILLIER, L. ET AL.: "ab18f11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone 841197 3' similar to contains Alu repetitive element." XP002103197 see the whole document ---	44,45, 67,70
X	DATABASE EMBL - EMEST15 Entry HSAA21198, entry AA121198, 21 November 1996 HILLIER, L. ET AL.: "zl88g08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone 511742 5'." XP002103200 see the whole document ---	44,45, 60,62, 67,70
X	DATABASE EMBL - EMEST15 Entry HSAA21174, Acc.no. AA121174, 21 November 1996 HILLIER, L. ET AL.: "zl88g08.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 511742 3'." XP002103202 see the whole document ---	44,45, 60,62, 67,70
X	DATABASE EMBL - EMEST17 Entry HSW22160, Acc.no. W22160, 9 May 1996 NATHANS, J.: "63A6 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional." XP002103201 see the whole document ---	44,45, 60,62, 67,70
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X	MIKI Y ET AL: "A STRONG CANDIDATE FOR THE BREAST AND OVARIAN CANCER SUSCEPTIBILITY GENE BRCA1" SCIENCE, vol. 266, no. 12, 7 October 1994, pages 66-71, XP000202410 see the whole document -& DATABASE EMBL - EMEST5 Entry/Acc.no. AF039241, 17 January 1998 MIKI, Y. ET AL.: "Homo sapiens clone 11-67js mRNA,partial sequence." XP002103205 see the whole document ---	44,45, 60,62, 67,70
X	DATABASE EMBL - EMEST18 Entry MM1140465, Acc.no. AA221749, 15 February 1997 MARRA, M. ET AL.: "my28g01.r1 Barstead mouse pooled organs MPLRB4 Mus musculus cDNA clone 697200 5' similar to TR:E239664 E239664 CHROMOSOME XIV READING FRAME ORF YNL021W." XP002103206 see the whole document ---	44,45, 60,62, 67,70
X	NAGASE T ET AL: "PREDICTION OF THE CODING SEQUENCES OF UNIDENTIFIED HUMAN GENES VI.THE CODING SEQUENCES OF 80 NEW GENES (KIAA0201-KIAA0280) DEDUCED BYANALYSIS OF CDNA CLONES FROM CELL LINE KG-1 AND BRAIN" DNA RESEARCH, vol. 3, no. 5, 1 January 1996, pages 321-329, XP002059454 see the whole document -& DATABASE EMBL - EMHUM1 Entry HSD455, Acc.no. D87455, 9 November 1996 NOMURA, N.: "Human mRNA for KIAA0266 gene, complete cds." XP002103207 see the whole document ---	44,45, 60,62, 67,70

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Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL - EMEST16 Entry HSAA51187, Acc.no. AA151187, 15 December 1996 HILLIER, L. ET AL.: "zo03c11.r1 Stratagene colon (#937204) Homo sapiens cDNA clone 566612 5'." XP002103208 see the whole document ---	44,45, 60,62, 67,70
X	DATABASE EMBL - EMHUM2 Entry HSU50839, Acc.no. U50839, 9 March 1997 LATIF, F. ET AL.: "Homo sapiens g16 protein (g16) mRNA, complete cds." XP002103209 see the whole document ---	44,45, 60,64, 67,70
X	LI, H. ET AL.: "Isolation and sequence analysis of the human syntaxin-encoding gene." GENE, vol. 143, 1994, pages 303-4, XP002103182 see the whole document ---	44,45, 47,48, 59,60, 65, 70-72, 74,83,84
X	DATABASE EMBL - EMEST11 Entry HS1188646, Acc.no. AA285170, 5 April 1997 STRAUSBERG, R.: "zs48f04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700735 3'." XP002103210 see the whole document ---	44,45, 59,60, 67-70
X	FISHER, D.Z. ET AL.: "cDNA sequencing of nuclear lamins A and C reveals primary and secondary structural homolgy to intermediate filament proteins." PROC.NAT'L.ACAD.SCI.USA, vol. 83, September 1986, pages 6450-4, XP002103184 see figure 2 ---	44,45, 59,60, 67-70
X	DATABASE EMBL - EMEST16 Entry HSAA54222, Acc.no. AA454222, 11 June 1997 HILLIER, L. ET AL.: "zx48g12.s1 Soares testis NHT Homo sapiens cDNA clone 795526 3' similar to gb:D42040 RING3 PROTEIN (HUMAN)" XP002103189 see the whole document ---	67,69

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Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	DATABASE EMBL - EMEST20 Entry MMAA84412, Acc.no. AA184412, 19 February 1997 MARRA, M. ET AL.: "mt34f07.r1 Soares mouse 3NbMS Mus musculus cDNA clone 622981 5' similar to SW:OXYB_HUMAN P22059 OXYSTEROL-BINDING PROTEIN." XP002103194 see the whole document	67-70
A	WO 96 29409 A (LUDWIG INST CANCER RES ;UNIV LEIDEN (NL)) 26 September 1996 see the whole document	1-11, 17-33, 39-52, 58-61, 67-117
A	WO 92 20356 A (LUDWIG INST CANCER RES) 26 November 1992 see the whole document, particularly the claims	1-11, 17-33, 39-52, 58-61, 67-117
A	WO 95 23874 A (LUDWIG INST CANCER RES) 8 September 1995 see page 5, line 10-14; claims 3,4,7; examples 33,36,43,44	1-4
A	FRANZÉN, B. ET AL.: "Analysis of polypeptide expression in benign and malignant human breast lesions: down-regulation of cytokeratins." BRITISH JOURNAL OF CANCER, vol. 73, 1996, pages 1632-8, XP002104551 see abstract	1,2,4-9, 13
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A	BOON T ET AL: "Tumor antigens recognized by T cells" IMMUNOLOGY TODAY, vol. 18, no. 6, June 1997, page 267-268 XP004068293 see the whole document ---	
A	SAHIN, U. ET AL.: "Human neoplasms elicit multiple specific immune responses in the autologous host." PROC.NATL.ACAD.SCI.USA, vol. 92, December 1995, pages 11810-3, XP002091914 cited in the application see the whole document ---	
P,X	DATABASE EMBL - EMHUM1 Entry/Acc.no. AC004022, 22 January 1998 HINDS, K. ET AL.: "Homo sapiens BAC clone GS155M11 from 7q21-q22, complete sequence." XP002091837 from nt.330-810 ---	1,2
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P,X	GÜRE, A.O. ET AL.: "Human lung cancer antigens recognized by autologous antibodies: definition of a novel cDNA derived from the tumor suppressor gene locus on chromosome 3p21.3" CANCER RESEARCH, vol. 58, 1 March 1998, pages 1034-41, XP002103188 see the whole document ---	1,2,4,5, 9,14,18, 21,22, 27,44, 45,49, 50,55, 59,60, 64, 67-70, 83,84
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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	NAGASE, T. ET AL.: "Prediction of the coding sequence of unidentified human genes. IX. The complete sequence of 100 new cDNA clones from barin which can code for large proteins in vivo." DNA RESEARCH, vol. 5, 28 February 1998, pages 31-39, XP002103187 see figure 1; table 3 -& DATABASE EMBL Entry/acc.no. AB011172, 10 April 1998 NAGASE, T. ET AL.: "Homo sapiens mRNA for KIAA0600 protein, partial cds." XP002104556 see the whole document ---	44,45, 67-70, 83,84
P,X	JONES, M.H. ET AL.: "Identification and characterization of BRDT: a testis-specific gene related to the bromodomain genes RING3 and Drosophila fsh." GENOMICS, vol. 45, no. 3, 1 November 1997, pages 529-34, XP002103185 see page 529, right-hand column, paragraph 2 see page 530, left-hand column, paragraph 2; figure 1 see page 532, right-hand column, paragraph 2 ---	44,45, 59,60, 67-70, 83,84
P,X	ISHIKAWA K ET AL: "Prediction of the coding sequences of unidentified human genes. X The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro" DNA RESEARCH, vol. 5, no. 321, 30 June 1998, pages 169-176, XP002089186 see abstract; figures 1,2; table 2 ---	44,59, 60,63, 67-70
E	US 5 858 723 A (MUELLER-LANTZSCH NIKOLAUS ET AL) 12 January 1999 Also against claims 108,109,116,117 see the whole document ---	1,2, 4-10,31, 32,40, 42,43, 49,50, 58-60, 67,69, 71,72, 74-79, 82-84, 99-104

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
E	WO 98 40483 A (HUMAN GENOME SCIENCES INC ;GREENE JOHN M (US); LI YI (US); ROSEN C) 17 September 1998 Also against claims 74,76-80,82-85,88,89, 99-104,108,109,111,116,117. See seq. 24 and the claims. ---	1,2, 4-10,14, 18, 21-24, 27,28, 31,32, 36,40, 44,45, 47-50, 55, 58-60, 64,67-72
E	WO 98 08866 A (WISTAR INST) 5 March 1998 see the whole document ---	1,2
E	WO 98 48015 A (CHUGAI RES INST MOLECULAR MED ;JONES MICHAEL H CHUGAI RESEARC (JP)) 29 October 1998 see whole document, particularly the claims. & DATABASE WPI Derwent Publications Ltd., London, GB; AN 98-583658 XP002103211 see abstract ---	18,22, 23, 27-29, 31,32, 40, 44-50, 58-60, 67-72, 74, 76-78, 85,88, 89,102, 103
E	WO 98 32853 A (GENETICS INST) 30 July 1998 see seq. 7 and 8 see page 6, line 23 - page 8, line 12; claims 20-22 see page 21, line 17 - page 22, line 11 ---	18,21, 22,24, 27-29, 44,45, 47-50, 53,59, 60,62, 67-72, 74, 76-80,82

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
T	SCANLAN, M.J. ET AL.: "Isoforms of the human PDZ-73 protein exhibit differential tissue expression" BIOCHIMICA ET BIOPHYSICA ACTA, vol. 1445, no. 1, 1999, pages 39-52, XP002104553 also for claims 77-80,82-84,116. see the whole document ---	
T	DRABKIN, H.A. ET AL.: "DEF-3(g16/NY-LU-12), an RNA binding protein from the 3p21.3 homozygous deletion region in SCLC" ONCOGENE, vol. 18, 1999, pages 2589-97, XP002104554 see the whole document -----	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 98/14679

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Although claims 85-111 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

2. [ ] Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [X] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

1-14,17-36,39-55,58-64,67-117; see additional sheets, pages 3-4.

4. [ ] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest.

[X] No protest accompanied the payment of additional search fees.

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-11,17-33,39-52,58-61,67-117, all partially

The nucleic acid sequence of Seq.ID 1, fragments or complements thereof, and the corresponding polypeptide(s) encoded thereby, and immunogenic and/or HLA binding fragments thereof, optionally as part of a complex with a HLA molecule, an expression vector comprising said nucleic acid, and optionally a human HLA molecule, a host cell transformed with said vector, and an antibody against said polypeptide(s).
Also a method of diagnosing of a disorder characterised by overexpression of said polypeptide(s) and a method for determining regression, progression or onset of a disease associated with overexpression of said polypeptide(s), using agents that specifically bind to said nucleic acid, said polypeptide(s) or complexes of (fragments of) said polypeptide(s) and a HLA molecule. A kit comprising two polynucleotides for the detection of said nucleic acid
Also pharmaceutical preparations
- which enrich the presence of said polypeptide-HLA complex, optionally comprising an adjuvant, or
- which inhibits the expression of said polypeptide(s), or
- comprising an agant that selectively binds said polypeptide, optionally as a conjugate with a diagnostic or therapeutic compound, or
- comprising said nucleic acid, optionally in an expression vector, optionally in a host cell, or
- comprising said polypeptide(s), optionally in combination with an adjuvant, or
- comprising cytolytic T cells, specific for said polypeptide-HLA complex, or
- comprising an antibody against said polypeptide(s).

Inventions 2-119: claims 1-11,13,15,17-33,35,37, 39-52,54,56,58-61,63,65,67-117, all partially (1)

Inventions 2-119: Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:2-40,66,89-169 (odd numbers), 170,172,174, and 176-210, where invention 2 is limited to Seq.ID:2 and corresponding polypeptides encoded thereby, invention 3 is limited to Seq.ID:3 and corresponding polypeptides encoded thereby,.........., and invention 119 is limited to Seq.ID:210 and corresponding polypeptides encoded thereby.

Invention 120: claims claims 1-10,13,17-32,35, 39-51,54,58-60,63,67-117, all nartially

Idem as subject 1 but limited to the DNA sequences seq.ID:211 and 329 and corresponding polypeptides encoded thereby.

Inventions 121-452: claims 1-10,13,16-32,35,38-51, 54,57-60,63,66-117, all partially (1)

Inventions 121-452: Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:212-328, and 330-543, where invention 121 is limited to Seq.ID:211 and corresponding polypeptides encoded thereby, invention 122 is limited to Seq.ID:212 and corresponding polypeptides encoded thereby,.........., and invention 452 is limited to Seq.ID:543 and corresponding polypeptides encoded thereby.

Invention 453: claims 1-10,12,17-32,34,39-51,53, 58-60,62,67-117, all partially

Idem as subject 1 but limited to the DNA sequences seq.ID:544 and 554 and corresponding polypeptides encoded thereby.

Inventions 454 and 455: claims 1-10,12,17-32,34, 39-51,53,58-60,62,67-117, all partially

Inventions 454 and 455: Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:546 and 548, where invention 454 is limited to Seq.ID:546 and corresponding polypeptides encoded thereby, and invention 455 is limited to Seq.ID:548 and corresponding polypeptides encoded thereby.

Invention 456: claims 1-10,12,17-32,34,39-51,53, 58-60,62,67-117, all partially

Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:550, 552, 556, 558 and 560 and corresponding polypeptides encoded thereby.

Inventions 457-582: claims 1-10,12-14,17-32,34-36, 39-51,53-55,58-60,62-64,67-117, all partially (1)

Inventions 457-582: Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:562-586 (even numbers),

588-683,686,687,689,691,692,692, and 696-706, where invention 457 is limited to Seq.ID:562 and corresponding polypeptides encoded thereby, invention 458 is limited to Seq.ID:564 and corresponding polypeptides encoded thereby,........., and invention 582 is limited to Seq.ID:706 and corresponding polypeptides encoded thereby.

Invention 583: claims 1-10,14,17-32,36,39-51,55, 58-60,64,67-117, all partially

Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:707, 709, 711 and 712 and corresponding polypeptides encoded thereby.

Inventions 584-592: claims 1-117, all partially (1)

Inventions 584-592: Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:799-815 (odd numbers), where invention 584 is limited to Seq.ID:799 and corresponding polypeptides encoded thereby, invention 585 is limited to Seq.ID:801 and corresponding polypeptides encoded thereby,........., and invention 592 is limited to Seq.ID:815 and corresponding polypeptides encoded thereby).

For the sake of conciseness, the subject matter of the first invention is explicitly defined, the other subject matters are defined by analogy thereto.

(1) In as far as the claims searched for a group of inventions refer to specific groups of sequences, only those claims which refer to the groups comprising the nucleic acid sequence of a particular invention, and/or its corresponding polypeptide sequence(s), form parts of that invention.

Due to the fact that extensive sequence homologies were found between several groups of sequences during the additional searches, some of the sequences have been grouped, whereby each of these groups comprising two or more such homologous sequences is considered to be one invention.

Claims searched during primary and additional searches:
1-14,17-36,39-55,58-64,67-117, limited to:
Invention 1, seq.ID.1
Invention 52, seq.ID.111, and 112 (transl.)
Invention 61, seq.ID.129, and 130 (transl.)
Invention 71, seq.ID.149, and 150 (transl.)
Invention 72, seq.ID.151, and 152 (transl.)
Invention 116, seq.ID.206
Invention 120, seq.ID.211 and 329; (related sequences)
Invention 137, seq.ID.228
Invention 139, seq.ID.330

Invention 219, seq.ID.411
Invention 453, seq.ID.544, and 545 (transl.),
and seq.ID.554, and 555 (transl.);
(related sequences)
Invention 454, seq.ID.546, and 547 (transl.)
Invention 455, seq.ID.548, and 548 (transl.)
Invention 456, seq.ID.550, and 551 (transl.),
and seq.ID.552, and 553 (transl.),
and seq.ID.556, and 557 (transl.),
and seq.ID.558, and 559 (transl.),
and seq.ID.560, and 561 (transl.);
(related sequences)
Invention 547 seq.ID.665
Invention 548, seq.ID.666
Invention 554, seq.ID.672
Invention 558, seq.ID.676
Invention 563, seq.ID.681
Invention 566, seq.ID.686
Invention 583, seq.ID.707, and 708 (transl.),
and seq.ID.709, and 710 (transl.),
and seq.ID.711,
and seq.ID.712;
(related sequences).

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